

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2003, 18:30:22 ; Search time 41.422 Seconds
(without alignments)
1631.015 Million cell updates/sec

Title: US-09-987-190-2
Perfect score: 145
Sequence: 1 KYSLPELDYFSAEPYISQINEIXYTX 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFM=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09987190 @cgm 1.1 275 @rnatc 02042003_092632_19211 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002:*

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2: /SID2/gcgdata/geneseq/emb1/NA1981.DAT:*
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6: /SID2/gcgdata/geneseq/emb1/NA1985.DAT:*
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13: /SID2/gcgdata/geneseq/emb1/NA1992.DAT:*
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16: /SID2/gcgdata/geneseq/emb1/NA1995.DAT:*
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18: /SID2/gcgdata/geneseq/emb1/NA1997.DAT:*
19: /SID2/gcgdata/geneseq/emb1/NA1998.DAT:*
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22: /SID2/gcgdata/geneseq/emb1/NA2001A.DAT:*
23: /SID2/gcgdata/geneseq/emb1/NA2001B.DAT:*
24: /SID2/gcgdata/geneseq/emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	55.9	631	21	Fusarium venenatum
2	79	54.5	612	21	Malassezia fungus
3	77	53.1	600	22	C. glutamicum codin
4	77	53.1	1143	22	C. melaleucola sup
5	77	53.1	309400	22	C. glutamicum codin
6	74	51.0	97	21	Human Mn-superoxid
7	74	51.0	414	21	Human secreted pro
8	74	51.0	552	20	Human manganese su
9	74	51.0	561	15	Human manganese su
10	74	51.0	561	15	Human manganese su
11	74	51.0	561	15	Human manganese su
12	74	51.0	561	15	Human manganese su
13	74	51.0	594	21	Human manganese su
14	74	51.0	600	9	Sequence of Formu
15	74	51.0	600	9	Sequence of Formu
16	74	51.0	600	9	CDNA of formula VI
17	74	51.0	600	9	CDNA of formula VI
18	74	51.0	600	16	Human manganese su
19	74	51.0	600	16	Human manganese su
20	74	51.0	600	16	Human manganese su
21	74	51.0	600	16	Human manganese su
22	74	51.0	609	13	Human manganese su
23	74	51.0	681	21	Mn-SOD (Ile59Thr).
24	74	51.0	813	8	Human manganese su
25	74	51.0	813	9	Sequence encoding
26	74	51.0	813	14	CDNA encoding huma
27	74	51.0	813	17	MnSOD CDNA. Homo
28	74	51.0	813	17	Human manganese su
29	74	51.0	813	20	Human manganese su
30	74	51.0	813	21	Human native manga
31	74	51.0	813	21	CDNA encoding a hu
32	74	51.0	849	24	Human manganese su
33	74	51.0	966	16	Human manganese su
34	74	51.0	969	17	Human manganese su
35	74	51.0	976	15	Human manganese-co
36	74	51.0	976	20	Human HGMV inducib
37	74	51.0	976	20	Human manganese co
38	74	51.0	977	20	Human SOD2 DNA. H
39	74	51.0	1007	17	Manganese superoxi
40	74	51.0	1008	14	MnSOD DNA (exons 1
41	74	51.0	1026	24	Human CDNA diftere
42	74	51.0	1026	24	lung cancer relate
43	74	51.0	1046	16	Human manganese su
44	74	51.0	1438	21	Nucleotide sequenc
45	74	51.0	1492	24	Rat sequence diffe
			2504	22	Human breast cance

ALIGNMENTS

RESULT 1
AAAF07909
ID AAAF07909 standard; cDNA; 631 BP.
XX
AC AAAF07909;
XX
PT 13-MAR-2001 (first entry)
XX
DE Fusarium venenatum EST SEQ ID NO:432.
XX
KW Multiple gene expression; filamentous fungal cell; EST;
XX expressed sequence tag; Fusarium venenatum; Aspergillus niger;
XX Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KW culture condition; environmental stress; spore morphogenesis;
KW metabolic pathway engineering; catabolic pathway engineering; ss.
XX
XX Fusarium venenatum.
XX

DE C glutamicum coding sequence fragment SEQ ID NO: 3227.
 XX
 XX Corynebacterium; amino acid synthesis; vitamin; saccharide;
 KM organic acid synthesis; ds.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN EP1108790-A2.
 XX
 PD 20-JUN-2001.
 XX
 PF 18-DEC-2000; 2000EP-0127688.
 XX
 PR 16-DEC-1999; 99JP-0377484.
 PR 07-APR-2000; 2000JP-0159162.
 PR 03-AUG-2000; 2000JP-0280988.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 XX Tateishi N, Senoh A, Ikeda M, Ozaki A;
 XX WPI; 2001-376931/40.
 DR P-PSDB; AAG92973.
 XX
 XX Novel polynucleotides derived from Corynebacterium bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analysing
 PT expression profile or pattern of a gene and identifying homologous gene
 PT
 XX
 PS Claim 8; SEQ ID NO: 3227; 246bp + Sequence Listing; English.
 XX
 XX The present invention provides a number of nucleotide and protein
 CC sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of corynebacterium bacterium, measuring expression amount and
 CC analysing the expression profile or expression pattern of a gene derived
 CC from Corynebacterium bacterium, and identifying a homologue of a gene derived
 CC from corynebacterium bacterium. Corynebacterium bacteria are useful for producing
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a nucleic acid described
 CC in the exemplification of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC European Patent Office.
 XX
 SO Sequence 600 BP; 143 A; 197 C; 146 G; 114 T; 0 other;
 XX
 XX Alignment Scores:
 Pred. No.: 0.00018 Length: 600
 Score: 77.00 Matches: 13
 Percent Similarity: 74.07% Conservative: 7
 Best Local Similarity: 48.15% Mismatches: 7
 Query Match: 53.10% Indels: 0
 DB: 22 Gaps: 0
 US-09-987-190-2 (1-30) x AAH68192 (1-600)
 QY 2 TySerLeuProGluLeuAspTyrGluPhseSerAlaThrGluProTyrIleSerGlyGln 21
 DB 10 TACCAACTCCGAGAACTGACTACGATACGACGCTCTCGAGCCACATCGCGCTGAA 69
 QY 22 IleaNGluile**TyrThr 28
 DB 70 ATCATGAGGCTTACCACTCC 90
 RESULT 4
 ID AAS00520 standard; DNA; 1143 BP.
 XX
 AC AAS00520;
 XX
 DT 09-MAY-2001 (first entry)

XX
 DE C. melassecola superoxide dismutase DNA.
 XX
 XX Superoxide dismutase; sod; corynebacterium microorganism; metabolite; ds;
 KM vitamin; D-pantothenic acid; L-lysine; amplification; animal nutrition.
 XX
 OS Corynebacterium melassecola.
 XX
 PN EP1077261-A2.
 XX
 PD 21-FEB-2001.
 XX
 PF 02-AUG-2000; 2000EP-0116669.
 XX
 PR 13-AUG-1999; 99US-0373731.
 XX
 PA (DEGS) DEGUSSA-HUELS AG.
 XX (CNRS) CNRS CENT NAT RECH SCI.
 XX
 XX Merkmann M, Guyonvarch A, Marx A;
 XX WPI; 2001-212718/22.
 DR P-PSDB; AAU00514.
 XX
 XX New DNA encoding superoxide dismutase of Corynebacterium, useful for
 PT producing transformants with increased production of metabolites,
 PT particularly lysine
 PT
 XX
 PS Claim 1; Page 13-14; 19pp; English.
 XX
 XX The sequence represents Corynebacterium melassecola superoxide dismutase
 CC (sod) DNA. Corynebacterium microorganisms may be transformed with a sod DNA
 CC sequence and the sod gene can be amplified. Sod is then often
 CC overexpressed in corynebacterium bacteria. Corynebacterium that overexpress sod
 CC are used for production of metabolites, particularly nucleotides,
 CC vitamins and amino acids, especially D-pantothenic acid or, specifically,
 CC L-lysine. These metabolites are useful in human or animal nutrition and
 CC as pharmaceuticals. Overexpression of sod in corynebacterium increases the
 CC yield of particular metabolites.
 XX
 SO Sequence 1143 BP; 273 A; 323 C; 288 G; 259 T; 0 other;
 XX
 XX Alignment Scores:
 Pred. No.: 0.000409 Length: 1143
 Score: 77.00 Matches: 13
 Percent Similarity: 74.07% Conservative: 7
 Best Local Similarity: 48.15% Mismatches: 7
 Query Match: 53.10% Indels: 0
 DB: 22 Gaps: 0
 US-09-987-190-2 (1-30) x AAS00520 (1-1143)
 QY 2 TySerLeuProGluLeuAspTyrGluPhseSerAlaThrGluProTyrIleSerGlyGln 21
 DB 347 TACCAACTCCGAGAACTGACTACGATACGACGCTCTCGAGCCACATCGCGCTGAA 406
 QY 22 IleaNGluile**TyrThr 28
 DB 407 ATCATGAGGCTTACCACTCC 427
 RESULT 5
 ID AAH68534 standard; DNA; 309400 BP.
 XX
 AC AAH68534;
 XX
 DT 26-SEP-2001 (first entry)

DE C glutamicum coding sequence fragment SEQ ID NO: 7069.
 XX
 XX Corynebacterium; amino acid synthesis; vitamin; saccharide;
 KW organic acid synthesis; ds.
 XX
 XX Corynebacterium glutamicum.
 OS
 PN BPI108790-A2.
 XX
 XX 20-JUN-2001.
 PD
 XX
 XX 18-DEC-2000; 2000EP-0127688.
 PF
 XX
 XX 16-DEC-1999; 99JP-0377484.
 PR 07-APR-2000; 2000JP-0159152.
 PR 03-AUG-2000; 2000JP-0280988.
 XX
 XX (RYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PT Tetselshi N, Senoh A, Ikeda M, Ozaki A;
 DR WPI; 2001-376931/40.
 XX
 XX Novel polynucleotides derived from Corynebacterium bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analysing
 PT expression profile or pattern of a gene and identifying homologous gene
 PT
 XX Disclosure; SEQ ID NO: 7069; 246bp + Sequence Listing; English.
 PS
 XX The present invention provides a number of nucleotide and protein
 CC sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of Corynebacterium bacterium, measuring expression amount and
 CC analysing the expression profile or expression pattern of a gene derived
 CC from Corynebacterium bacterium, and identifying a homologue of a gene derived
 CC from Corynebacterium bacterium. Corynebacterium bacteria are useful for producing
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a nucleic acid described
 CC in the exemplification of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC European Patent Office.
 CC
 XX
 XX Sequence 309400 BP; 70133 A; 86477 C; 83115 G; 69675 T; 0 other;
 SQ
 Alignment Scores:
 e: No: 0.528 Length: 309400
 e: 77.00 Matches: 13
 Percent Similarity: 74.07% Conservativeness: 7
 Best Local Similarity: 48.15% Mismatches: 7
 Query Match: 53.10% Indels: 0
 DB: 22 Gaps: 0
 US-09-987-190-2 (1-30) x AAH68534 (1-309400)
 QY 2 TyTserleupProGluLeuAapTyTyrGluPheserAlarhGluProTyTyrIleSerGly 21
 DB 126401 TACGAACCTCCGAGAACTGACATACGACATGACGCTCTCGAGCCACATCGCCCTGAA 126460
 QY 22 IleAangluile**TyTyr 28
 DB 126461 ATCATGAGCTTCACCACTCC 126481
 RESULT 6
 AAQ94270
 ID AAQ94270 standard; cDNA; 97 BP.
 XX
 XX AAQ94270;
 XX
 XX 24-MAY-1996 (first entry)
 XX

DE Human Mn-superoxide dismutase (Lys29) N-terminal coding sequence.
 XX
 XX hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;
 KW autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;
 KW osteoarthritis; wound healing; ds.
 XX
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT mat_peptide 4..97
 FT /tag= a
 FT /note= "only encodes partial mature protein
 sequence, i.e. N-terminal amino acids 1-31"
 XX
 XX EP676472-A1.
 PN
 XX
 XX 11-OCT-1995.
 PD
 XX
 XX 10-MAR-1988; 88EP-0107460.
 PF
 XX
 XX 24-DEC-1987; 87DE-3744038.
 PR 14-MAR-1987; 87DE-3708306.
 PR 26-MAY-1987; 87DE-3717695.
 PR 10-JUL-1987; 87DE-3722884.
 XX
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA
 XX Hauptmann R, Heckl K, Krystek E, Maurer-Fogy I;
 PI Ostermann E, Spevak W, Stralowa C, Wiche-Castanon M;
 PI Zoephel A;
 XX
 XX WPI; 1995-346092/45.
 DR
 XX
 XX Genes encoding recombinant human manganese superoxide dismutase -
 PT for treatment, prevention and diagnosis of inflammatory diseases
 PT
 XX Claim 8; Page 5; 54pp; German.
 PS
 XX
 XX A human placental cDNA library was screened with a probe derived
 CC from published sequences of human liver MnSOD. Two sequences were
 CC isolated which encoded the majority (either amino acids 22-198 or
 CC 26-198) of hMnSOD. To complete the 5'-ends of the cDNA sequences,
 CC a double-stranded fragment (AAQ94270) coding for an initial Met
 CC residue followed by amino acids 1-31 was synthesised using yeast
 CC preferred codons. Recombinant, full-length hMn-SOD is useful for
 CC treating, preventing or diagnosing inflammatory, degenerative,
 CC neoplastic and rheumatic disorders; in wound healing and in
 CC autoimmune diseases.
 CC
 XX
 XX Sequence 97 BP; 30 A; 30 C; 15 G; 22 T; 0 other;
 SQ
 Alignment Scores:
 e: No: 6.12e-05 Length: 97
 e: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservativeness: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: 16 Gaps: 0
 US-09-987-190-2 (1-30) x AAQ94270 (1-97)
 QY 1 LysTyTserleupProGluLeuAapTyTyrGluPheserAlarhGluProTyTyrIleSerGly 20
 DB 4 AAGCACTCTTGGCCAGACTTGCCTACGACTACGCTCTTAAGCAACACATCAATGCT 63
 QY 21 GlnIleAangluile**TyTyr 28
 DB 64 CAATCATGCAATGACCACTCT 87
 RESULT 7
 AAC02178
 ID AAC02178 standard; cDNA; 414 BP.
 XX
 XX

AC		AAC02178;	
XX			
DT	06-OCT-2000	(first entry)	
DE			
KW	Human secreted protein 5' EST, SEQ ID NO: 2176.		
KX			
KM	Human; 5' EST, expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.		
OS	Homo sapiens.		
PN	EPI033401-A2.		
PD	06-SEP-2000.		
XP	21-FEB-2000; 2000EP-0200610.		
PF			
PR	26-FEB-1999; 99US-0122487.		
XZ	(GEST) GENSET.		
P1	Dumas Milne Edwards J, Duclert A, Giordano J;		
XX			
DR	WPI; 2000-500381/45.		
DR	P-PDB; AAC02172.		
XX			
PT	New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures - Claim 1; SEQ ID 2176; 71bp + CD-ROM; English.		
PS			
CC	The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.		
CC			
CC			
CC			
CC			
CC			
XX			
●	Sequence 414 BP; 89 A; 124 C; 126 G; 73 T; 2 other;		
●			
Alignment Scores:			
Pred. No.:	0.000391	Length:	414
Score:	74.00	Matches:	12
Percent Similarity:	78.57%	Conservative:	10
Best Local Similarity:	42.86%	Mismatches:	6
Query Match:	51.03%	Indels:	0
DB:	21	Gaps:	0
US-09-987-190-2 (1-30) x AAC02178 (1-414)			
OY	1 LysTYSerLeuProGluleuNAepTYrGLuPhSeSxAlArThrgLuPoTyrlleSargLy 20		
Db	182 AAGCACAGCCTCCCCGCACTGCCCTACGACTACGGCGGCCTCGAACTCATCAACGCG 241		
OY	21 GinlleASnglule***TYrrThr 28		
Db	242 CAGATCATGCAGCTGCACCACGACG 265		
RESULT 8			
ID	AAZ08755 standard; cDNA; 552 BP.		
XC	AAZ08755;		
XX			

```

DT 03-NOV-1999 (first entry)
XX
XX Human manganese superoxide dismutase exon 3-deleted isoform cDNA.
XX
XX Human, manganese superoxide dismutase; MnSOD; exon 3 deleted isoform;
XX MnSOD E3(-); diagnosis; viral infection; HIV; oncogenesis; tumour;
XX KM UV-induced damage; post ischaemia reperfusion damage; anti-inflammatory;
XX KW cytotoxic; cardiotoxic; cancer; ss.
XX
XX Homo sapiens.
XX OS
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 1..552
XX FT /*tag= a
XX FT /product= "MnSOD E3(-)"
XX FT /note= "manganese superoxide dismutase exon 3-deleted
XX FT isoform"
XX
XX W09943697-A1.
XX
XX 02-SEP-1999.
XX
XX 25-FEB-1999; 99MO-US04129.
XX
XX 25-FEB-1998; 98US-0075948.
XX
XX (UYCO-) UNIV & COMMUNITY COLLEGE.
XX
XX Anziano PQ;
XX
XX WPI; 1999-527592/44.
XX
XX P-PSDB; AAY29656.
XX
XX
XX A new isoform useful for diagnosing oxidative stress, and treating
XX viral infections
XX
XX Claim 2; Page 12; 64pp; English.
XX
XX
XX The present sequence encodes an isoform of manganese superoxide
XX dismutase (MnSOD), which is a splice-variant lacking exon 3 of the full
XX length MnSOD (i.e. MnSOD E3(-)). MnSOD E3(-) may be useful in the
XX treatment of a wide variety of disorders including viral infections,
XX particularly HIV, and may be used for the prevention of oncogenesis,
XX tumour promotion and invasiveness, and UV-induced damage, for protection
XX of cardiac tissue against post ischaemia reperfusion damage, as an
XX anti-inflammatory agent, to reduce the cytotoxic and cardiotoxic effects
XX of anti-cancer drugs, and to improve the longevity of living cells.
XX
XX
XX Sequence 552 BP; 145 A; 135 C; 153 G; 119 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 0.000565 Length: 552
XX Score: 74.00 Matches: 12
XX Percent Similarity: 78.57% Conservative: 10
XX Best local Similarity: 42.86% Mismatches: 6
XX Query Match: 51.03% Indels: 0
XX DB: 20 Gaps: 0
XX
XX
XX US-09-987-190-2 (1-30) x AA208755 (1-552)
XX
XX 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
XX Db 73 AAGCAGACGCTCCCGCCGACCTGACCTGACGCTACGCGCCCTGGAACATCAACGCG 132
XX
XX 21 GlnIleAsnGluIle***TyrThr 28
XX |||||
XX |||||
XX Db 133 CAGATCATGCGAGCTGCACACAGC 156
XX
XX RESULT 9
XX AA073585
XX ID AA073585 standard; DNA; 561 BP.
XX

```

```

AC      AAQ73585;
XX
XX      25-JUN-1995 (first entry)
XX
XX      Human manganese superoxide dismutase variant gene.
DE
XX      MnSOD; tetramer; pulmonary oxygen toxicity; mitochondrial; mutant;
XX      88.
KM
XX      Homo sapiens.
OS
XX      Homo sapiens.
XX
XX      MO9421283-A.
XX
XX      29-SEP-1994.
XX
XX      24-MAR-1994; 94WO-US03185.
XX
XX      24-MAR-1993; 93US-0036604.
XX
XX      (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX
XX      Wegner C, Wolyniec W;
XX
XX      WPI; 1994-316659/39.
XX
XX      Improved inhibition of pulmonary oxygen toxicity - by
XX      prophylactic, topical admin. of human mitochondrial manganese
XX      superoxide dismutase
XX
XX      Claim 7; Page 26; 41pp; English.
XX
XX      The sequence is that of a mutant human manganese superoxide
XX      dismutase tetramer. Mutations of the native protein provide
XX      a protein which, when applied topically, can inhibit pulmonary
XX      oxygen toxicity.
XX      See also AAQ73582-4.
XX
XX      Sequence 561 BP, 159 A, 127 C, 139 G, 136 T, 0 other;
SQ
XX
XX      Alignment Scores:
XX      Pred. No.: 0.000577 Length: 561
XX      Score: 74.00 Matches: 12
XX      Percent Similarity: 78.57% Conservative: 10
XX      Best Local Similarity: 42.86% Mismatch: 6
XX      Query Match: 51.03% Indels: 0
XX      DB: 15 Gaps: 0
XX
XX      US-09-987-190-2 (1-30) x AAQ73585 (1-561)
XX
XX      1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 200
XX      ::::::::::::::::::::
XX      4 AAGCACTCTTGGCAGACTTGGCCATACGACTACGCTCTAGAACACACATCATGCT 630
XX      ::::::::::::::::::::
XX
XX      21 GlnIleAsnGluIle**TyrThr 28
XX      ||||| :::::
XX      64 CAATTCATGCAATTCGACCACTCT 87
XX
XX      RESULT 10
XX      ID AAQ73582 standard; DNA; 561 BP.
XX      AAQ73582;
XX
XX      AC AAQ73582;
XX
XX      DT 25-JUN-1995 (first entry)
XX
XX      Human manganese superoxide dismutase gene.
XX
XX      MnSOD; tetramer; pulmonary oxygen toxicity; mitochondrial; mutant;
XX      88.
XX
XX      Homo sapiens.
XX
XX      MO9421283-A.
XX

```

```

XX PD 29-SEP-1994.
XX PF 24-MAR-1994;          94WO-US03185.
XX PR 24-MAR-1993;         93US-0036604.
XX PA      (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX PI      Wegner C,   Wolyniec WW;
XX DR WPI; 1994-316659/39.

PT Improved inhibition of pulmonary oxygen toxicity - by
PT prophylactic, topical admin. of human mitochondrial manganese
PS superoxide dismutase
PS Claim 6; Page 25; 41pp; English.

CC The sequence is that of the native human manganese superoxide
CC dismutase tetramer. Mutations in this sequence, esp. CAG for AAG at
CC codon 30 or CAT for CAG at codon 32 provides a protein which, when
CC applied topically, can inhibit pulmonary oxygen toxicity.
CC See also AAQ73583-5.
XX SQ Sequence 561 BP, 160 A, 127 C, 139 G, 135 T; 0 other;

Alignment Scores:
Pred. No.:           0.000577             Length:       561
Score:              74.00                  Matches:      12
Percent Similarity: 78.57%                 Conservative: 10
Best Local Similarity: 42.86%               Mismatches:    6
Query Match:        51.03%                  Indels:        0
DB:                 15                      Gaps:          0

US-09-987-190-2 (1-30) x AAQ73582 (1-561)

OY      1 LysTyrSerLeuProGluIleuAspTyrgLuuPheSerAlaThrGluProTryrIleSery 200
|||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||::||
Dd      4 AAGCACTCTTTGCCAGACTGCATACGACTCGGTCTTAGAACCAACAATCATGCT 633
|||||:::::::::::|||||
OY      21 GluIleAasnGlulle**tyrThr 28
|||||:::::::::::|||||
Db      64 CAATCATTGAATTCACCACTCT 87
|||||:::::::::::|||||

RESULT 11
AAQ73583
ID AAQ73583 standard; DNA; 561 BP.
XX AC AAQ73583;
XX DT      25-JUN-1995 (first entry)
DE Human manganese superoxide dismutase variant gene.
KW MnSOD; tetramer; pulmonary oxygen toxicity; mitochondrial; mutant; ss.
XX OS Homo sapiens.
XX PN WO9421283-A.
XX PD 29-SEP-1994.
XX PF 24-MAR-1994;          94WO-US03185.
XX PR 24-MAR-1993;         93US-0036604.
XX PA      (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX PI      Wegner C,   Wolyniec WW;
XX DR WPI; 1994-316659/39.
```

XX Improved inhibition of pulmonary oxygen toxicity - by
 PT propylactic, topical admin. of human mitochondrial manganese
 PT superoxidizedismutase
 XX
 PS Claim 7, Page 26; 41pp; English.
 XX
 CC The sequence is that of a mutant human manganese superoxide
 CC dismutase tetramer. Mutations of the native protein provide
 CC a protein which, when applied topically, can inhibit pulmonary
 CC oxygen toxicity.
 CC See also AAQ73582-5.
 XX
 SQ Sequence 561 BP; 159 A; 128 C; 139 G; 135 T; 0 other;
 Alignment Scores:
 Pred. No.: 0.000577 Length: 561
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 Gaps: 0
 DB: 15
 US-09-987-190-2 (1-30) x AAQ73583 (1-561)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheserAlaThrGluProTyrIleSerGly 20
 DB 4 AAGCAGCTTTGGCAGACTTGCCATACGACTACGCTGCTAGAACACACATCATGCT 63
 QY 21 GlnIleAsnGluIle***TyrThr 28
 DB 64 CAATCATGCATATGCACCACTCT 87
 RESULT 12
 AAQ73584
 ID AAQ73584 standard; DNA; 561 BP.
 AC AAQ73584;
 XX
 DT 25-JUN-1995 (first entry)
 XX
 DE Human manganese superoxide dismutase variant gene.
 XX
 KM MnSOD; tetramer; pulmonary oxygen toxicity; mitochondrial; mutant;
 KM ss.
 XX
 OS Homo sapiens.
 PA WO9421283-A.
 XX
 PD 29-SEP-1994.
 XX
 PF 24-MAR-1994; 94MO-US03185.
 XX
 PR 24-MAR-1993; 93US-0036604.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 XX
 PI Wegner C, Wolyniec WW;
 XX
 DR WPI; 1994-316659/39.
 XX
 PT Improved inhibition of pulmonary oxygen toxicity - by
 PT propylactic, topical admin. of human mitochondrial manganese
 PT superoxidizedismutase
 XX
 PS Claim 7; Page 27; 41pp; English.
 XX
 CC The sequence is that of a mutant human manganese superoxide
 CC dismutase tetramer. Mutations of the native protein provide
 CC a protein which, when applied topically, can inhibit pulmonary
 CC oxygen toxicity.
 CC See also AAQ73582-5.

XX SQ Sequence 561 BP; 160 A; 126 C; 139 G; 136 T; 0 other;
 Alignment Scores:
 Pred. No.: 0.000577 Length: 561
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 Gaps: 0
 DB: 15
 US-09-987-190-2 (1-30) x AAQ73584 (1-561)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheserAlaThrGluProTyrIleSerGly 20
 DB 4 AAGCAGCTTTGGCAGACTTGCCATACGACTACGCTGCTAGAACACACATCATGCT 63
 QY 21 GlnIleAsnGluIle***TyrThr 28
 DB 64 CAATCATGCATATGCACCACTCT 87
 RESULT 13
 AAZ39779
 ID AAZ39779 standard; cDNA; 594 BP.
 AC AAZ39779;
 XX
 DT 06-MAR-2000 (first entry)
 XX
 DE Human manganese superoxide dismutase (MnSOD) protein encoding cDNA.
 XX
 KM Manganese superoxide dismutase; MnSOD; EC5OD; proteoglycan; human;
 KM endothelial; oxidative damage; pulmonary inflammatory injury; cancer;
 KM lung disease; hypoxia; ischemia; reperfusion injury; arthritis;
 KM hyperoxia; atherosclerosis; lupus erythematosus; hypertension;
 KM neutrophil-mediated inflammation; ss.
 XX
 OS Homo sapiens.
 PA WO9558547-A1.
 XX
 PN 18-NOV-1999.
 XX
 PD 06-MAY-1999; 99MO-US09921.
 XX
 PR 08-MAY-1998; 98US-0075019.
 XX
 PA (WEBB-) WEBB-WARING INST BIOMEDICAL RES.
 XX
 PI McCord JM, Gao B, Flores SC;
 XX
 DR WPI; 2000-062283/05.
 DR P-PSDB; AAY55846.
 XX
 PT Modified manganese superoxide dismutase, methods of production and
 PT antibodies -
 XX
 PS Claim 6; Page 71-72; 83pp; English.
 XX
 CC The invention provides a nucleic acid molecule encoding a genetically
 CC modified manganese superoxide dismutase (MnSOD). The nucleic acid
 CC comprises a first nucleic acid sequence encoding an enzymatically active
 CC portion of MnSOD; and a second nucleic acid sequence encoding a peptide
 CC (EC5OD) that binds to polyanionic polysaccharides or proteoglycans on
 CC endothelial cell surfaces. The protein protects a mammal, especially
 CC humans, from oxidative damage and especially from conditions consisting
 CC of pulmonary inflammatory injury, lung disease, cancer, hypoxia, ischemia
 CC reperfusion injury, hyperoxia, atherosclerosis, arthritis, lupus
 CC erythematosus, hypertension and neutrophil-mediated inflammation. The
 CC lung disease is infant or adult respiratory distress syndrome.
 CC interstitial lung disease or asthma. The mutant MnSOD also protects
 CC organs of mammals from pre- and post-transplantation oxidative damage.
 CC MnSOD is positively charged at physiological pH and has a longer plasma

CC half-life of about 4 hours compared to 6-15 minutes for cytosolic Cu,Zn
 CC SOD (following intravenous injection). EC50D has a substantial advantage
 CC over both Cu,ZnSOD and MnSOD because of its ability to bind to the
 CC endothelium. EC50D is hard to produce in mammalian cell culture systems,
 CC so a fusion of EC50D and MnSOD therefore overcomes these problems. The
 CC present sequence represents a cDNA encoding a human MnSOD protein.
 XX
 XX Sequence 594 BP; 166 A; 144 C; 154 G; 130 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	0.000621	594	12	10	0	0
Percent Similarity:	74.00					
Best Local Similarity:	78.57%					
Query Match:	42.86%					
DB:	51.03%					
	21					

US-09-987-190-2 (1-30) x AA239779 (1-594)

1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 1 AAGCACAGCTCTCCCGACCTGCGCTACGACTACGCGCGCTGGAACCTGCATCAACGCG 60

Qy 21 GlnIleAsnGluIle**TyrThr 28
 Db 61 CAGATCATGACGCTGCACACACAGC 84

RESULT 14

ID AAN81219 standard; cDNA; 600 BP.

AAN81219;

03-OCT-1990 (first entry)

XX Sequence of Formula IIb encoding modified portion of human manganese
 DE superoxide dismutase (hMnSOD).

XX Human manganese superoxide dismutase derivative; clone B88;
 KW formula IIb; enzyme; EC-1.15.1.1.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 4..600
 FT /*tag= a

XX EP282899-A.

XX 21-SEP-1988.

XX 10-MAR-1988; 88EP-0103754.

XX 24-DEC-1987; 87DE-3744038.

XX 14-MAR-1987; 87DE-3708306.

XX (BOEH) BOEHRINGER INGELHEIM.

XX Heckl K, Spevak W, Ostermann E, Zophel A, Krystek E, Maurer-Fogy I;

XX Wliche-Castanon MJ, Stralowa C, Hauptmann R;

XX WPI; 1988-265361/38.

XX P-PSDB; AAP80603.

XX Prodn. of human manganese superoxidizedismutase peptide(s) -

XX PT and DNA coding sequences, for control and diagnosis of eg

XX PT inflammatory diseases

XX PS Disclosure; ; pp; German.

XX The patent is for polypeptides, esp. non-glycosylated, having the

XX enzymatic, biological and immunological properties of hMnSOD that are

XX prepd. by genetic engineering methods. Also new are DNA sequences

CC encoding all or part of the polypeptides and replicating vectors,
 CC expression plasmids and transformed host cells contg. these sequences.
 CC hMnSOD catalyses disproportionation of the superoxide radical and can be
 CC used in the prevention, diagnosis and treatment of inflammatory,
 CC degenerative, neoplastic and rheumatoid disorders; for wound healing; in
 CC autoimmune disease and in organ transplantation. It can also be used to
 CC improve the storage stability of liq. and solid foods. AAN81219 is
 CC derived from Formula Ib (AAN81826).
 XX
 XX Sequence 600 BP; 172 A; 135 C; 150 G; 143 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	0.000629	600	12	10	0	0
Percent Similarity:	74.00					
Best Local Similarity:	78.57%					
Query Match:	42.86%					
DB:	51.03%					
	9					

US-09-987-190-2 (1-30) x AAN81219 (1-600)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 4 AAGCACTCTTGCAGACTTGCATACGACTACGCGCTCTAGAACACACATCAATGCT 63

Qy 21 GlnIleAsnGluIle**TyrThr 28
 Db 64 CAATCATGCAATTGCACCACTCT 87

RESULT 15

ID AAN81218 standard; cDNA; 600 BP.

AAN81218;

03-OCT-1990 (first entry)

XX Sequence of Formula Iia encoding modified portion of human manganese
 DE superoxide dismutase (hMnSOD).

XX Human manganese superoxide dismutase derivative; clone B88;
 KW formula Iia; enzyme; EC-1.15.1.1.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 4..600
 FT /*tag= a

XX EP282899-A.

XX 21-SEP-1988.

XX 10-MAR-1988; 88EP-0103754.

XX 24-DEC-1987; 87DE-3744038.

XX 14-MAR-1987; 87DE-3708306.

XX (BOEH) BOEHRINGER INGELHEIM.

XX Heckl K, Spevak W, Ostermann E, Zophel A, Krystek E, Maurer-Fogy I;

XX Wliche-Castanon MJ, Stralowa C, Hauptmann R;

XX WPI; 1988-265361/38.

XX P-PSDB; AAP80602.

XX Prodn. of human manganese superoxidizedismutase peptide(s) -

XX PT and DNA coding sequences, for control and diagnosis of eg

XX PT inflammatory diseases

XX PS Disclosure; ; pp; German.

XX The patent is for polypeptides, esp. non-glycosylated, having the

enzymatic, biological and immunological properties of hMnSOD that are prep'd. by genetic engineering methods. Also new are DNA sequences encoding all or part of the polypeptides and replicating vectors, CC expression plasmids and transformed host cells contg. these sequences. CC hMnSOD catalyses disproportionation of the superoxide radical and can be CC used in the prevention, diagnosis and treatment of inflammatory, CC degenerative, neoplastic and rheumatoid disorders; for wound healing; in CC autoimmune disease and in organ transplantation. It can also be used to CC improve the storage stability of liq. and solid foods. AAN81218 is CC derived from Formula Ia (AAN81825).

XX
SQ Sequence 600 BP; 173 A; 134 C; 150 G; 143 T; 0 other;

Alignment Scores:
Pred. No.: 0.000629 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x AAN81218 (1-600)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSercly 20
Db 4 AAGCAGCTTTGGCCAGCTTGCATACGACTACGCTGCTCTAGAACACCATCATGCT 63

Qy 21 GlnIleAsnGluIle***TyrThr 28
Db 64 CAATCATGCAATTGCACCACTCT 87

RESULT 16
AAN81224
ID AAN81224 standard; cDNA; 600 BP.
AC AAN81224;
DT 03-OCT-1990 (first entry)
XX
DE cDNA of formula VIIa encoding complete human manganese
DE superoxide dismutase (hMnSOD).
XX
KW Human manganese superoxide dismutase derivative; clone BS8;
KW formula VIIa; enzyme; EC-1.15.1.1.
XX
OS Homo sapiens.
XX
EP282899-A.
XX
21-SEP-1988.
XX
PF 10-MAR-1988; 88BP-0103754.
XX
PR 24-DEC-1987; 87DE-3744038.
XX
PR 14-MAR-1987; 87DE-3708306.
XX
PA (BOEH) BOEHRINGER INGELHEIM.
XX
XX Heckl K, Spevak W, Ostermann E, Zophel A, Krystek E, Maurer-Fogy I;
PI Wlitchke-Castanon MJ, Stralowa C, Hauptmann R;
XX
DR WPI; 1988-265361/38.
XX
XX Prodn. of human manganese superoxidedismutase peptide(s) -
PT and DNA coding sequences, for control and diagnosis of eg
PT inflammatory diseases
XX
PS Disclosure; ; 7pp; German.
XX
XX The patent is for polypeptides, esp. non-glycosylated, having the
CC enzymatic, biological and immunological properties of hMnSOD that are
CC prep'd. by genetic engineering methods. Also new are DNA sequences
CC encoding all or part of the polypeptides and replicating vectors,

expression plasmids and transformed host cells contg. these sequences. CC hMnSOD catalyses disproportionation of the superoxide radical and can be CC used in the prevention, diagnosis and treatment of inflammatory, CC autoimmune disease and in organ transplantation. It can also be used to CC improve the storage stability of liq. and solid foods. Oligo VIIa CC (XhoI/XbaI) (AAN81222) was ligated to Oligo VIIb (XbaI/NotI) (AAN81223) CC and then used to produce cDNA encoding the entire hMnSOD of formula VIIa CC and formula VIIb (AAN81225).

XX
SQ Sequence 600 BP; 173 A; 133 C; 150 G; 144 T; 0 other;

Alignment Scores:
Pred. No.: 0.000629 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x AAN81224 (1-600)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSercly 20
Db 4 AAGCAGCTTTGGCCAGCTTGCATACGACTACGCTGCTCTAGAACACCATCATGCT 63

Qy 21 GlnIleAsnGluIle***TyrThr 28
Db 64 CAATCATGCAATTGCACCACTCT 87

RESULT 17
AAN81225
ID AAN81225 standard; cDNA; 600 BP.
AC AAN81225;
DT 03-OCT-1990 (first entry)
XX
DE cDNA of formula VIIb encoding complete human manganese
DE superoxide dismutase (hMnSOD).
XX
KW Human manganese superoxide dismutase derivative; clone BS8;
KW formula VIIb; enzyme; EC-1.15.1.1.
XX
OS Homo sapiens.
XX
EP282899-A.
XX
21-SEP-1988.
XX
PF 10-MAR-1988; 88BP-0103754.
XX
PR 24-DEC-1987; 87DE-3744038.
XX
PR 14-MAR-1987; 87DE-3708306.
XX
PA (BOEH) BOEHRINGER INGELHEIM.
XX
XX Heckl K, Spevak W, Ostermann E, Zophel A, Krystek E, Maurer-Fogy I;
PI Wlitchke-Castanon MJ, Stralowa C, Hauptmann R;
XX
DR WPI; 1988-265361/38.
XX
XX Prodn. of human manganese superoxidedismutase peptide(s) -
PT and DNA coding sequences, for control and diagnosis of eg
PT inflammatory diseases
XX
PS Disclosure; ; 7pp; German.
XX
XX The patent is for polypeptides, esp. non-glycosylated, having the
CC enzymatic, biological and immunological properties of hMnSOD that are
CC prep'd. by genetic engineering methods. Also new are DNA sequences
CC encoding all or part of the polypeptides and replicating vectors,
CC expression plasmids and transformed host cells contg. these sequences.

CC hMnSOD catalyses disproportionation of the superoxide radical and can be used in the prevention, diagnosis and treatment of inflammatory, CC degenerative, neoplastic and rheumatoid disorders; for wound healing; in CC autoimmune disease and in organ transplantation. It can also be used to CC improve the storage stability of liq. and solid foods. Oligo Via CC (XhoI/XbaI) (AA081222) was ligated to oligo VIB (XbaI/NcoI) (AA081223) CC and then used to produce cDNA encoding the entire hMnSOD of formula VIIA CC (AA081224) and formula VIIB.

XX SQ Sequence 600 BP; 172 A; 134 C; 150 G; 144 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	0.000629	74.00	12	10	0	0
Percent Similarity:	78.57%	78.57%	42.86%	6	0	0
Best Local Similarity:	51.03%	51.03%	Indels:	0	0	0
Query Match:	9	Indels:	0	0	0	0

US-09-987-190-2 (1-30) x AA081225 (1-600)

1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 4 AAGCAGCTCTTGGCCAGACTTGCATACGACTACGCTGCTTGAACACACATCATGCT 63

Qy 21 GlnIleAngIuile**TyrThr 28
 64 CAATCATGCAATTCACACACTCT 87

RESULT 18

AA094271 standard; cDNA; 600 BP.

AC AA094271;

DT 17-MAY-1996 (first entry)

XX Human manganese superoxide dismutase (Lys29) coding sequence.

DE hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;

KW autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;

KW osteoarthritis; wound healing; ss.

OS Homo sapiens.

XX Location/Qualifiers

FT Key 1..600

FT CDS /product= Met_hMn-SOD (Lys29)

XX EPE76472-A1.

XX 11-OCT-1995.

XX 10-MAR-1988; 88EP-0107460.

XX 24-DEC-1987; 87DE-3744038.

XX 14-MAR-1987; 87DE-3708306.

XX 26-MAY-1987; 87DE-3717695.

XX 10-JUL-1987; 87DE-3722884.

XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.

XX Hauptmann R, Heckl K, Krystek E, Maurer-Fogy I;

XX Ostermann E, Spevak W, Stratawa C, Wiche-Castanon M;

XX Zsoephel A;

XX WPI; 1995-346092/45.

XX P-PSDB; AAR75191.

XX Genes encoding recombinant human manganese superoxide dismutase -

XX for treatment, prevention and diagnosis of inflammatory diseases

PS Claim 8; Page 6; 54pp; German.

XX The present sequence codes for a Met residue followed by the 198
 CC amino acid long hMn-SOD mature polypeptide having a Lys residue
 CC at position 29. The cDNA can be inserted into expression vectors
 CC containing appropriate signal sequences, etc. for expression of
 CC recombinant hMn-SOD. The N-terminal Met residue can be removed,
 CC e.g. by treatment with CNBr or CNCl. Mature hMn-SOD is useful for
 CC treating, preventing or diagnosing inflammatory, degenerative,
 CC neoplastic and rheumatic disorders; in wound healing and in
 CC autoimmune diseases.

XX SQ Sequence 600 BP; 173 A; 134 C; 150 G; 143 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	0.000629	74.00	12	10	0	0
Percent Similarity:	78.57%	78.57%	42.86%	6	0	0
Best Local Similarity:	51.03%	51.03%	Indels:	0	0	0
Query Match:	16	Indels:	0	0	0	0

US-09-987-190-2 (1-30) x AA094271 (1-600)

1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 4 AAGCAGCTCTTGGCCAGACTTGCATACGACTACGCTGCTTGAACACACATCATGCT 63

Qy 21 GlnIleAngIuile**TyrThr 28
 64 CAATCATGCAATTCACACACTCT 87

RESULT 19

AA094272 standard; cDNA; 600 BP.

AC AA094272;

DT 17-MAY-1996 (first entry)

XX Human manganese superoxide dismutase (Gln29) coding sequence.

DE hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;

KW autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;

KW osteoarthritis; wound healing; ss.

OS Homo sapiens.

XX Location/Qualifiers

FT Key 1..600

FT CDS /product= Met_hMn-SOD (Gln29)

XX EPE76472-A1.

XX 11-OCT-1995.

XX 10-MAR-1988; 88EP-0107460.

XX 24-DEC-1987; 87DE-3744038.

XX 14-MAR-1987; 87DE-3708306.

XX 26-MAY-1987; 87DE-3717695.

XX 10-JUL-1987; 87DE-3722884.

XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.

XX Hauptmann R, Heckl K, Krystek E, Maurer-Fogy I;

XX Ostermann E, Spevak W, Stratawa C, Wiche-Castanon M;

XX Zsoephel A;

XX WPI; 1995-346092/45.

XX P-PSDB; AAR75192.

PT Genes encoding recombinant human manganese superoxide dismutase -
 PT for treatment, prevention and diagnosis of inflammatory diseases
 XX
 XX
 PS Claim 8; Page 6; 54pp; German.
 XX
 CC The present sequence codes for a Met residue followed by the 198
 CC amino acid long hMn-SOD mature polypeptide having a Gln residue
 CC at position 29. The cDNA can be inserted into expression vectors
 CC containing appropriate signal sequences, etc. for expression of
 CC recombinant hMn-SOD. The N-terminal Met residue can be removed.
 CC e.g. by treatment with CNBr or CNCl. Mature hMn-SOD is useful for
 CC treating, preventing or diagnosing inflammatory, degenerative,
 CC neoplastic and rheumatic disorders; in wound healing and in
 CC autoimmune diseases.
 CC
 SQ Sequence 600 BP; 172 A; 135 C; 150 G; 143 T; 0 other;
 Alignment Scores:
 Pred. No.: 0.000629 Length: 600
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: 16 Gaps: 0
 US-09-987-190-2 (1-30) x AAQ94272 (1-600)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 4 AAGCAGCTCTTTGCCAGACTTCCCATACGACTACGCTGCTCTAGAACACACATCAATGCT 63
 QY 21 GlnIleAsnGluIle**TyrThr 28
 Db 64 CAATCATGCATTCGACCACTCT 87
 RESULT 20
 AAQ94277
 ID AAQ94277 standard; cDNA; 600 BP.
 AC AAQ94277;
 XX
 DT 23-MAY-1996 (first entry)
 XX
 DE Human manganese superoxide dismutase (lys29) coding sequence.
 XX
 KM hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;
 KM autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;
 KM osteoarthritis; wound healing; ss.
 OS Homo sapiens.
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT CDS 1..600
 FT /*tag= a
 FT /product= Met hMn-SOD(Lys29)
 FT /note= "the first 31 codons are provided by a
 FT synthetic linker sequence"
 XX
 XX EP676472-A1.
 PN 11-OCT-1995.
 PD 10-MAR-1988; 88BP-0107460.
 PF 24-DEC-1987; 87DE-3744038.
 PR 14-MAR-1987; 87DE-3708306.
 PR 26-MAY-1987; 87DE-3717695.
 PR 10-JUL-1987; 87DE-3722884.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX Hauptmann R, Heckl K, Krystek E, Maurer-Fogy I,
 PI

PI Ostermann E, Spevak W, Stralowa C, Wiche-Castanon M;
 PI Zepherl A;
 XX
 DR WPI; 1995-346092/45.
 XX
 PT Genes encoding recombinant human manganese superoxide dismutase -
 PT for treatment, prevention and diagnosis of inflammatory diseases
 XX
 XX
 PS Claim 8; Page 17; 54pp; German.
 XX
 CC The present sequence codes for a Met residue followed by the 198
 CC amino acid long hMn-SOD mature polypeptide having a Lys residue
 CC at position 29. The cDNA can be inserted into expression vectors
 CC containing appropriate signal sequences, etc. for expression of
 CC recombinant hMn-SOD. The N-terminal Met residue can be removed.
 CC e.g. by treatment with CNBr or CNCl. Mature hMn-SOD is useful for
 CC treating, preventing or diagnosing inflammatory, degenerative,
 CC neoplastic and rheumatic disorders; in wound healing and in
 CC autoimmune diseases.
 CC
 SQ Sequence 600 BP; 173 A; 133 C; 150 G; 144 T; 0 other;
 Alignment Scores:
 Pred. No.: 0.000629 Length: 600
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: 16 Gaps: 0
 US-09-987-190-2 (1-30) x AAQ94277 (1-600)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 4 AAGCAGCTCTTTGCCAGACTTCCCATACGACTACGCTGCTCTAGAACACACATCAATGCT 63
 QY 21 GlnIleAsnGluIle**TyrThr 28
 Db 64 CAATCATGCATTCGACCACTCT 87
 RESULT 21
 AAQ94278
 ID AAQ94278 standard; cDNA; 600 BP.
 AC AAQ94278;
 XX
 DT 23-MAY-1996 (first entry)
 XX
 DE Human manganese superoxide dismutase (Gln29) coding sequence.
 XX
 KM hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;
 KM autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;
 KM osteoarthritis; wound healing; ss.
 OS Homo sapiens.
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT CDS 1..600
 FT /*tag= a
 FT /product= Met hMn-SOD(Gln29)
 FT /note= "the first 31 codons are provided by a
 FT synthetic linker sequence"
 XX
 XX EP676472-A1.
 PN 11-OCT-1995.
 PD 10-MAR-1988; 88BP-0107460.
 PF 24-DEC-1987; 87DE-3744038.
 PR 14-MAR-1987; 87DE-3708306.
 PR 26-MAY-1987; 87DE-3717695.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX Hauptmann R, Heckl K, Krystek E, Maurer-Fogy I,
 PI

PR 10-JUL-1987; 87DE-3722884.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX
PI Hauptmann R, Heckl K, Krystek E, Maurer-Fogy I;
PI Ostermann E, Spevak W, Stratawa C, Wiche-Castanon M,
PI Zoeschel A;
XX
DR WPI; 1995-346092/45.
XX
PT Genes encoding recombinant human manganese superoxide dismutase -
XX for treatment, prevention and diagnosis of inflammatory diseases
XX
PS Claim 8; Page 17-18; 54pp; German.
XX
CC The present sequence codes for a Met residue followed by the 198
CC amino acid long hmn-SOD mature polypeptide having a Gln residue
CC at position 29. The CDNA can be inserted into expression vectors
CC containing appropriate signal sequences, etc. for expression of
CC recombinant hmn-SOD. The N-terminal Met residue can be removed,
e.g. by treatment with CNBr or CNCl. Mature hmn-SOD is useful for
treating, preventing or diagnosing inflammatory, degenerative,
neoplastic and rheumatic disorders; in wound healing and in
autoimmune diseases.
CC
SQ Sequence 600 BP; 172 A; 134 C; 150 G; 144 T; 0 other;
XX
XX
Alignment Scores:
Pred. No.: 0.000629 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 16 Gaps: 0
US-09-987-190-2 (1-30) x AAQ20194 (1-600)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
DB 4 AAGCAGCTTTGCCGACTTCCGACACGACGCTGCTGGAACGACACATCATCT 63
QY 21 GlnIleAsngIuile**TyrThr 28
DB 64 CAATCATGCAATGCACCATCT 87
RESULT 22
AAQ20194
ID AAQ20194 standard; DNA; 609 BP.
AAQ20194;
DT 01-APR-1992 (first entry)
XX
DE Mn-SOD (Ile59Thr).
XX
KM Manganese superoxide dismutase; vector; anti-inflammatory; ds.
XX
OS Homo sapiens.
XX
PN EP462836-A.
XX
PD 27-DEC-1991.
XX
PF 20-JUN-1991; 91EP-0305596.
XX
PR 19-OCT-1990; 90JP-0279286.
XX
PR 20-JUN-1990; 90JP-0159925.
XX
PA (MITK) MITSUI TOATSU CHEM INC.
XX
PI Takahashi S, Makino T, Asanagi M, Yoshino C;
XX
DR WPI; 1992-001187/01.

DR P-PSDB; AAR20015.
XX
XX New recombinant vector plasmid - expresses human manganese,
PT superoxide dismutase, used as antiinflammatory agent
XX
XX Disclosure; Fig 8; 22pp; English.
XX
XX A vector was constructed contg. lac/P1 ligated promoter which has
CC this human Mn-SOD structural gene. The gene encodes modified human
CC Mn-SOD in which the 59th isoleucine is converted to threonine.
XX
SQ Sequence 609 BP; 171 A; 148 C; 157 G; 133 T; 0 other;
XX
XX
Alignment Scores:
Pred. No.: 0.000641 Length: 609
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 13 Gaps: 0
US-09-987-190-2 (1-30) x AAQ20194 (1-609)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
DB 6 AAGCAGAGCCCTCCCGACTGCTGACGACGCGCTGGAACCTCATCATCAGCG 65
QY 21 GlnIleAsngIuile**TyrThr 28
DB 66 CAGATCATGCACTGCACCATCAGC 89
RESULT 23
AA239781
ID AA239781 standard; DNA; 681 BP.
XX
AC AA239781;
XX
XX 06-MAR-2000 (first entry)
XX
DE Human manganese superoxide dismutase (MnSOD) mutant protein DNA.
XX
XX Manganese superoxide dismutase; MnSOD; EC503; proteoglycan; human;
KM endothelial; oxidative damage; pulmonary inflammatory injury; cancer;
KM lung disease; hypoxia; ischemia; reperfusion injury; arthritis;
KM hyperoxia; atherosclerosis; lupus erythematosus; hypertension;
KM neutrophil-mediated inflammation; mutant; ss.
XX
XX Synthetic.
XX
OS Homo sapiens.
XX
XX WO958547-A1.
XX
XX 18-NOV-1999.
XX
XX 06-MAY-1999; 99WO-US09921.
XX
XX 08-MAY-1998; 98US-0075019.
XX
XX (WEBB-) WEBB-WARING INST BIOMEDICAL RES.
XX
XX McCord JM, Gao B, Flores SC;
XX
XX WPI; 2000-062283/05.
XX
XX P-PSDB; AAY55849.
XX
XX Modified manganese superoxide dismutase, methods of production and
PT antibodies -
XX
XX Claim 11; Page 74-75; 83pp; English.
XX
XX The invention provides a nucleic acid molecule encoding a genetically
CC modified manganese superoxide dismutase (MnSOD). The nucleic acid
CC comprises a first nucleic acid sequence encoding an enzymatically active

CC portion of MnSOD; and a second nucleic acid sequence encoding a peptide
CC (EC50D) that binds to polyanionic polysaccharides or proteoglycans on
CC endothelial cell surfaces. The protein protects a mammal, especially
CC humans, from oxidative damage and especially from conditions consisting
CC of pulmonary inflammatory injury, lung disease, cancer, hypoxia, ischemia
CC reperfusion injury, hyperoxia, atherosclerosis, arthritis, lupus
CC erythematosis, hypertension and neutrophil-mediated inflammation. The
CC lung disease is infant or adult respiratory distress syndrome,
CC interstitial lung disease or asthma. The mutant MnSOD also protects
CC organs of mammals from pre- and post-transplantation oxidative damage.
CC MnSOD is positively charged at physiological pH and has a longer plasma
CC half-life of about 4 hours compared to 6-15 minutes for cytosolic Cu,Zn
CC SOD (following intravenous injection). EC50D has a substantial advantage
CC over both Cu, ZnSOD and MnSOD because of its ability to bind to the
CC endothelium. EC50D is hard to produce in mammalian cell culture systems,
CC so a fusion of EC50D and MnSOD therefore overcomes these problems. The
CC present sequence represents a DNA encoding a human MnSOD mutant protein.
CC This comprises the MnSOD sequence, and a 78 basepair EC50D tail-encoding
CC fragment.

Sequence 681 BP, 185 A; 170 C; 189 G; 137 T; 0 other;

Alignment Scores:
Pred. No.: 0.00074 Length: 681
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 21 Gaps: 0

US-09-987-190-2 (1-30) x AAN71370 (1-681)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 7 AAGCAGCGCCCTCCCGACTGCTCCCTACGACTACGCGCCCTGGAACCTCACATCAACCG 66

Qy 21 GlnIleAsnGluIle**TyrThr 28
Db 67 CAGATCATGCGACTGCACACACAGC 90

RESULT 24
ID AAN71370 standard; DNA, 813 BP.

AC AAN71370;

DT 14-MAY-1991 (first entry)

Sequence encoding human manganese superoxide dismutase.

Human MSOD; hydrogen peroxide; ischaemia; lesions; inflammation;
KM free radicals; ds.

Key Location/Qualifiers

FT CDS 43..711

FT mat_peptide

FT 115..708

FT /*tag= a

FT /*tag= b

FT /product= mature MSOD

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

XX New DNA coding for polypeptide of human manganese superoxide-
PT dismutase - useful e.g. for treating inflammation, and new
PT expression vectors and transformed cells
XX
XX Disclousure; fig 1; 46pp; French.
XX
XX This purified cDNA encodes both prepro- and mature-manganese
CC superoxide dismutase (MSOD). It is one strand of a double stranded
CC molecule contained in a recombinant vehicle. The MSOD produced
CC catalyses the reaction of hydrogen ions and the SOD radical anion to
CC form hydrogen peroxide and water. It is useful in veterinary and
CC pharmaceutical compsns. for e.g. reducing lesions of reperfusion
CC following ischaemia, to prolong survival time isolated organs and
CC for treating inflammation. See also AAN71371-72.
XX
SQ Sequence 813 BP, 218 A; 204 C; 213 G; 178 T; 0 other;

Alignment Scores:
Pred. No.: 0.000928 Length: 813
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 8 Gaps: 0

US-09-987-190-2 (1-30) x AAN71370 (1-813)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 115 AAGCAGCGCCCTCCCGACTGCTCCCTACGACTACGCGCCCTGGAACCTCACATCAACCG 174

Qy 21 GlnIleAsnGluIle**TyrThr 28
Db 175 CAGATCATGCGACTGCACACACAGC 198

RESULT 25
ID AAN81158 standard; cDNA, 813 BP.

AC AAN81158;

DT 22-OCT-1990 (first entry)

DE cDNA encoding human manganese superoxide dismutase.

KM Human manganese superoxide dismutase; ds cDNA; oxygen free radicals.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 43..711

FT /*tag= a

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

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FT

FT

FT

FT

FT

Recombinant human manganese superoxidizedismutase -
PT used for treating, eg reperfusion injury, inflammation,
PT arthritis, bronchial pulmonary dysplasia or lung fibrosis.

```

XX Die closure; ; pp: English.
XX
CC The cDNA encodes human manganese superoxide dismutase, and is
CC inserted into a plasmid, eg pMSB-4 (ATCC 53250).
XX
SQ Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 other;

Alignment Scores:
Pred. No.: 0.000928 Length: 813
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x AAN81158 (1-813)
Oy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
115 AAGCACAGCCTCCCGACCTGCGCTACGACTACGCGCGCTCGAAGCTCAGATCAACGCG 174
Oy 21 GlnIleAsnGluIle***TyrThr 28
1175 CAGATCATGCACTGCACACACAGC 198

RESULT 26
AAQ53193
ID AAQ53193 standard; cDNA; 813 BP.
AC AAQ53193;
XX
DT 21-JUN-1994 (first entry)
XX
DE MnsOD cDNA.
XX
KM MnsOD; manganese superoxide dismutase; N-terminal; catalyst;
KM reperfusion injury; ischaemia; superoxide; SO; molecular oxygen;
KM anti-inflammatory; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 43..711
FT /*tag= a
FT /*product= MnsOD
XX
XX US5270195-A.
XX
XX 14-DEC-1993.
XX
XX 22-NOV-1985; 85US-0801090.
XX
XX 29-OCT-1986; 86IE-0002851.
XX
XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
XX
XX Beck Y, Hartman JR;
XX
XX WPI; 1993-404931/50.
XX
XX P-PSDB; AAR44801.
XX
XX Expression plasmid in Escherichia coli host system - encodes
XX human manganese superoxidodismutase analogue, useful for e.g.
XX treating inflammation
XX
XX Claim 1; Fig 1a-1c; 27pp; English.
XX
XX The sequence encodes a manganese superoxide dismutase which can be used
XX to catalyse the reduction of superoxide (SO) radicals to hydrogen
XX peroxide and molecular oxygen. It can be used to reduce
XX reperfusion injury following ischaemia and prolong the survival of
XX excised organs. It can also be used as a long acting

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```

CC anti-inflammatory drug.
XX
SQ Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 other;

Alignment Scores:
Pred. No.: 0.000928 Length: 813
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x AAQ53193 (1-813)
Oy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
115 AAGCACAGCCTCCCGACCTGCGCTACGACTACGCGCGCTCGAAGCTCAGATCAACGCG 174
Oy 21 GlnIleAsnGluIle***TyrThr 28
1175 CAGATCATGCACTGCACACACAGC 198

RESULT 27
AAT34277
ID AAT34277 standard; cDNA; 813 BP.
AC AAT34277;
XX
DT 24-OCT-1996 (first entry)
XX
DE Human manganese superoxide dismutase cDNA.
XX
KM Manganese superoxide dismutase; MnsOD; reperfusion injury;
KM ischaemia; bronchial pulmonary dysplasia; inflammation;
KM anti-inflammatory; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 43..711
FT /*tag= a
FT sig_peptide 43..114
FT /*tag= b
FT mat_peptide 115..708
FT /*tag= c
XX
XX US5540911-A.
XX
XX 30-JUL-1996.
XX
XX 22-NOV-1985; 85US-0801090.
XX
XX 29-OCT-1986; 86IE-0002851.
XX
XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
XX
XX Beck Y, Hartman JR;
XX
XX WPI; 1996-361912/36.
XX
XX P-PSDB; AAM00018.
XX
XX Use of recombinant human manganese superoxide dismutase - for
XX treating inflammation or bronchial pulmonary dysplasia, reducing
XX reperfusion injury or prolonging organ survival
XX
XX Claim 1; Fig 1A-1C; 27pp; English.
XX
XX A cDNA clone (AAT34277) codes for human manganese superoxide dismutase
XX (MnsOD) (AAM00018), an enzyme that catalyses the reduction of
XX superoxide radicals to H2O2 and O2. It was isolated from a human T-
XX cell library cloned into vector gcl0 using probes (see also AAT34283-
XX 84) based on portions of mature MnsOD. The MnsOD gene was also
XX identified (see also AAT34278-82). The cDNA can be used for the

```

CC prodn. of recombinant MnSOD using e.g. Escherichia coli cells as
 CC hosts. The MnSOD is useful for reducing reperfusion injury,
 CC treating inflammation or bronchial pulmonary dysplasia and for
 CC prolonging survival of excised organs.

XX Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	0.000928	813	12	10	6	0
Percent Similarity:	74.00					
Best Local Similarity:	78.57%					
Query Match:	42.86%					
DB:	51.03%					
	17					

US-09-987-190-2 (1-30) x AAT34277 (1-813)

Qy 1 LysTyrSerLeuPProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSercly 20

115 AAGCAGAGCCTCCCGACCTGCTCCTACGACTACGCGCGCTCGAAGCTCAGATCAACGCG 174

Qy 21 GlnIleAsnGluIle**TyrThr 28

Db 175 CAGATCATGCGCTGCACACAGC 198

RESULT 28

AAT15589

AC AAT15589;

DT 06-APR-1996 (first entry)

DE Human manganese superoxide-dismutase cDNA.

XX Human; manganese superoxide-dismutase; T-lymphocyte; probe; cDNA;
 KW Escherichia coli; plasmid pMS-4; N-terminal truncation; cloning;
 KM aminopeptidase; antiinflammatory; oxygen free radical scavenger;
 KM synovial inflammation; arthritis; lung fibrosis; ds.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 43..711

FT sig_peptide /tag= a

FT mat_peptide /product= Manganese superoxide-dismutase

FT /note= "EC-1.15.1.1"

FT /tag= b

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

XX The sequence encodes a human manganese superoxide-dismutase
 CC (MnSOD), and has been isolated from a human T-lymphocyte cDNA
 CC library in phase lambda-gt10 in Escherichia coli. The sequence of the
 CC a 5'-probe (AAT15591) and a 3'-probe (AAT15592). The sequence of the
 CC insert in plasmid pMS-4 (obtained by subcloning in plasmid pBR322)
 CC is shown. The cDNA may be expressed in e.g. E. coli for production
 CC of recombinant MnSOD. The MnSOD product may be cleaved with
 CC Aeromonas proteolytica aminopeptidase to produce an N-terminally
 CC truncated analogue with lysine and optionally histidine residues
 CC removed. The MnSOD analogue may be used in therapy of conditions
 CC associated with generation of oxygen free radicals, particularly
 CC synovial inflammation, arthritis and lung fibrosis (claimed).

XX Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	0.000928	813	12	10	6	0
Percent Similarity:	74.00					
Best Local Similarity:	78.57%					
Query Match:	42.86%					
DB:	51.03%					
	17					

US-09-987-190-2 (1-30) x AAT15589 (1-813)

Qy 1 LysTyrSerLeuPProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSercly 20

Db 115 AAGCAGAGCCTCCCGACCTGCTCCTACGACTACGCGCGCTCGAAGCTCAGATCAACGCG 174

Qy 21 GlnIleAsnGluIle**TyrThr 28

Db 175 CAGATCATGCGCTGCACACAGC 198

RESULT 29

AAX24998

AC AAX24998;

DT 05-JUL-1999 (first entry)

DE Human native manganese superoxide dismutase cDNA.

XX Human; native manganese superoxide dismutase; protein engineering;
 KW Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KM enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
 KM inflammation; reperfusion injury; therapy; ss.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 43..711

FT sig_peptide /tag= a

FT mat_peptide /tag= b

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

FT /tag= c

PT New recombinant human manganese superoxide dismutase proteins
 XX Disclosure; Page 52-53; 61pp; English.
 XX
 CC This cDNA sequence codes for human manganese superoxide dismutase
 CC (hmnSOD, see AAW98169). Novel hmnSOD proteins having catalytic
 CC activity which differs from this natural hmnSOD are claimed. The
 CC modified proteins exhibit reduced or no product inhibition, or have
 CC greater activity, or both, compared to natural hmnSOD. The
 CC modifications involve one or amino acid substitutions within
 CC the active site of the enzyme, especially at residues His-26,
 CC His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and His-163
 CC (see also AAW98171-77). Nucleic acids encoding the modified hmnSOD
 CC proteins are also claimed. The modified hmnSOD proteins, or
 CC expression vectors in which modified hmnSOD nucleic acid is linked
 CC to a promoter (preferably mammalian), can be used to protect a cell
 CC line from damage caused by superoxide radicals (claimed). They can
 CC also be used to treat subjects suffering from, or at risk of,
 CC cytotoxicity caused by superoxide radicals (claimed). As such,
 CC they can be used as antioxidants in the treatment of a variety of
 CC disorders, including inflammation (claimed), reperfusion injury
 CC following ischemia (claimed), and cellular damage caused by
 CC chemotherapeutic agents.
 CC
 SQ Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 0.000928 Length: 813
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: 20 Gaps: 0
 US-09-987-190-2 (1-30) x AAW24998 (1-813)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 115 AAGCAGACGCTCCCGACCTGCGCTACGACGCGCCCTGGAACCTCAACGCG 174
 QY 21 GlnIleAsnGluIle***TyrThr 28
 Db 175 CAGATCATGCAGCTGCACACGAC 198
 RESULT 30
 AAW63891
 ID AAW63891 standard; cDNA; 813 BP.
 XX
 XX AAW63891;
 DE 04-DEC-2000 (first entry)
 XX
 DE cDNA encoding a human manganese superoxide dismutase.
 XX
 KW Human; manganese superoxide dismutase; hmn SOD; superoxide radical;
 KW superoxide radical damage; cytotoxicity; inflammation; ischemia;
 KW reperfusion injury; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 43..711
 FT CDS
 FT /*tag= a
 FT /transl_except= (pos: 505..507, aa: Xaa)
 FT /transl_except= (pos: 511..513, aa: Ala)
 FT /product= "manganese superoxide dismutase"
 FT /note= "Xaa is Gln or Glu"
 FT 43..114
 FT /*tag= b
 FT mat_peptide 115..708
 FT /*tag= c
 PN US6107070-A.

XX
 PD 22-AUG-2000.
 XX
 PF 10-SEP-1998; 98US-0151052.
 XX
 FR 10-SEP-1997; 97US-0927230.
 XX
 PA (UYFL) UNIV FLORIDA.
 XX
 PI Silverman DN, Nick HS;
 XX WPI; 2000-578537/54.
 XX DR P-PSDB; AAB08204.
 DR
 XX
 PT Novel human manganese superoxide dismutase protein useful as
 PT antioxidant for treating cytotoxicity caused by superoxide radicals,
 PT inflammation and reperfusion injury following ischemia -
 XX
 XX Disclosure; Columns 25-26; 27pp; English.
 CC
 CC The present sequence encodes a human manganese superoxide dismutase
 CC protein (hmn SOD). The specification describes a modified hmn SOD which
 CC has a catalytic activity which differs from natural hmn SOD in that it
 CC exhibits reduced or no product inhibition compared to natural hmn
 CC SOD. The natural hmn SOD is especially modified with one or more
 CC substitutions in amino acids 26, 30, 34, 74, 143, 159, 161 and 163.
 CC The modified hmn SOD is useful for protecting a cell from damage caused
 CC by superoxide radicals and for treating a subject suffering from
 CC cytotoxicity caused by superoxide radicals. The protein is useful for
 CC treating inflammation and reperfusion injury following ischemia.
 CC
 SQ Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 0.000928 Length: 813
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: 21 Gaps: 0
 US-09-987-190-2 (1-30) x AAW63891 (1-813)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 115 AAGCAGACGCTCCCGACCTGCGCTACGACGCGCCCTGGAACCTCAACGCG 174
 QY 21 GlnIleAsnGluIle***TyrThr 28
 Db 175 CAGATCATGCAGCTGCACACGAC 198
 RESULT 31
 ABA94453
 ID ABA94453 standard; cDNA; 849 BP.
 XX
 XX ABA94453;
 DE 09-APR-2002 (first entry)
 XX
 DE Human manganese superoxide dismutase (hSODm) encoding cDNA.
 XX
 KW Human manganese superoxide dismutase; antiinflammatory; antiarthritic;
 KW antirheumatic; vasotropic; osteopathic; hSODm; human; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 100..768
 FT CDS
 FT /*tag= a
 FT /product= "hSODm"
 FT 100..171
 FT mat_peptide 172..765
 FT

```
FT XX /+tag= c
XX PN US6326003-B1.
XX PD 04-DEC-2001.
XX PF 14-OCT-1986; 86US-0918534.
XX PR 14-OCT-1986; 86US-0918534.
XX PS (CHIR ) CHIRON CORP.
XX PI Halliwell RA, Bell GT, Mullenbach GT;
XX DR WPI; 2002-129495/17.
XX DR P-PSDB; ABB07330.
XX PT Treating inflammatory joint disease such as osteoarthritis, rheumatoid
XX PT arthritis and post ischemic tissue injury, comprises injecting human
XX PS manganese superoxide dismutase -
XX PS Example 2; Fig 4; 14pp; English.
XX CC The invention relates to a method of treating a patient with inflammatory
XX CC joint disease. The method involves intra-articularly injecting into the
XX CC afflicted joint a solution of human manganese superoxide dismutase
XX CC (hSODm). The treatment is used to treat an inflammatory joint disease,
XX CC particularly osteoarthritis or rheumatoid arthritis. The method can also
XX CC be used to treat post ischemic tissue injury. The present sequence
XX CC represents a cDNA encoding the hSODm.
XX SQ Sequence 849 BP; 256 A; 197 C; 227 G; 169 T; 0 other;

Alignment Scores:
Pred. No.: 0.00098 Length: 849
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 24 Gaps: 0

US-09-987-190-2 (1-30) x ABA94453 (1-849)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 172 AAGCAGACGCGCTCCCGAGCTGCGCCGCTGGAACCTCAGATCAGCCG 231
21 GlnIleAsnGluIle**TyrThr 28
232 CAGATCATGCACTGCACACACAGC 255

RESULT 32
AAQ94279
ID AAQ94279 standard; cDNA; 966 BP.
XX AC AAQ94279;
XX XX
XX PT 23-MAY-1996 (first entry)
XX DE Human manganese superoxide dismutase (Gln29) CDS and partial 3'-UTR.
XX KM hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;
XX KM autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;
XX KM osteoarthritis; wound healing; ss.
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT mat_peptide 1..594
XX FT /+tag= a
XX FT /product= hMn-SOD (Gln29)
XX PN EP676472-A1.
```

```
XX PD 11-OCT-1995.
XX PF 10-MAR-1988; 88EP-0107460.
XX PR 24-DEC-1987; 87DE-3744038.
XX PR 14-MAR-1987; 87DE-3708306.
XX PR 26-MAY-1987; 87DE-3717695.
XX PR 10-JUL-1987; 87DE-3722884.
XX PS (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX PI Hauptmann R, Heckl K, Krystek E, Maurer-Fogy I;
XX PI Ostermann E, Spevak W, Stralowa C, Wiche-Castanon M;
XX PI Zoepfel A;
XX DR WPI; 1995-346092/45.
XX XX
XX PT Genes encoding recombinant human manganese superoxide dismutase -
XX PT for treatment, prevention and diagnosis of inflammatory diseases
XX PS Claim 8; Page 6 and Page 18; 54pp; German.
XX CC The present sequence codes for the 198 amino acid long hMn-SOD
XX CC mature polypeptide having a Gln residue at position 29. The cDNA
XX CC can be inserted into expression vectors containing appropriate
XX CC signal sequences, etc. for expression of recombinant hMn-SOD.
XX CC Mature hMn-SOD is useful for treating, preventing or diagnosing
XX CC inflammatory, degenerative, neoplastic and rheumatic disorders;
XX CC in wound healing and in autoimmune diseases.
XX SQ Sequence 966 BP; 279 A; 191 C; 216 G; 280 T; 0 other;

Alignment Scores:
Pred. No.: 0.00116 Length: 966
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 16 Gaps: 0

US-09-987-190-2 (1-30) x AAQ94279 (1-966)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 1 AAGCAGCTTTGCGAGACTTGCCATGACGACTGCTCTAGAACACACATCAATGCT 60
21 GlnIleAsnGluIle**TyrThr 28
61 CAATCATGCAATTGCACCACTCT 84

RESULT 33
AAT31018
ID AAT31018 standard; cDNA to mRNA; 969 BP.
XX AC AAT31018;
XX XX
XX PT 26-SEP-1996 (first entry)
XX DE Human manganese superoxide dismutase cDNA.
XX KM Gene therapy; hypoxia related enhancer element; HREB; ischemia;
XX KM reperfusion; promoter; superoxide dismutase; ss.
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT CDS 61..729
XX FT /+tag= a
XX PN W09620276-A1.
XX PD 04-JUL-1996.
```

XX 13-NOV-1995; 95WO-1B00996.
XX 23-DEC-1994; 94US-0365486.
XX (STRI) SRI INT.
XX Bihopric NH, Green CJ, Laderoute KR, Murphy B;
XX Webster KA;
XX WPI, 1996-321849/32.
XX P-PSDB; AAM00453.
XX Chimeric gene contg. therapeutic gene linked to HHEE - partic. for
XX expressing SOD etc. in hypoxic tissue to reduce tissue injury caused
XX by ischaemia or reperfusion
XX
XX Disclosure; Page 94-95; 118pp; English.
XX A CDNA sequence (AAT31018) codes for human manganese superoxide
XX dismutase (AAM00453), an enzyme that catalyses the decomposition
XX of the superoxide anion to peroxide. Agents such as superoxide
XX dismutase are able to increase the salvage of heart muscle cells.
XX The gene may be used in novel therapeutic constructs also
XX contg. a tissue-specific promoter and a hypoxia response enhancer
XX element. Expression of the gene is enhanced in the target tissue
XX under hypoxic conditions, such as those encountered during
XX ischaemia and reperfusion.
XX
XX Sequence 969 BP; 277 A; 208 C; 244 G; 240 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 0.00116 Length: 969
XX Score: 74.00 Matches: 12
XX Percent Similarity: 78.57% Conservative: 10
XX Best Local Similarity: 42.86% Mismatches: 6
XX Query Match: 51.03% Indels: 0
XX DB: 17 Gaps: 0
XX
XX US-09-987-190-2 (1-30) x AAT31018 (1-969)
XX
XX Oy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
XX Db 133 AAGCACAGCCTCCCGACTGACCTACGCGCCCTGGAACCTCACAACGCG 192
XX Oy 21 GlnIleAenGluIle**TyrThr 28
XX Db 193 CAGATCATGACGCTGCACACGACG 216
XX
XX JUT 34
XX AAG67474
XX ID AAG67474 standard; cDNA; 976 BP.
XX AC AAG67474;
XX XX
XX DT 31-MAY-1995 (first entry)
XX XX
XX DE Human manganese-contg. superoxide dismutase SOD-2 cDNA.
XX XX
XX KW Human superoxide dismutase; mSOD; hSOD2; neurodegeneration;
XX KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
XX KW Hallervorden-Spatz disease; olivopontocerebellar atrophy;
XX KW familial amyotrophic lateral sclerosis; FALS; diagnosis; mutant SOD;
XX KW reverse transcription polymerase chain reaction; SSCP analysis; ss.
XX
XX Homo sapiens.
XX OS
XX XX
XX FH Key Location/Qualifiers
XX FT 95..763
XX FT CDS /tag= a
XX FT /note= "precursor of manganese-contg. SOD"
XX FT sig_peptide 95..166
XX FT /tag= b

FT mat_peptide /note= "amino acids -24 to -1 of signal peptide"
FT 167..763
FT /tag= c
FT /product= mature_mSOD
FT polyA_site 976
FT /tag= d
XX
XX W09419493-A.
XX
XX 01-SEP-1994.
XX
XX 28-FEB-1994; 94MO-US02089.
XX
XX 26-FEB-1993; 93US-0023980.
XX
XX (GHO) GEN HOSPITAL CORP.
XX PA (MAST) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Brown R, Horvitz HR, Rosen DR;
XX
XX WPI; 1994-294353/36.
XX DR P-PSDB; AAR61337.
XX
XX The presence of a mutation in a gene encoding a superoxide
XX dismutase (SOD1, SOD2 or SOD3) indicates an increased likelihood of
XX developing a cell death disease, specifically a neurodegenerative
XX disease. The use of SOD polypeptides to treat amyotrophic lateral
XX sclerosis and diseases involving a deleterious mutation in the
XX glutathione peroxidase-encoding gene, the catalase-encoding gene
XX and the nitric oxide-encoding gene is claimed. The specification
XX includes sequences for human SOD1, hSOD2 and hSOD3, but because the
XX print quality is poor, the hSOD2 sequence has been retrieved from
XX GENBANK (Accession number Y00985).
XX
XX SQ Sequence 976 BP; 252 A; 219 C; 262 G; 243 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 0.00117 Length: 976
XX Score: 74.00 Matches: 12
XX Percent Similarity: 78.57% Conservative: 10
XX Best Local Similarity: 42.86% Mismatches: 6
XX Query Match: 51.03% Indels: 0
XX DB: 15 Gaps: 0
XX
XX US-09-987-190-2 (1-30) x AAG67474 (1-976)
XX
XX Oy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
XX Db 167 AAGCACAGCCTCCCGACTGACCTACGCGCCCTGGAACCTCACAACGCG 226
XX Oy 21 GlnIleAenGluIle**TyrThr 28
XX Db 227 CAGATCATGACGCTGCACACGACG 250
XX
XX RESULT 35
XX ID AAX33940
XX XX AAX33940 standard; DNA; 976 BP.
XX AC AAX33940;
XX XX
XX DT 30-JUN-1999 (first entry)
XX XX
XX DE Human HCMV inducible gene, seq ID NO 7.
XX XX
XX KW HCMV inducible gene; cig; human; human cytomegalovirus; interferon;
XX KW anti-viral therapy; anti-HCMV therapy; detection; diagnosis;
XX KW drug screening; ds.

XX Homo sapiens.
 OS
 XX MO9913075-A2.
 PN
 XX
 XX 18-MAR-1999.
 PD
 XX
 XX 08-SEP-1998; 98WO-US18638.
 PF
 XX
 XX 22-SEP-1997; 97US-0059725.
 PR
 XX 08-SEP-1997; 97US-0058180.
 PR
 XX (UYPR-) UNIV PRINCETON.
 PA
 XX
 XX Cong J, Schenk T, Zhu H;
 PI
 XX WPI: 1999-243729/20.
 DR
 XX P-PSDB; AAY05370.
 DR

New isolated human genes

Claim 2; Page 99-100; 184pp; English.

XX This sequence represents a human gene of the invention, that is induced
 CC to express by both HCMV and interferon (IFN), designated HCMV-inducible
 CC genes (cig or cigs). The invention also relates to genes that are
 CC repressed in the presence of HCMV infection, designated HCMV-repressible
 CC genes (crg or crgs). The products can be used to obtain agents which can
 CC be used for anti-viral therapy, particularly anti-HCMV therapy. They can
 CC also be used for the development of drugs that would allow for higher
 CC dosage IFN treatments without the concomitant toxicity normally
 CC associated with administering high levels of IFN. The products can also
 CC be used for detection, diagnosis and drug screening.
 XX

SO Sequence 976 BP; 252 A; 219 C; 262 G; 243 T; 0 other;

Alignment Scores:

Pred. No.: 0.00117 Length: 976
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: Gaps: 0

US-09-987-190-2 (1-30) x AAX33940 (1-976)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 |||||
 167 AAGCAGAGCTCTCCCGACCTGCTCCCTGACGCGCCCTGGAACCTCACATCAACCG 226

Qy 21 GlnIleAsnGluIle**TyrThr 28
 |||||
 227 CAGATCATGACGCTGCACACACG 250

RESULT 36
 AAX08429
 ID AAX08429 standard; DNA; 976 BP.
 XX
 XX AAX08429;

XX 28-JUN-1999 (first entry)

XX Human manganese containing superoxide dismutase gene.

XX Manganese containing superoxide dismutase; MnSOD; IDDM;
 XX diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell;
 XX fatty acid; lipotoxic; cytotoxic; cytokine; osteoporosis;
 XX inflammatory disease; autoimmune disease; neurodegenerative disease;
 XX ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 XX

FT CDS 75..763
 FT /*tag= a
 FT /product= "Manganese containing superoxide dismutase"

XX MO9906059-A2.

XX 11-FEB-1999.

XX 30-JUL-1998; 98WO-US15781.

XX 03-MAR-1998; 98US-0055092.

XX 30-JUL-1997; 97US-0055092.

XX (BETA-) BETAGENE INC.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Clark SA, Hohmeier H, Koyama K, Lee Y, Newgard CB;
 PI Ohneda M, Shimabukuro, Thigpen A, Unger RH;
 PI
 XX WPI: 1999-153448/13.
 DR P-PSDB; AAW96317.
 DR

PT Protection of mammalian cells against immunotoxicity or lipotoxicity
 PT - used for treating, e.g. diabetes, obesity, wasting syndromes,
 PT osteoporosis, inflammatory diseases, autoimmune diseases or
 PT neurodegenerative diseases

PS Disclosure; Page 232-233; 253pp; English.

XX Manganese containing superoxide dismutase (MnSOD) can be used to
 CC protect cells against cytokine mediated killing. Inhibition of
 CC cytokine mediated immunotoxicity of cells can be achieved by
 CC blocking free radical production or the accumulation of free
 CC radicals in that cell. Treatment of insulin dependent diabetes
 CC mellitus (IDDM) can be achieved by by blocking nitric oxide (NO)
 CC production in a pancreatic beta cell and by providing a composition
 CC comprising an agent that reduces levels of fatty acids in the cells
 CC and protects beta-cells of the subject against lipid-mediated cell
 CC death. Cells can also be protected against nitric oxide mediated
 CC cytotoxicity by introducing into the cell an antioxidant agent.
 CC The methods can be used for protecting cells against immunotoxicity
 CC mediated by, e.g. IL-1 beta, IL-1 alpha, gamma IFN, TNF alpha, TNF
 CC beta, IL-8, IL-2, IL-6, IL-7, IL-9, IL-14, IL-17,
 CC granulocyte-macrophage colony stimulating factor or monocyte
 CC chemottractant protein-1. The methods can be used for the treatment
 CC of e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity,
 CC wasting syndromes, short stature, osteoporosis, inflammatory
 CC diseases, autoimmune diseases, or neurodegenerative diseases.
 XX

SO Sequence 976 BP; 252 A; 219 C; 262 G; 243 T; 0 other;

Alignment Scores:
 Pred. No.: 0.00117 Length: 976
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: Gaps: 0

US-09-987-190-2 (1-30) x AAX08429 (1-976)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 |||||
 167 AAGCAGAGCTCTCCCGACCTGCTCCCTGACGCGCCCTGGAACCTCACATCAACCG 226

Qy 21 GlnIleAsnGluIle**TyrThr 28
 |||||
 227 CAGATCATGACGCTGCACACACG 250

RESULT 37
 AAV73824
 ID AAV73824 standard; DNA; 977 BP.
 XX

PT treating inflammation or bronchial pulmonary dysplasia, reducing
 PT reperfusion injury or prolonging organ survival
 XX
 PS Example 8; Fig 6A-6B; 27pp; English.
 XX
 CC DNA fragments (AA134278-82) cover the 6 exons of the human manganese
 CC superoxide dismutase gene. The fragment given in AA134278 covers
 CC the promoter region and exons 1 and 2. The MnSOD gene was isolated
 CC from human placental DNA using a MnSOD cDNA clone (see also AA134277)
 CC as probe. The isolated gene can be introduced into mammalian cell
 CC hosts for the prodn. of MnSOD (see also AA00018), useful for the
 CC treatment of e.g. ischaemia and inflammation.
 XX
 SQ Sequence 1007 BP; 154 A; 330 C; 397 G; 126 T; 0 other;
 Alignment Scores:
 Pred. No.: 0.00122 Length: 1007
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: 17 Gaps: 0
 US-09-987-190-2 (1-30) x AA134278 (1-1007)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 DB 833 AAGCAGACGCTCCCGACCTGCTAGACTACGCGCCCTGGAACCTCACATCAACCG 892
 QY 21 GlnIleAsnGluIle***TyrThr 28
 DB 893 CAGATCATGCGACTGACACACAGC 916
 RESULT 39
 ID AA063914 standard; DNA; 1008 BP.
 AC AA063914;
 XX
 XX 21-JUN-1994 (first entry)
 DT
 XX
 DE MnSOD DNA (exons 1 and 2).
 XX
 KM MnSOD; manganese superoxide dismutase; N-terminal; catalyst;
 KM reperfusion injury following ischaemia; superoxide; SO; molecular oxygen;
 KM anti-inflammatory; bs.
 XX
 XX Homo sapiens.
 Key Location/Qualifiers
 FT exon 421..510
 FT /*tag= a
 FT exon 783..986
 FT /*tag= b
 FT stem_loop 74..102
 FT /*tag= c
 FT stem_loop 214..233
 FT /*tag= d
 FT repeat_unit 289..300
 FT /*tag= e
 FT /*rpt_type= direct
 FT /note= "repeat 3"
 FT repeat_unit 405..415
 FT /*tag= f
 FT /*rpt_type= direct
 FT /note= "repeat 3"
 FT repeat_unit 361..370
 FT /*tag= g
 FT /*rpt_type= direct
 FT /note= "repeat 4"
 FT repeat_unit 373..383
 FT /*tag= h
 FT /*rpt_type= direct

FT GC_signal /note= "repeat 4"
 FT 71..76
 FT /*tag= i
 FT /note= "SP1 binding site"
 FT 247..257
 FT /*tag= j
 FT /note= "SP1 binding site"
 FT 296..307
 FT /*tag= k
 FT /note= "SP1 binding site"
 FT 324..334
 FT /*tag= l
 FT /note= "SP1 binding site"
 FT misc_RNA 1008
 FT /*tag= m
 FT /note= "Represents sequence of undefined length
 between exons 2 and 3."
 FT US5270195-A.
 FT 14-DEC-1993.
 FT 22-NOV-1985; 85US-0801090.
 FT 29-OCT-1986; 86IE-0002851.
 FT (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
 FT Beck Y, Hartman JR;
 FT WPI; 1993-404931/50.
 FT Expression plasmid in Escherichia coli host system - encodes
 FT human manganese superoxidisedismutase analogue, useful for e.g.
 FT treating inflammation
 XX Disclosure; Fig 6a-6d; 27pp; English.
 XX
 XX The sequence shows part of the genomic DNA that encodes a
 CC manganese superoxide dismutase which can be used
 CC to catalyse the reduction of superoxide (SO) radicals to hydrogen
 CC peroxide and molecular oxygen. It can be used to reduce
 CC reperfusion injury following ischaemia and prolong the survival of
 CC excised organs. It can also be used as a long acting
 CC anti-inflammatory drug. See sequences (AA063914-17) for other fragments.
 XX
 SQ Sequence 1008 BP; 154 A; 330 C; 397 G; 126 T; 1 other;
 Alignment Scores:
 Pred. No.: 0.00122 Length: 1008
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: 14 Gaps: 0
 US-09-987-190-2 (1-30) x AA063914 (1-1008)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 DB 833 AAGCAGACGCTCCCGACCTGCTAGACTACGCGCCCTGGAACCTCACATCAACCG 892
 QY 21 GlnIleAsnGluIle***TyrThr 28
 DB 893 CAGATCATGCGACTGACACACAGC 916
 RESULT 40
 ID ABK84524 standard; cDNA; 1026 BP.
 AC ABK84524;
 XX
 DT 14-AUG-2002 (first entry)

XX Human cDNA differentially expressed in granulocytic cells #1095.
 DE XX
 KW Human; se; granulocytic cell; DNA chip; bacterial infection;
 KW viral infection; parasitic infection; protozoal infection;
 KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; periodontal disease;
 KW granulocyte activation; chronic inflammation; allergy.
 KW
 XX Homo sapiens.
 OS
 PN WO200228999-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 03-OCT-2001; 2001WO-US30821.
 XX
 PF 03-OCT-2000; 2000US-237189P.
 PA (GENE-) GENE LOGIC INC.
 XX Beazer-Barclay Y, Weisman SM, Yamaga S, Vockley J;
 PI WPI; 2002-435328/46.
 XX
 DR Detecting granulocyte activation by detecting differential expression
 XX of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity -
 XX
 PS Claim 1; SEQ ID No 1095; 114bp; English.
 CC The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) GA by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)
 CC for an agent capable of modulating GCA or an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the
 CC gene expression profile; (3) detecting (M4) an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease, by detecting the
 CC level of expression in a sample of the tissue of gene(s) from Gs, where
 CC the level of expression of the gene is indicative of inflammation;
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
 CC an allergic response in a subject, exposure of a subject to a pathogen
 CC or sterile inflammatory disease, by contacting a tissue having
 CC inflammation with an agent that modulates the expression of gene(s)
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating GA; M3 is useful for screening an agent capable of modulating
 CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease; also bacterial infection, viral infection,
 CC parasitic infection, protozoal infection, fungal infection and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 1026 BP; 283 A; 216 C; 245 G; 282 T; 0 other;

Alignment Scores:
 Pred. No.: 0.00125 Length: 1026
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: 24 Gaps: 0
 US-09-987-190-2 (1-30) x ABX84524 (1-1026)
 QY 1 LysTyrSerLeuPProGluLeuAspTyrGluPheSerAlaThrGluProTyrTlleSercly 20
 Db 77 AAGCAGAGCCTCCCGACCTGCTCCCTACGACTACGCGCCCTCGAACTCACATCACGCG 136
 QY 21 GlnTleAngGluIle***TyrThr 28
 Db 137 CAGATCATGCAGCTGCACACGAC 160

Search completed: April 8, 2003, 02:21:59
 Job time : 65.422 secs

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OM protein - protein search, using sw model

Run on: April 9, 2003, 14:01:45 ; Search time 3.99083 Seconds
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Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database: SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	25	83.3	234 1	SODM_CANAL
2	10	33.3	233 1	SODM_YEAST
3	8	26.7	206 1	SODM_MYCAV
4	8	26.7	206 1	SODM_MYCLP
5	7	23.3	206 1	SODM_MYCFO
6	7	23.3	206 1	SODM_MYCSM
7	7	23.3	206 1	SODM_NOCAS
8	7	23.3	207 1	SODF_MYCTU
9	7	23.3	488 1	GCS2_BACSU
10	7	23.3	1034 1	CAP2_SYNY3
11	6	20.0	130 1	Y142_LEUWC
12	6	20.0	137 1	UK14_HUMAN
13	6	20.0	201 1	SODM_PROFR
14	6	20.0	207 1	3WGH_LISMO
15	6	20.0	207 1	SODM_CHLEP
16	6	20.0	278 1	PURU_HAELN
17	6	20.0	334 1	MENC_MYCLE
18	6	20.0	347 1	UTR2_YEAST
19	6	20.0	360 1	ITD2_HALNI
20	6	20.0	428 1	HEMY_HAELN
21	6	20.0	535 1	TCE1_AVEA3
22	6	20.0	535 1	TCE2_AVEA3
23	6	20.0	561 1	YDDA_ECOLI
24	6	20.0	879 1	BALL_MOUSE
25	6	20.0	881 1	BALL_HUMAN
26	6	20.0	948 1	UVRA_NEIMA
27	6	20.0	949 1	UVRA_NEIMA
28	6	20.0	950 1	UVRA_NEIMA
29	6	20.0	1325 1	BCC3_ACEXY
30	5	16.7	74 1	V194_FOWPV
31	5	16.7	85 1	YKX2_CAEEL
32	5	16.7	101 1	YKX5_CHLEA
33	5	16.7	109 1	Y265_UREPA

34	5	16.7	115 1	ANFC_SCYCA
35	5	16.7	115 1	SMD2_SCHPO
36	5	16.7	124 1	REV_SIVCZ
37	5	16.7	125 1	Y364_AQUAE
38	5	16.7	127 1	Y026_NPYOP
39	5	16.7	129 1	VAL2_ABMVM
40	5	16.7	129 1	VAL2_TMOV
41	5	16.7	132 1	VAL3_PHVU
42	5	16.7	133 1	TATB_VIBCH
43	5	16.7	137 1	UK14_CAPHI
44	5	16.7	138 1	EXD1_VIBCH
45	5	16.7	140 1	LCA_TIRIVU
46	5	16.7	141 1	APGB_MOUSE
47	5	16.7	144 1	VE6_HPV54
48	5	16.7	145 1	YBAG_YEAST
49	5	16.7	149 1	ARGR_BACBD
50	5	16.7	149 1	ARGR_BACLI
51	5	16.7	149 1	ARGR_BACST
52	5	16.7	149 1	ARGR_BACSU
53	5	16.7	157 1	IBP_BUCAI
54	5	16.7	162 1	YLF6_CAEEL
55	5	16.7	165 1	RIMM_RICCN
56	5	16.7	169 1	CALB_HUMAN
57	5	16.7	169 1	CALB_MOUSE
58	5	16.7	170 1	CALB_DROME
59	5	16.7	170 1	CALC_DROME
60	5	16.7	171 1	Y162_MERTH
61	5	16.7	173 1	HR12_MOUSE
62	5	16.7	175 1	CALC_RAT
63	5	16.7	175 1	FLAW_KLEPN
64	5	16.7	175 1	NU6W_FELCA
65	5	16.7	177 1	RELX_MESAU
66	5	16.7	177 1	YDAB_MYCBO
67	5	16.7	180 1	TAAS_WHEAT
68	5	16.7	180 1	Y788_RICPR
69	5	16.7	182 1	RIMM_VIBCH
70	5	16.7	185 1	RELI_HUMAN
71	5	16.7	185 1	RELX_MOUSE
72	5	16.7	188 1	V230_FOWPV
73	5	16.7	191 1	KIRP_HUMAN
74	5	16.7	191 1	KIRP_MOUSE
75	5	16.7	191 1	KIRP_RAT
76	5	16.7	200 1	NUPL_XENIA
77	5	16.7	200 1	SODM_AGABI
78	5	16.7	202 1	SODF_MERTH
79	5	16.7	203 1	TAAS_HORVU
80	5	16.7	203 1	PTH_ANASP
81	5	16.7	207 1	YNO2_CAEEL
82	5	16.7	208 1	KGUA_HAELN
83	5	16.7	210 1	SODF_SUDAC
84	5	16.7	210 1	SODF_SUDSO
85	5	16.7	211 1	FIXI_AZOCA
86	5	16.7	211 1	SODF_ACIAM
87	5	16.7	211 1	SODF_PYRAE
88	5	16.7	212 1	UL03_HAVER
89	5	16.7	214 1	GTH3_ARATH
90	5	16.7	216 1	LUXM_VIRBA
91	5	16.7	225 1	TN12_MOUSE
92	5	16.7	226 1	DTXR_CORDI
93	5	16.7	226 1	NHB2_RHORN
94	5	16.7	228 1	RPE_STROO
95	5	16.7	231 1	FLGD_ECOLI
96	5	16.7	232 1	FLGD_SALTY
97	5	16.7	236 1	YBEP_ECOLI
98	5	16.7	239 1	DCUR_ECOLI
99	5	16.7	242 1	TPIS_MYCFL
100	5	16.7	243 1	DP3E_ECOLI
101	5	16.7	243 1	YC22_MERJA
102	5	16.7	244 1	T2FC_YEAST
103	5	16.7	244 1	Y181_MYCTU
104	5	16.7	245 1	RNPH_BACSU
105	5	16.7	245 1	SODM_NEUCR
106	5	16.7	247 1	TRAF_ECOLI

P23259	scylliorhinu
O14036	schizosacch
P17280	chimpanzee
O66689	aquifex aeo
O10297	orygia pseu
P21944	abutilon mo
O06658	tomato mott
O06925	pepper huas
P57063	vibrio chol
P80601	capra hircu
O52044	vibrio chol
O29145	trichosurus
O3CQY1	mus musculu
O21018	human papil
P38210	saccharomyc
O9K973	bacillus ha
O86130	bacillus li
O31408	bacillus st
P17893	bacillus su
P57640	buchnera ap
O03598	caenorhabdi
O32167	rickettsia
P06705	homo sapien
O63810	mus musculu
P48451	dtrosophila
O24810	dtrosophila
O27850	methanobact
P22760	mus musculu
P28470	rattus norv
P04668	klebsiella
P48928	felis silve
O64121	mesocricetu
P46830	mycobacteri
P16347	triticum ae
O05978	rickettsia
O9K973	vibrio chol
P04808	homo sapien
P47932	mus musculu
O93505	fowlpox vir
O99828	homo sapien
O92064	mus musculu
O9E010	rattus norv
P05221	xenopus lae
O9P246	agarcia bl
O60056	methanobact
P07596	hordium vul
O0Y744	anabaena sp
Q11965	caenorhabdi
P44310	haemophilus
O08713	bullefolobus
P08057	sulfolobus
O68571	azotirizobiu
O9P913	acidianus a
O93724	pyrobaculum
P28942	equine help
P42761	arabidopsis
P54298	vibrio harv
O54907	mus musculu
P33120	corynebacte
P29379	rhodococcus
Q01028	streptococ
P15936	escherichia
P16321	salmonella
P76359	escherichia
P39271	escherichia
P48779	mycoplasma
O36007	escherichia
O58619	methanococc
P05148	saccharomyc
O07423	mycobacteri
P28619	bacillus su
O9Y788	neurospora
P14497	escherichia

107	5	16.7	249	1	TN12_HUMAN	043508	homo sapien	180	5	16.7	362	1	AROB_HAEN	P43879	haemophilus
108	5	16.7	250	1	TRMD_TREPA	083878	treponema p	181	5	16.7	363	1	MBHS_BRJA	P12635	bradyrhizob
109	5	16.7	251	1	BIOC_ECOLI	P12999	escherichia	182	5	16.7	366	1	YN10_YEAS	P13930	saccharomyc
110	5	16.7	251	1	BIOC_ERMHE	006898	erwinia her	183	5	16.7	372	1	PRS2_MERTM	P42811	methanobact
111	5	16.7	253	1	DF10_YEAST	P40526	saccharomyc	184	5	16.7	374	1	RECA_STRCO	050487	streptomyce
112	5	16.7	259	1	Y500_METUA	Q57923	methanococc	185	5	16.7	374	1	RECA_STRLI	P48294	streptomyce
113	5	16.7	260	1	RCEH_RHOSH	P11846	rhodobacter	186	5	16.7	374	1	RFAG_ECOLI	P25740	escherichia
114	5	16.7	260	1	S3AD_STAM	P44827	staphylococc	187	5	16.7	375	1	MBHS_CITFR	Q46053	citrobacter
115	5	16.7	260	1	VBRL_ICMV	008595	indian caas	188	5	16.7	375	1	PROB_SYNY3	P73071	synecocyst
116	5	16.7	269	1	AAKB_RAT	P80386	rattus norv	189	5	16.7	375	1	SOX3_MOUSE	P53784	mus musc
117	5	16.7	272	1	Y439_MYCCE	P47677	mycoplasma	190	5	16.7	376	1	HOSC_THETH	087718	thermus the
118	5	16.7	276	1	YJIC_ECOLI	P33374	escherichia	191	5	16.7	376	1	PEXE_MOUSE	Q97080	mus muscu
119	5	16.7	281	1	SODP_BACSU	035023	bacillus su	192	5	16.7	377	1	MYG_NORMA	P31537	nordictis ma
120	5	16.7	288	1	HEMK_MYCLE	P45832	mycobacteri	193	5	16.7	377	1	PEXE_HUMAN	P76381	homo sapien
121	5	16.7	289	1	ATPG_PASWU	Q916b6	pasteurella	194	5	16.7	379	1	WZA_ECOLI	Q65038	escherichia
122	5	16.7	298	1	CD38_RABIT	Q9m203	oryctolagus	195	5	16.7	379	1	WZA_SALTI	Q82554	salmonella
123	5	16.7	299	1	RR42_SCHPO	Q60124	schizosacch	196	5	16.7	379	1	WZA_SALTY	Q82554	salmonella
124	5	16.7	302	1	Y091_METUA	Q57556	methanococc	197	5	16.7	387	1	Y4PF_RHISN	P55615	rhizobium s
125	5	16.7	304	1	HEMK_MYCTU	Q10602	mycobacteri	198	5	16.7	388	1	FETB_MOUSE	Q9qkx1	mus muscu
126	5	16.7	304	1	HEMK_THEVO	Q97809	thermoplas	199	5	16.7	389	1	MTSA_LACTIC	P34877	lactococcus
127	5	16.7	304	1	NPX4_RAT	Q932n4	rattus norv	200	5	16.7	390	1	TRPB_MERTM	P26992	methanobact
128	5	16.7	305	1	PIR_ECOLI	P03067	escherichia	201	5	16.7	392	1	PSMR_SULTO	Q975u2	sulfobobus
129	5	16.7	308	1	HEMZ_THENC	Q9h1b8	thermoplas	202	5	16.7	394	1	DUS4_HUMAN	Q31115	homo sapien
130	5	16.7	309	1	SOX3_XENLA	P55863	xenopus lae	203	5	16.7	396	1	APA4_HUMAN	P66727	homo sapien
131	5	16.7	310	1	PYRB_HALNL	Q9hnm4	halobacteri	204	5	16.7	396	1	P53_ONCMY	P25035	oncorhynch
132	5	16.7	310	1	PYRB_LACLA	Q9cft79	lactococcus	205	5	16.7	398	1	A23D_DROME	Q44093	drosophila
133	5	16.7	310	1	VCAP_BPT3	P20324	bacterioph	206	5	16.7	398	1	FTS2_WOLPE	P54485	wolbachia s
134	5	16.7	311	1	MRAP_BACSU	Q07876	bacillus su	207	5	16.7	409	1	YOPM_YERPE	P17778	yersinia pe
135	5	16.7	312	1	SOX3_CHICK	P48433	gallus gall	208	5	16.7	411	1	EP1G_TRYCR	P34715	trypanosoma
136	5	16.7	312	1	YDIR_ECOLI	P77378	escherichia	209	5	16.7	411	1	LCYB_SYNP7	Q55276	synecococc
137	5	16.7	313	1	FIXB_ECOLI	P15574	escherichia	210	5	16.7	412	1	CSP_PLAFA	P02893	plasmogium
138	5	16.7	315	1	PHSS_DESBA	P13063	desulfovibr	211	5	16.7	412	1	PGKP_ALCEU	P03033	alcaligenes
139	5	16.7	316	1	BGMN_LACAC	Q07685	lactobacilli	212	5	16.7	412	1	RBAL_CAEEL	P50919	caenorhabdi
140	5	16.7	316	1	CBT_ECOLI	Q47083	escherichia	213	5	16.7	413	1	PGKC_ALCEU	P50319	alcaligenes
141	5	16.7	318	1	ANX4_CANRA	P50994	canis famli	214	5	16.7	415	1	YO12_YEAST	P35193	saccharomyc
142	5	16.7	319	1	YQOP_BACSU	P54553	bacillus su	215	5	16.7	416	1	TR16_CHICK	P18519	gallus gall
143	5	16.7	320	1	BIRA_SALTU	P37416	salmonella	216	5	16.7	417	1	SAHH_SULSO	P50252	bulfiolobus
144	5	16.7	321	1	BIRA_ECOLI	P06709	escherichia	217	5	16.7	417	1	TR16_MOUSE	Q920u1	mus muscu
145	5	16.7	322	1	YVBF_ECOLI	P77757	escherichia	218	5	16.7	418	1	EP1G_ORYSA	Q92r17	oryza sativ
146	5	16.7	324	1	GLXA_RHIME	087389	rhizobium m	219	5	16.7	419	1	GLPB_ECOLI	P13033	escherichia
147	5	16.7	325	1	YRBG_ECOLI	P43394	escherichia	220	5	16.7	423	1	TIG_BACSU	P80638	bacillus su
148	5	16.7	326	1	MENC_MYCTU	006419	mycobacteri	221	5	16.7	424	1	BM10_HUMAN	Q95359	homo sapien
149	5	16.7	330	1	PG11_ARATH	Q9m5j9	arabidopsis	222	5	16.7	424	1	CSP_PLAFT	P13814	plasmogium
150	5	16.7	330	1	PG12_ARATH	Q9m5j8	arabidopsis	223	5	16.7	425	1	K2C1_XENLA	P26171	rhodobacter
151	5	16.7	331	1	GALR_STRTR	Q9zb11	streptococc	224	5	16.7	425	1	TR16_RAT	Q9k8f3	anabaena sp
152	5	16.7	333	1	PAP2_VACCC	P21033	vaccinia vi	225	5	16.7	427	1	TIG_LACLA	P48077	cyanothora
153	5	16.7	333	1	PAP2_VACCV	P07617	vaccinia vi	226	5	16.7	427	1	TR16_HUMAN	P08138	homo sapien
154	5	16.7	333	1	PAP2_VARY	P33052	variola vir	227	5	16.7	428	1	APG2_METUA	P60336	methanococc
155	5	16.7	337	1	AL13_SCHPO	013953	schizosacch	228	5	16.7	428	1	BCH2_RHOCA	P26171	rhodobacter
156	5	16.7	338	1	GPDA_STRPN	Q97n61	streptococc	229	5	16.7	428	1	HEM1_ANASP	Q08393	anabaena sp
157	5	16.7	343	1	LICH_ACICA	Q43961	actinobact	230	5	16.7	431	1	TIG_BACHD	Q9k8f3	bacillus ha
158	5	16.7	344	1	MBHS_AZOCB	P13190	azotobacter	231	5	16.7	432	1	HEM1_CYPAP	P48077	cyanothora
159	5	16.7	346	1	ADH_MYCTU	P131975	mycobacteri	232	5	16.7	432	1	YRKQ_BACSU	P54444	bacillus su
160	5	16.7	347	1	ID12_LACLA	Q9c1f5	lactococcus	233	5	16.7	433	1	MTM1_YEAST	P35158	saccharomyc
161	5	16.7	348	1	NTRB_PROVU	P28788	proteus vul	234	5	16.7	435	1	HEM1_LISMO	Q8y6x4	listeria mo
162	5	16.7	349	1	NTRB_ECOLI	P06712	escherichia	235	5	16.7	437	1	HEM1_PAEWA	Q69108	paenibacilli
163	5	16.7	349	1	NTRB_KLEPN	P06218	klebsiella	236	5	16.7	439	1	NMT1_PSEAE	Q97r33	pseudomonas
164	5	16.7	349	1	NTRB_GALTU	P41788	salmonella	237	5	16.7	439	1	YD75_MYCTU	P17803	mycobacteri
165	5	16.7	349	1	US30_HCMVA	P09706	human cytom	238	5	16.7	443	1	SOX3_HUMAN	P41225	homo sapien
166	5	16.7	350	1	POT2_HAENI	P44731	haemophilus	239	5	16.7	444	1	C120_SYNY3	Q59990	synecocyst
167	5	16.7	350	1	Y098_SYNY3	Q55880	synecocyst	240	5	16.7	445	1	DCDA_CONGL	Q02220	saccharomyc
168	5	16.7	351	1	CBIG_SALTU	Q05631	salmonella	241	5	16.7	447	1	YKYS_YEAST	Q02220	saccharomyc
169	5	16.7	351	1	ID12_RHITO	Q98915	rhizobium 1	242	5	16.7	448	1	XANA_XANCP	P29955	xanthomonas
170	5	16.7	352	1	EGSA_THENC	Q9h1j6	thermoplas	243	5	16.7	448	1	YB00_METUA	Q58500	methanococc
171	5	16.7	352	1	RECA_CLOPE	P94666	clostridium	244	5	16.7	451	1	PTK6_HUMAN	Q13882	homo sapien
172	5	16.7	352	1	VATC_DEIRA	Q97wh0	delnoccocus	245	5	16.7	452	1	HEMF_RHOSH	P33770	rhodobacter
173	5	16.7	353	1	DRN2_MOUSE	P56542	mus muscu	246	5	16.7	452	1	HEMN_RHOSH	P95651	rhodobacter
174	5	16.7	356	1	AROB_CLOAB	Q97kms	clostridium	247	5	16.7	452	1	SELA_AQUAE	Q67140	aquifex aeo
175	5	16.7	356	1	SMRI_PODAN	Q08142	podopora a	248	5	16.7	457	1	PVAL_MOUSE	P28650	mus muscu
176	5	16.7	358	1	MBHS_AZOVI	P21950	azotobacter	249	5	16.7	458	1	NU4M_STRCA	Q21406	struthio ca
177	5	16.7	360	1	MBHS_RHILV	P18637	rhizobium 1	250	5	16.7	459	1	NU4M_CHICK	P18939	gallus gall
178	5	16.7	360	1	POT1_HAENI	P43168	haemophilus	251	5	16.7	459	1	NU4M_DASNO	Q21334	dasyus nov
179	5	16.7	360	1	VP3_ARMV	P24820	arabid msa	252	5	16.7	459	1	NU4M_MOUSE	P03911	mus muscu

253	5	16.7	459	1	NU4M_POIOR	Q95917 polypeternus	326	5	16.7	560	1	YML1_ARATH	O22752 arabidopsis
254	5	16.7	459	1	NU4M_RABIT	O79436 oryctolagus	327	5	16.7	581	1	KAPP_ARATH	P46014 arabidopsis
255	5	16.7	459	1	NU4M_RAT	P05508 rattus norv	328	5	16.7	583	1	FRDA_MYCTU	O10760 mycobacteri
256	5	16.7	460	1	NU4M_SCYCA	O79410 scyllorhinu	329	5	16.7	599	1	CENB_HUMAN	P07139 homo sapien
257	5	16.7	460	1	NU4M_SQUAC	O92454 squallus aca	330	5	16.7	599	1	CENB_MOUSE	P27790 mus musculu
258	5	16.7	461	1	NU4M_XENLA	P03912 xenopus lae	331	5	16.7	606	1	CENB_CRIGR	P48998 cricetus
259	5	16.7	462	1	YMO1_YEAST	Q04461 saccharomyc	332	5	16.7	606	1	Y4BO_RHISN	P55382 rhizobium s
260	5	16.7	463	1	SYS_AERPE	Q9yag3 aeropyrum p	333	5	16.7	621	1	FOR_THETI	O56303 thermococcu
261	5	16.7	464	1	IRLS_BURPS	O31396 burkholderi	334	5	16.7	625	1	BGAL_LACSK	Q48846 lactobacill
262	5	16.7	465	1	BGLC_RHIME	O92497 rhizobium m	335	5	16.7	626	1	GIDA_CLOAB	O97893 clostridium
263	5	16.7	466	1	SERA_SCHPO	P81228 eschiosacch	336	5	16.7	627	1	GIGB_BACSU	P39118 bacillus su
264	5	16.7	468	1	LIP2_RAT	P54318 rattus norv	337	5	16.7	628	1	BGAL_LACAC	O07664 lactobacill
265	5	16.7	469	1	GATB_THETH	Q91cx2 thermus the	338	5	16.7	628	1	LU_HUMAN	P50855 homo sapien
266	5	16.7	469	1	VL2_BPVI	P03109 bovine papi	339	5	16.7	629	1	GIDA_XYLFA	O9pbd4 xyliella fas
267	5	16.7	471	1	CA34_BOVIN	P08094 bos taurus	340	5	16.7	630	1	GIDA_CLOPE	O8xh11 clostridium
268	5	16.7	471	1	TIG_SYNY3	O55511 synechocyst	341	5	16.7	637	1	VATI_THEAC	O9hmt1 thermoplasm
269	5	16.7	473	1	RUM4_RHOGC	O91p88 rhodocyclu	342	5	16.7	640	1	SP10_YEAST	P31528 saccharomyc
270	5	16.7	475	1	GUNA_CLOCE	P17901 clostridium	343	5	16.7	645	1	SPD_BACSU	O03524 bacillus su
271	5	16.7	479	1	MP1P_DROME	P20483 drosophila	344	5	16.7	649	1	HEXB_STRPN	P14160 streptococc
272	5	16.7	480	1	GLTD_AZOBH	O05756 azospirillu	345	5	16.7	656	1	REP_BUCAP	O51889 buchiera ap
273	5	16.7	482	1	RNF9_HUMAN	Q9udv6 homo sapien	346	5	16.7	658	1	REP_BUCAP	O51889 buchiera ap
274	5	16.7	483	1	GATB_RICPR	O9ze11 rickettsia	347	5	16.7	660	1	MUTL_LACLA	O99xk7 streptococc
275	5	16.7	484	1	SCRB_VIBAL	P13394 vibrio algi	348	5	16.7	668	1	YGL3_YEAST	P53135 saccharomyc
276	5	16.7	489	1	PSD3_DAUCA	Q06364 daucus caro	349	5	16.7	675	1	CIBR_YEAST	P57031 paenibacill
277	5	16.7	489	1	RNF9_MOUSE	Q9wuh3 mus musculu	350	5	16.7	679	1	YHCB_YEAST	P38738 saccharomyc
278	5	16.7	491	1	GLV2_SYNY3	P72623 synechocyst	351	5	16.7	681	1	GFA2_HUMAN	O94808 homo sapien
279	5	16.7	491	1	ILVC_PASMU	O9clt1 pasteurilla	352	5	16.7	681	1	GFA2_MOUSE	O94808 mus musculu
280	5	16.7	492	1	SES3_HUMAN	P58005 homo sapien	353	5	16.7	684	1	Y492_MYCTU	O11157 mycobacteri
281	5	16.7	492	1	SES3_MOUSE	O9cyd7 mus musculu	354	5	16.7	688	1	CHLE_CHARE	P36447 chlamydomon
282	5	16.7	493	1	UGDH_MOUSE	O70475 mus musculu	355	5	16.7	688	1	YB9F_YEAST	P38437 saccharomyc
283	5	16.7	493	1	UGDH_RAT	O70199 rattus norv	356	5	16.7	690	1	HELS_METH	O26901 methanobact
284	5	16.7	494	1	UGDH_BOVIN	P12378 bos taurus	357	5	16.7	703	1	PPK_STRGR	O9ueh8 streptomyc
285	5	16.7	494	1	UGDH_HUMAN	O60701 homo sapien	358	5	16.7	705	1	DPO2_YEAST	P38121 saccharomyc
286	5	16.7	506	1	YCA6_GUTTH	O78439 guillardia	359	5	16.7	707	1	HS88_NEUCR	O74225 neurospora
287	5	16.7	507	1	SXA2_SCHPO	P32825 eschiosacch	360	5	16.7	712	1	DNL4_RHOMR	P49421 rhodothermu
288	5	16.7	510	1	G6PD_ASPNG	P48826 aspergillus	361	5	16.7	715	1	HELS_PYRAB	O9v089 pyrococcus
289	5	16.7	511	1	G6PD_EMENT	P41764 emericella	362	5	16.7	721	1	HEL5_PYRUV	O73946 pyrococcus
290	5	16.7	515	1	CP12_HUMAN	P05177 homo sapien	363	5	16.7	721	1	RNR_UREPA	O9p786 ureaplasma
291	5	16.7	516	1	DHCR_HUMAN	O15392 homo sapien	364	5	16.7	728	1	YJ85_YEAST	P51954 saccharomyc
292	5	16.7	521	1	VGLC_HSVBC	P14378 bovine hearp	365	5	16.7	731	1	TOPI_TREPA	O83409 streptococ
293	5	16.7	525	1	DIMH_CABEL	O17399 caenorhabdi	366	5	16.7	746	1	PPK_STRCO	O9kz46 streptococ
294	5	16.7	528	1	CTK1_YEAST	Q03957 saccharomyc	367	5	16.7	754	1	RRL1_INCUJ	P19703 influenza c
295	5	16.7	528	1	PRPR_ECOLI	P77743 escherichia	368	5	16.7	756	1	EFER_HUMAN	O59154 homo sapien
296	5	16.7	531	1	CE27_HUMAN	Q02318 h cytochrom	369	5	16.7	761	1	TOPI_MERJA	O9hy58 pseudomonas
297	5	16.7	531	1	FXM1_SCHPO	O09752 eschiosacch	370	5	16.7	765	1	YK07_YEAST	P53866 saccharomyc
298	5	16.7	532	1	IPA7_SHIFL	P18014 shigella fl	371	5	16.7	767	1	YNM4_YEAST	P53866 saccharomyc
299	5	16.7	535	1	CP27_RABIT	P17177 o cytochrom	372	5	16.7	768	1	KGP1_DROME	O03042 drosophila
300	5	16.7	537	1	CH61_MYCLE	P37578 mycobacteri	373	5	16.7	772	1	SYFB_UREPA	O9pgq3 ureaplasma
301	5	16.7	538	1	YAJ8_SCHPO	Q09908 eschiosacch	374	5	16.7	774	1	NEK1_MOUSE	P51954 mus musculu
302	5	16.7	541	1	PRPR_SALTY	P37702 arabidopsis	375	5	16.7	774	1	MNEV_HUMAN	O9hy58 pseudomonas
303	5	16.7	541	1	MYR0_ARATH	P74839 salmonella	376	5	16.7	781	1	YHY2_YEAST	P38890 saccharomyc
304	5	16.7	543	1	RRP3_YEAST	P29092 sinapis alb	377	5	16.7	785	1	TRK1_HCMVA	P09635 human cytom
305	5	16.7	544	1	MYR3_SINAT	P53003 saccharopol	378	5	16.7	788	1	LY14_YEAST	P40971 saccharomyc
306	5	16.7	546	1	PCCB_SACER	O28668 archaeoglob	379	5	16.7	790	1	KDGB_DROME	O01583 drosophila
307	5	16.7	546	1	TRCD_ARCFU	P06683 mus musculu	380	5	16.7	791	1	SYFB_RICCN	O92138 rickettsia
308	5	16.7	548	1	CO9_MOUSE	O00326 brasica na	381	5	16.7	818	1	YX07_CAEEL	O11114 caenorhabdi
309	5	16.7	550	1	YMA0_YEAST	Q02322 saccharomyc	382	5	16.7	819	1	AKH1_SERMA	B27725 serratia ma
310	5	16.7	551	1	AGLA_RHIME	Q92318 rhizobium m	383	5	16.7	825	1	XEP_BIFAN	O9aem9 bifidobacte
311	5	16.7	551	1	ILVD_PYRAB	Q9uz02 pyrococcus	384	5	16.7	830	1	RPOD_EUGGR	P23511 euglena gira
312	5	16.7	553	1	IAGA_SALTI	P43016 salmonella	385	5	16.7	831	1	NAH3_RAT	P26433 rattus norv
313	5	16.7	553	1	IAGA_SALTY	P43015 salmonella	386	5	16.7	832	1	NAH3_RABIT	P26432 oryctolagus
314	5	16.7	553	1	ILVD_METUA	O58672 methanococc	387	5	16.7	832	1	HSE_YEAST	P10961 saccharomyc
315	5	16.7	553	1	SYFA_TREPA	O83938 treponema p	388	5	16.7	834	1	NAH1_HUMAN	P48764 homo sapien
316	5	16.7	558	1	LCB1_YEAST	P25045 saccharomyc	389	5	16.7	836	1	MCBL_SFYKA	P25950 shope fibro
317	5	16.7	561	1	CEP1_USITWA	P49602 ustilago ma	390	5	16.7	838	1	PAS_MOUSE	P19056 mus musculu
318	5	16.7	562	1	EXG2_YEAST	P52911 saccharomyc	391	5	16.7	839	1	NAH3_DIDMA	O28382 didelphis m
319	5	16.7	562	1	SIS2_YEAST	P36024 saccharomyc	392	5	16.7	840	1	YHT1_YEAST	P38835 saccharomyc
320	5	16.7	563	1	LIP2_GEOON	P22394 geotrichum	393	5	16.7	841	1	IRG1_HCMVA	O42814 aspergillus
321	5	16.7	565	1	PRIM_THEMA	O9x1g3 thermotoga	394	5	16.7	846	1	ENV_HVILB	P092715 human cytom
322	5	16.7	565	1	NODU_BRJJA	P26027 bradyrhizob	395	5	16.7	851	1	MUTS_STRPY	P04562 streptococc
323	5	16.7	569	1	IF37_CAEEL	P30642 caenorhabdi	396	5	16.7	851	1	ENV_HVILMF	O99x18 human immun
324	5	16.7	570	1	POF3_SCHPO	O74991 schizosacch	397	5	16.7	853	1	ENV_HVILMF	P19551 human immun
325	5	16.7	577	1			398	5	16.7				

399	5	16.7	855	1	ENV_HV10Y	P20888 human immun	472	5	16.7	1400	1	RON_HUMAN	O04912 homo sapien
400	5	16.7	856	1	ENV_HV1B1	P033375 human immun	473	5	16.7	1411	1	YM42_YEAST	O03214 saccharomyc
401	5	16.7	856	1	ENV_HV1H2	P04578 human immun	474	5	16.7	1433	1	YGLM_BUNYV	P04505 bunywerera
402	5	16.7	856	1	ENV_HV1H3	P04624 human immun	475	5	16.7	1440	1	SYEP_HUMAN	P07814 homo sapien
403	5	16.7	856	1	ENV_HV1LH	P07626 human immun	476	5	16.7	1447	1	TOP2_DROME	P15348 drosophila
404	5	16.7	856	1	ENV_HV1LV	P03376 human immun	477	5	16.7	1474	1	A2MG_HUMAN	P10123 homo sapien
405	5	16.7	861	1	ENV_HV1LR	P03377 human immun	478	5	16.7	1482	1	P2P_HUMAN	P20742 homo sapien
406	5	16.7	861	1	SYL_HAE1R	P43827 haemophilus	479	5	16.7	1489	1	YGP0_YEAST	P53115 saccharomyc
407	5	16.7	865	1	ENV_HV1RH	P04579 human immun	480	5	16.7	1520	1	TOP2_CAEEL	O23670 caenorhabdi
408	5	16.7	870	1	SYV_CAMDE	O99pe4 campylobact	481	5	16.7	1526	1	TP2A_CRIGR	P11515 cricetus
409	5	16.7	878	1	SYA_BUCAT	P57483 buchnera ap	482	5	16.7	1526	1	TP2A_RAT	P41516 rattus norv
410	5	16.7	892	1	TNPA_STRFR	P20189 streptomyc	483	5	16.7	1528	1	TP2A_MOUSE	O01320 mus musculu
411	5	16.7	895	1	PMAI_CANAL	P28877 candida alb	484	5	16.7	1531	1	TP2A_HUMAN	P11388 homo sapien
412	5	16.7	900	1	LOXC_ARATH	P38418 arabidopsis	485	5	16.7	1533	1	TOP2_PIG	O46374 sus scrofa
413	5	16.7	900	1	MUTS_TREPA	O83348 treponema p	486	5	16.7	1547	1	TOP2_BOWMO	O16140 bombyx mori
414	5	16.7	904	1	DPOL_MYCTU	O07700 mycobacteri	487	5	16.7	1670	1	CA34_HUMAN	O01955 homo sapien
415	5	16.7	910	1	SYL_NEINA	O97w39 neisseria m	488	5	16.7	1695	1	KEP1A_MOUSE	O01371 mus musculu
416	5	16.7	911	1	DPOL_MYCLE	P46835 mycobacteri	489	5	16.7	1758	1	CA24_CAEEL	P17140 caenorhabdi
417	5	16.7	911	1	ITR1_HUMAN	P19827 homo sapien	490	5	16.7	1763	1	CA24_ASCSU	P27353 ascatis buu
418	5	16.7	919	1	PWP2_HUMAN	O15269 homo sapien	491	5	16.7	1822	1	ITB4_HUMAN	P16144 homo sapien
419	5	16.7	925	1	GLHR_ANTIPL	P35409 anthopleura	492	5	16.7	1829	1	RM1_MOUSE	O70472 mus musculu
420	5	16.7	928	1	KKRI_YEAST	P36003 saccharomyc	493	5	16.7	1829	1	Y296_HUMAN	O15015 homo sapien
421	5	16.7	935	1	ODOI_HAEIN	P45303 haemophilus	494	5	16.7	1888	1	YDT2_SCHPO	O14287 schizosacch
422	5	16.7	936	1	CDAS_HUMAN	O957h7 homo sapien	495	5	16.7	1906	1	KML5_CHICK	P11789 gallus gall
423	5	16.7	936	1	MSH4_HUMAN	O15457 homo sapien	496	5	16.7	1916	1	RIF1_YEAST	P29539 saccharomyc
424	5	16.7	951	1	SYV_ECOLI	P07118 escherichia	497	5	16.7	1980	1	MY9B_RAT	O63358 rattus norv
425	5	16.7	962	1	PTRA_ECOLI	P05458 escherichia	498	5	16.7	2052	1	UBR9_SCHPO	O13771 schizosacch
426	5	16.7	965	1	PTO9_YEAST	P32552 saccharomyc	499	5	16.7	2114	1	MY9B_MOUSE	O99706 mus musculu
427	5	16.7	988	1	SY1_STNY3	P73505 synechocyst	500	5	16.7	2150	1	SDC3_CAEEL	P34706 caenorhabdi
428	5	16.7	1015	1	PPOL_BOVIN	P18493 bos taurus	501	5	16.7	2158	1	MY9B_HUMAN	O13459 homo sapien
429	5	16.7	1036	1	YG35_YEAST	P53273 saccharomyc	502	5	16.7	2210	1	RRPL_EBOSM	O66802 ebola virus
430	5	16.7	1038	1	ITR4_HUMAN	P16162 homo sapien	503	5	16.7	2226	1	POLG_HPAV2	P26580 hepatitis a
431	5	16.7	1038	1	YKD3_YEAST	P360691 saccharomyc	504	5	16.7	2226	1	POLG_HPAV4	P26581 hepatitis a
432	5	16.7	1039	1	ITR4_MOUSE	O00651 mus musculu	505	5	16.7	2226	1	POLG_HPAV8	P26582 hepatitis a
433	5	16.7	1050	1	BU1B_HUMAN	O06566 homo sapien	506	5	16.7	2227	1	POLG_HPAVH	P08617 hepatitis a
434	5	16.7	1057	1	VP2_AHSV3	O89508 african hor	507	5	16.7	2227	1	POLG_HPAVL	P06441 hepatitis a
435	5	16.7	1058	1	CARB_LACPL	P77886 lactobacilli	508	5	16.7	2227	1	POLG_HPAVM	P13901 hepatitis a
436	5	16.7	1070	1	DNLI_XENLA	P51592 xenopus lae	509	5	16.7	2230	1	POLG_HPAV2	P14553 simian hepa
437	5	16.7	1074	1	SM5A_HUMAN	O13591 homo sapien	510	5	16.7	2261	1	RRPL_MUMPM	P30929 simian virus
438	5	16.7	1075	1	PST2_SCHPO	O13919 schizosacch	511	5	16.7	2298	1	CU05_HUMAN	O99735 homo sapien
439	5	16.7	1077	1	SM5A_MOUSE	O62217 mus musculu	512	5	16.7	2326	1	PGG2_RAT	O00657 rattus norv
440	5	16.7	1078	1	S24A_HUMAN	O95486 homo sapien	513	5	16.7	2358	1	YEBJ_ECOLI	P76347 escherichia
441	5	16.7	1087	1	PGDS_XENLA	P26619 xenopus lae	514	5	16.7	2504	1	FAS_HUMAN	P49375 homo sapien
442	5	16.7	1088	1	RRPO_ROTBR	P17468 bovine rota	515	5	16.7	2505	1	PAS_RAT	P12785 rattus norv
443	5	16.7	1088	1	RRPO_ROTBR	P12615 bovine rota	516	5	16.7	2524	1	NOTC_XENLA	P21783 xenopus lae
444	5	16.7	1088	1	RRPO_ROTBR	P17699 porcine rot	517	5	16.7	2555	1	PPS3_BACSU	P39647 bacillus su
445	5	16.7	1088	1	RRPO_ROTBR	P22678 simian 11 r	518	5	16.7	2660	1	YEBJ_ECOS7	O8x877 escherichia
446	5	16.7	1116	1	VP2_RDVF	O98632 rice dwarf	519	5	16.7	2920	1	CLR2_MOUSE	O970n0 mus musculu
447	5	16.7	1116	1	YK54_AQUAE	O67838 aquilex aeo	520	5	16.7	2923	1	CLR2_HUMAN	O9hcu4 homo sapien
448	5	16.7	1131	1	AC15_MOUSE	P35601 mus musculu	521	5	16.7	3014	1	CLR1_HUMAN	O9ny66 homo sapien
449	5	16.7	1133	1	VGLM_HANTB	P28728 hantaan vir	522	5	16.7	3034	1	CLR1_MOUSE	O35161 mus musculu
450	5	16.7	1133	1	VGLM_SEOUB	P13455 beoul vitus	523	5	16.7	3163	1	POLG_TUVVO	O20597 t genome po
451	5	16.7	1133	1	VGLM_SEOUB	P17880 beoul vitus	524	5	16.7	3164	1	POLG_TUVVU	B89509 e genome po
452	5	16.7	1134	1	VGLM_SEOUR	P28729 beoul vitus	525	5	16.7	3209	1	RELN_CHICK	O93574 gallus gall
453	5	16.7	1142	1	VGLM_SEOUR	O02391 gallus gall	526	5	16.7	3317	1	CADN_RAT	P58363 rattus norv
454	5	16.7	1148	1	VP2_RDVO	O55519 rice dwarf	527	5	16.7	3321	1	PCN2_HUMAN	O95613 homo sapien
455	5	16.7	1160	1	GLGI_CRIGR	O9z1e9 cricetus	528	5	16.7	3354	1	CADN_HUMAN	O9h2t1 homo sapien
456	5	16.7	1161	1	POL_SFVL	P23074 simian foam	529	5	16.7	3354	1	CADN_MOUSE	O99p24 mus musculu
457	5	16.7	1169	1	EX5B_BORBU	O51578 borrelia bu	530	5	16.7	3358	1	PGCV_MOUSE	O62059 mus musculu
458	5	16.7	1171	1	GLGI_RAT	O62638 rattus norv	531	5	16.7	3579	1	STAN_DROME	O62059 mus musculu
459	5	16.7	1172	1	CUI4_SCHPO	P41003 schizosacch	532	5	16.7	3587	1	SRF2_BACSU	O9v578 drosophila
460	5	16.7	1173	1	GIGA_ORYSA	O9aw17 oryza sativ	533	5	16.7	4344	1	DYHC_EMENT	O04747 bacillus su
461	5	16.7	1174	1	DP3A_YERPE	O68717 yersinia pe	534	5	16.7	4349	1	FAT2_HUMAN	O9ny68 homo sapien
462	5	16.7	1174	1	KCRF_STRPU	P18294 strongyloce	535	5	16.7	4351	1	FAT2_RAT	O88277 rattus norv
463	5	16.7	1175	1	GLGI_MOUSE	O61543 mus musculu	536	5	16.7	6486	1	TYCC_BACBR	O30409 b tyrocidin
464	5	16.7	1179	1	GLGI_HUMAN	O92896 homo sapien	537	5	16.7	14	1	UCO4_MAIZE	P80610 zea mays (m
465	5	16.7	1211	1	MI0L_HUMAN	O9bxc6 homo sapien	538	5	16.7	35	1	CDK6_MOUSE	P80021 sus scrofa
466	5	16.7	1225	1	KP4A_CHICK	O90640 gallus gall	539	5	16.7	35	1	NPF_MONEX	O64261 mus musculu
467	5	16.7	1230	1	SR20_CANAL	O9z212 candida alb	540	5	16.7	39	1	LHB3_RHOAC	P1967 rhodopsin ex
468	5	16.7	1268	1	624B_HUMAN	O95487 homo sapien	541	5	16.7	41	1	LHB3_RHOAC	P26780 rhodopsin pseudo
469	5	16.7	1276	1	PMP6_CHLPN	O92889 chlamydia p	542	5	16.7	41	1	S108_BOVIN	P28782 bos taurus
470	5	16.7	1298	1	YTFN_HAEIN	O57523 haemophilus	543	5	16.7	41	1	LCA_MACGI	P19122 macropus gi
471	5	16.7	1377	1	CID_DROME	P19538 drosophila	544	5	16.7	42	1	LCA_MACGI	P19122 macropus gi

545	4	13.3	46	1	OPT_BOVIN	P58874	bos taurus	618	4	13.3	88	1	CX9A	CONTE	O99U58	conus texti
546	4	13.3	47	1	YOBF_ECOLI	P76265	escherichia	619	4	13.3	88	1	VL1Q	HELIP	O25964	helicobacte
547	4	13.3	50	1	COAB_BP22	P03618	bacterioph	620	4	13.3	88	1	VL1Q	VACCC	P10077	vaccinia vi
548	4	13.3	52	1	ATP8_PENMO	O9mgd7	penaeus mon	621	4	13.3	88	1	VK03	VACCC	P20669	vaccinia vi
549	4	13.3	52	1	LECA_VICSA	P16350	vicia sativ	622	4	13.3	88	1	VK03	VACCV	P18378	vaccinia vi
550	4	13.3	53	1	LECI_LATOC	P12306	lactyrus oc	623	4	13.3	89	1	FL1Q	ECOLI	P33134	escherichia
551	4	13.3	53	1	LECI_LATOC	P12307	lactyrus oc	624	4	13.3	89	1	FL1Q	ERWCA	P34201	erwinia car
552	4	13.3	53	1	LECA_LATAP	P07441	lactyrus ap	625	4	13.3	89	1	FL1Q	SALTU	P54701	salmonella
553	4	13.3	53	1	LECA_LATAP	P07442	lactyrus ar	626	4	13.3	89	1	GON3	PORNO	P51922	portichthys
554	4	13.3	53	1	LECA_VICCR	P02868	vicia cracc	627	4	13.3	89	1	YAL1	BACLI	O99162	bacillus li
555	4	13.3	54	1	LECA_LATCI	P07440	lactyrus ci	628	4	13.3	90	1	AF1Q	HUMAN	O13015	homo sapien
556	4	13.3	54	1	LECA_LATCI	P07443	lactyrus hi	629	4	13.3	90	1	AF1Q	MOUSE	P29783	mus musculu
557	4	13.3	54	1	LECA_LATOD	P02869	lactyrus od	630	4	13.3	90	1	GON3	DICLA	O91a09	diceritarch
558	4	13.3	54	1	LECA_LATSI	P07444	lactyrus ti	631	4	13.3	90	1	GON3	PAGMA	P51921	pagrus majo
559	4	13.3	55	1	LECA_LATSA	P12308	lactyrus sa	632	4	13.3	90	1	GON3	SPAAU	P51923	sparus majo
560	4	13.3	57	1	YCS7_HAEIN	P44143	haemophilus	633	4	13.3	90	1	IFI1	MYCSP	P38037	mycoplasma
561	4	13.3	58	1	YCS8_BPPE3	P03629	bacterioph	634	4	13.3	90	1	PAK2	SVYV3	P74554	mycobocyst
562	4	13.3	59	1	RLJ30_STANM	O06444	staphylococ	635	4	13.3	90	1	RPOL	SULAC	P46217	sulfolobus
563	4	13.3	59	1	RLJ35_MYCCE	P47439	mycoplasma	636	4	13.3	90	1	RPOZ	STRCO	O3Kx61	etereptomyce
564	4	13.3	59	1	RLJ35_MYCCE	P75447	mycobacter	637	4	13.3	90	1	Z600	DROME	P22469	drosophila
565	4	13.3	60	1	YRH1_AZOV1	O44557	azotobacter	638	4	13.3	91	1	INAT	ECOLI	P19767	escherichia
566	4	13.3	64	1	YCS3_ARCFU	O29015	archaeoglob	639	4	13.3	91	1	INSA	SHIFL	P19763	shigella fl
567	4	13.3	66	1	ATNG_HUMAN	P54710	homo sapien	640	4	13.3	91	1	Y97	ADRO7	P05668	human adeno
568	4	13.3	66	1	COPE_HBUPF	O32620	helicobacte	641	4	13.3	92	1	Y86	MERTH	O26972	methanobact
569	4	13.3	66	1	KED2_ECOLI	P13967	escherichia	642	4	13.3	93	1	LSM5	YEAST	P40089	saccharomyc
570	4	13.3	66	1	SECE_ARCFU	O29714	archaeoglob	643	4	13.3	93	1	S108	HUMAN	P05109	homo sapien
571	4	13.3	66	1	Y13G_BP74	P39500	bacterioph	644	4	13.3	93	1	Y435	MERTU	O57877	methanococc
572	4	13.3	67	1	RROZ_LISIN	O92a12	listeria in	645	4	13.3	93	1	YCBI	PSRDE	P29943	pseudomonas
573	4	13.3	67	1	RROZ_LISMO	O92673	listeria mo	646	4	13.3	94	1	GATC	AQURAE	O67994	quatrifex aeo
574	4	13.3	67	1	YANI_YEAST	P39561	saccharomyc	647	4	13.3	94	1	RPCI	BP434	P16117	bacterioph
575	4	13.3	70	1	CSPJ_SALTI	P58726	salmonella	648	4	13.3	95	1	FXV6	HUMAN	O9H0q3	homo sapien
576	4	13.3	70	1	PSY2_FRBDI	P14878	fremyella d	649	4	13.3	95	1	NOLP	RHILP	P33717	rhizobium 1
577	4	13.3	70	1	RROZ_CLOPE	O841x9	clostridium	650	4	13.3	95	1	RAG1	ORYSA	O01884	oryza sativ
578	4	13.3	71	1	Y647_MERTU	O58063	methanococc	651	4	13.3	95	1	RS14	CARRU	O9A14	carsonella
579	4	13.3	72	1	CHH_ERORO	P58845	procambatus	652	4	13.3	95	1	YBUC	ECOLI	P46119	escherichia
580	4	13.3	72	1	HPIT_ECTVA	P38941	ectochlorho	653	4	13.3	96	1	CH10	AMOPS	P26005	amoeba prot
581	4	13.3	72	1	RPON_THEVO	O979K0	thermoplasm	654	4	13.3	96	1	CH10	CHRYI	P31295	chromatium
582	4	13.3	72	1	VB11_VACCV	O01229	vaccinia vi	655	4	13.3	96	1	CH10	LEGMI	P61615	legionella
583	4	13.3	73	1	COAB_BPFD	P03617	bacterioph	656	4	13.3	96	1	CH10	LEGPN	P66879	legionella
584	4	13.3	73	1	SMS2_PLAVE	P21780	platichtyus	657	4	13.3	97	1	Y4D6	STRCO	P37977	streptomyces
585	4	13.3	73	1	UH11_H8V7J	P52358	human herpes	658	4	13.3	97	1	YCIS	HAEIN	P44129	haemophilus
586	4	13.3	73	1	Y43_BPRI8	P18243	bacterioph	659	4	13.3	98	1	ELIA	PHYCP	P15571	phytophthor
587	4	13.3	74	1	ATPL_RICCN	O925j1	rickettsia	660	4	13.3	98	1	ELIA	PHYME	P35698	plytrophthor
588	4	13.3	74	1	MIH_PROBO	O10987	procambatus	661	4	13.3	98	1	NULM	SIGHI	O21567	sigmodon hi
589	4	13.3	74	1	SMS2_MYOSC	P09876	tyrocephala	662	4	13.3	99	1	BXAL	SAMCY	P33718	samia cyth
590	4	13.3	74	1	V777_TBPEA	O83756	treponema p	663	4	13.3	99	1	YG42	CAMTE	O9PM44	campylobact
591	4	13.3	75	1	GLUC_AMICA	P33528	ania calva	664	4	13.3	99	1	YO10	BEHPI	P51712	bacterioph
592	4	13.3	75	1	WCHB_ECOLI	O9ym53	escherichia	665	4	13.3	100	1	BXAX	SAMCY	P33749	samia cyth
593	4	13.3	75	1	VC12_SPVKA	P32221	swinepox vi	666	4	13.3	100	1	CHLB	PLRSC	P37854	pleurozium
594	4	13.3	75	1	YODD_ECOLI	P76328	escherichia	667	4	13.3	100	1	CHLB	POLCU	P37852	polycrithum
595	4	13.3	75	1	YRK1_BACSU	P54436	bacillus su	668	4	13.3	100	1	ES6Y	MYCLE	O49945	mycobacteri
596	4	13.3	77	1	VG43_BPMU5	O05255	mycobacteri	669	4	13.3	100	1	VE7	HPV22	O92686	rickettsia
597	4	13.3	77	1	YDH1_PLAPS	P14587	plasmodium	670	4	13.3	100	1	VE7	HPV22	P50760	human papil
598	4	13.3	79	1	SPD1_ARABI	P46802	araneus bic	671	4	13.3	100	1	Y953	MERTU	O98303	methanococc
599	4	13.3	80	1	IFI_DEIRA	O9ysk1	deinococcus	672	4	13.3	100	1	YISI	SHISO	P16939	shigella so
600	4	13.3	80	1	PSAC_SKECO	O96804	skelotonema	673	4	13.3	101	1	DMT1	ALIMI	O9Pue0	alligator m
601	4	13.3	81	1	PSAC_ODOSI	P49477	odontella s	674	4	13.3	101	1	NIFU	ANAVA	O53349	anabena va
602	4	13.3	82	1	CZ_OXYNO	P05526	oxytricha n	675	4	13.3	101	1	SMO3	YEAST	P33331	saccharomyc
603	4	13.3	83	1	N19M_BOVIN	O02371	bos taurus	676	4	13.3	101	1	VG7	BPB03	O37867	bacterioph
604	4	13.3	83	1	PGCA_PIG	O29011	sus scrofa	677	4	13.3	101	1	YH65	YEAST	P38831	saccharomyc
605	4	13.3	83	1	PSAK_SYNN	P20453	synechococc	678	4	13.3	101	1	YH65	YEAST	O40481	saccharomyc
606	4	13.3	83	1	PROK_SULAC	P39463	sulfolobus	679	4	13.3	102	1	ANTR	RANCA	P08011	xana catesb
607	4	13.3	84	1	CPPA_NIEGO	P07048	neisseria g	680	4	13.3	102	1	GP4D	CHLMU	O64440	chlamydia m
608	4	13.3	85	1	CYC6_PLEBO	P00117	plectonema	681	4	13.3	102	1	GP4D	CHLPS	O46262	chlamydia p
609	4	13.3	85	1	PSAK_SYNTU	P23318	synechococc	682	4	13.3	102	1	GP4D	CHLIR	P08765	chlamydia t
610	4	13.3	85	1	YPBS_BACSU	P54160	bacillus su	683	4	13.3	102	1	RP5W	PSEPU	P15552	pseudomonas
611	4	13.3	86	1	OXIR_PIG	O97661	sus scrofa	684	4	13.3	102	1	VE7	HPV20	P07078	human papil
612	4	13.3	86	1	PSAK_PORPU	P51370	porphyra pu	685	4	13.3	103	1	ACPH	CLOAB	O97h14	clostridium
613	4	13.3	87	1	FXV4_RAT	O63113	rattus norv	686	4	13.3	103	1	CHLB	ARABE	P37843	araucaria h
614	4	13.3	87	1	PSAK_GUTH	O74444	gulliardia	687	4	13.3	103	1	CHLB	BATTR	P37844	bazzania tr
615	4	13.3	87	1	VP08_BPAPS	O991u0	bacterioph	688	4	13.3	103	1	CHLB	BOUAR	P37845	equisetum a
616	4	13.3	87	1	Y04A_BP74	P07083	bacterioph	689	4	13.3	103	1	CHLB	BOUSC	O32214	equisetum s
617	4	13.3	87	1	YBBD_ECOLI	P30977	escherichia	690	4	13.3	103	1	CHLB	ISOEC	O32450	isoetes ech

691	4	13.3	103	1	CHLB_LYCANA	P37847 lycopodium	764	4	13.3	115	1	HYPA_AQUAE	O67133 aquilex aeo
692	4	13.3	103	1	CHLB_LYCOCO	P37848 lycopodium	765	4	13.3	115	1	RK22_ASTRLO	P34770 aetasia lon
693	4	13.3	103	1	CHLB_METECO	P37849 metasequonia	766	4	13.3	115	1	RL24_SYNY3	P73304 synecocyst
694	4	13.3	103	1	CHLB_NEPX	P37850 nephrolepis	767	4	13.3	115	1	SMS1_PROAN	O97670 protoplenus
695	4	13.3	103	1	CHLB_OSMCL	P37851 osmundia cla	768	4	13.3	115	1	YBR2_YEAST	P28829 saccharomyc
696	4	13.3	103	1	CHLB_SELMO	P37856 selaginella	769	4	13.3	115	1	YD30_HELPY	O25888 helicobacte
697	4	13.3	103	1	CHLB_ZAMFI	P37857 zamia flesch	770	4	13.3	115	1	YL22_CABEL	P24415 caenorhabdi
698	4	13.3	103	1	HE2_HUMAN	O08648 homo sapien	771	4	13.3	116	1	RPBY_ARATH	Q38859 arabidopsis
699	4	13.3	103	1	PRO2_STRPN	O97644 streptococc	772	4	13.3	116	1	RT13_DAVCA	P23209 daucus caro
700	4	13.3	103	1	S112_HUMAN	O96f64 homo sapien	773	4	13.3	116	1	RT13_TOBAC	P05488 nicotiana t
701	4	13.3	103	1	YPA1_LEGPN	P26880 legionella	774	4	13.3	116	1	RT13_WHEAT	P07924 triticum ae
702	4	13.3	103	1	YPC6_CLAPU	P22368 claviceps p	775	4	13.3	116	1	Y828_PYRHO	O58558 pyrococcus
703	4	13.3	104	1	NEUY_LAMFL	P48097 lampetra fl	776	4	13.3	116	1	Y157_AQUAE	O67709 aquilex aeo
704	4	13.3	104	1	RL30_KLULA	P38664 kluyveromyc	777	4	13.3	117	1	RBS1_HYDMR	O59459 hydrogenvi
705	4	13.3	104	1	PRO2_STRPY	P28575 streptococc	778	4	13.3	117	1	RPOZ_IACIA	O59459 lactococcus
706	4	13.3	104	1	THIO_BOVIN	O97680 bos taurus	779	4	13.3	118	1	ELI1_PHYCR	P44802 phytophthor
707	4	13.3	104	1	THIO_CALTA	O96d33 callithrix	780	4	13.3	118	1	KDGL_HAEN	P44424 haemophilus
708	4	13.3	104	1	THIO_CHICK	O08629 gallus gall	781	4	13.3	118	1	PAND_CAUCR	Q96602 caulobacter
709	4	13.3	104	1	THIO_HORSE	O97508 equus caball	782	4	13.3	118	1	VNS2_IATRS	O82729 influenza a
710	4	13.3	104	1	THIO_HUMAN	P10599 homo sapien	783	4	13.3	118	1	YD30_HELPY	O92345 helicobacte
711	4	13.3	104	1	THIO_MACMU	P29451 macaca mula	784	4	13.3	118	1	YUSI_BACSU	O32175 bacillus su
712	4	13.3	104	1	THIO_MOUSE	P10639 mus musculus	785	4	13.3	119	1	AMCY_MEREX	P04172 methylolact
713	4	13.3	104	1	THIO_OPFHA	O98cxi ophiophagus	786	4	13.3	119	1	RL19_MYCPN	P75133 mycoplasma
714	4	13.3	104	1	THIO_PIG	P82460 sus scrofa	787	4	13.3	119	1	VATF_HUMAN	O16864 homo sapien
715	4	13.3	104	1	THIO_RABIT	P08628 oryctolagus	788	4	13.3	119	1	VATF_RAT	P50408 rattus norv
716	4	13.3	104	1	THIO_SHEEP	P11232 rattus norv	789	4	13.3	119	1	VP26_HYSEB	P28974 equine hepr
717	4	13.3	104	1	VER7_HPV26	P50413 ovis aries	790	4	13.3	120	1	PAND_RALSO	O8XVU6 ralestonia s
718	4	13.3	104	1	VER7_HPV26	P36824 human papil	791	4	13.3	120	1	RL7A_HALNI	O9XU68 halobacteri
719	4	13.3	104	1	VSH7_DICDI	P13327 diacyosteli	792	4	13.3	120	1	VACL_ECOLI	P45557 escherichia
720	4	13.3	104	1	Y907_HAEN	P44072 haemophilus	793	4	13.3	120	1	YJY8_YEAST	P47091 saccharomyc
721	4	13.3	105	1	N1FW_ANASP	O44149 anabaena sp	794	4	13.3	121	1	FLIO_ECOLI	P22566 escherichia
722	4	13.3	105	1	SMS2_ICTPU	P01172 ictalurus p	795	4	13.3	121	1	LCA_MACRG	P07458 macrocopus ru
723	4	13.3	106	1	PUTX_PSEPU	P00259 pseudomonas	796	4	13.3	121	1	PFDB_MERTH	O26774 methanobact
724	4	13.3	106	1	SECE_HAEN	P43805 haemophilus	797	4	13.3	121	1	RBS_ALVHS	P24682 alvinococh
725	4	13.3	106	1	Y1P1_VIBCH	O9Kk29 vibrio chol	798	4	13.3	121	1	TTTH_CAREL	O21882 caenorhabdi
726	4	13.3	106	1	Y368_METUA	O57814 methanococc	799	4	13.3	122	1	HEX9_ADETI	P04376 lupata aden
727	4	13.3	106	1	Y488_ARCFU	O29762 archaeoglob	800	4	13.3	122	1	S109_BOVIN	P28736 bos taurus
728	4	13.3	107	1	IF1C_MAIZE	P46616 zea mays (m	801	4	13.3	123	1	CRCB_PYRAB	O5V0X2 pyrococcus
729	4	13.3	107	1	IF1C_ORYSA	P13135 oryza sativ	802	4	13.3	123	1	CRCB_PYRAB	O59171 pyrococcus
730	4	13.3	107	1	PPDC_ECOLI	P08372 escherichia	803	4	13.3	123	1	KAD1_RAT	P39069 rattus norv
731	4	13.3	107	1	VNS1_PYM	P28888 pneumonia v	804	4	13.3	123	1	LCA_PAPCY	P12065 papio cynoc
732	4	13.3	107	1	YFHP_HAEN	P46672 haemophilus	805	4	13.3	123	1	LSM6_YEAST	O06406 saccharomyc
733	4	13.3	107	1	YNIU_AZOVI	O44540 azotobacter	806	4	13.3	123	1	NB4M_NEUCR	P42114 neurospora
734	4	13.3	108	1	GLRX_YEAST	P17695 saccharomyc	807	4	13.3	123	1	RL7A_METKA	O8C703 methanopyru
735	4	13.3	108	1	NIGM_BOVIN	O02374 bos taurus	808	4	13.3	123	1	YO30_MYCLE	O60601 mycobacteri
736	4	13.3	108	1	PT91_YEAST	O02772 saccharomyc	809	4	13.3	124	1	AT14_YEAST	O12349 saccharomyc
737	4	13.3	108	1	VAPI_BACNO	O45560 bacteroides	810	4	13.3	124	1	YABJ_BACSU	B37552 bacillus su
738	4	13.3	109	1	C550_NITWI	P00085 nitrobacter	811	4	13.3	124	1	YMO2_CAREL	P34493 caenorhabdi
739	4	13.3	109	1	FEL2_FELCA	P30440 felis silve	812	4	13.3	125	1	CU14_MANSE	P13229 manduca sex
740	4	13.3	109	1	PRVA_HUMAN	P20472 homo sapien	813	4	13.3	125	1	FABL_HALBI	P81653 halaelurus
741	4	13.3	109	1	WMTM_LAMBD	O46953 escherichia	814	4	13.3	125	1	FABL_RHSPA	P80856 rhandia sap
742	4	13.3	109	1	VPJF_ECOLI	P25528 escherichia	815	4	13.3	125	1	MINK_CAYPO	O60409 cavia porce
743	4	13.3	110	1	FER_ECOLI	P18852 saccharomyc	816	4	13.3	125	1	RPC9_SCHPO	O09177 schizosacch
744	4	13.3	110	1	GBG_YEAST	P18852 saccharomyc	817	4	13.3	125	1	SECG_BORBU	O51063 borrelia bu
745	4	13.3	110	1	H1S2_CLOAB	O97Kh6 clostridium	818	4	13.3	125	1	VG61_BPM15	P01170 lophus ame
746	4	13.3	110	1	NJOK_RICCN	O92G98 rickettsia	819	4	13.3	125	1	Y568_METUA	O57968 methanococ
747	4	13.3	110	1	NJOK_RICPR	O28029 bos taurus	820	4	13.3	125	1	Y811_SUTJO	O97376 methanococ
748	4	13.3	110	1	VATF_BOVIN	P81316 methanococc	821	4	13.3	125	1	Y811_SUTJO	O97376 methanococ
749	4	13.3	110	1	YBSA_METJA	P08701 escherichia	822	4	13.3	125	1	Y944_HELPY	O25598 helicobacte
750	4	13.3	111	1	IMWI_ECOLI	O15453 homo sapien	823	4	13.3	126	1	ALDR_LACLA	O34113 lactococcus
751	4	13.3	112	1	NBR2_HUMAN	P47389 mycoplasma	824	4	13.3	126	1	PAND_PSEAE	O94858 pseudomonas
752	4	13.3	112	1	R8FA_MYCPE	O96f65 chlamydia p	825	4	13.3	126	1	Y681_MYCPU	O50735 mycoplasma
753	4	13.3	112	1	RS6_CHLPN	P03289 human adeno	826	4	13.3	126	1	YA42_SCHPO	O09723 schizosacch
754	4	13.3	112	1	Y112_ADR02	O67257 aquilex aeo	827	4	13.3	127	1	YMO6_SUISO	O97919 sulfobolus
755	4	13.3	112	1	YCO1_AQUAE	O67257 aquilex aeo	828	4	13.3	127	1	CRCB_THEMA	O9XU68 thermotoga
756	4	13.3	113	1	IF1C_WHEAT	O24700 synecococc	829	4	13.3	127	1	RT12_CHOCH	P48858 chionox cr
757	4	13.3	113	1	RL24_SYNP6	O54187 onchocerca	830	4	13.3	127	1	TRM1_ECOLI	P18026 escherichia
758	4	13.3	114	1	D2_ONCVO	O64193 lactocacill	831	4	13.3	127	1	TRM6_ECOLI	P18808 escherichia
759	4	13.3	114	1	DCHS_LACHU	O97168 streptomyc	832	4	13.3	127	1	TRM7_ECOLI	P33730 escherichia
760	4	13.3	114	1	GWJ2_STRCO	P15758 oenothera b	833	4	13.3	127	1	YUGF_ECOLI	P39317 escherichia
761	4	13.3	114	1	Y941_ARCFU	O23221 archaeoglob	834	4	13.3	127	1	YL35_ARCFU	O28145 archaeoglob
762	4	13.3	114	1	ANFC_TRISC	P55208 tritakis scy	835	4	13.3	127	1	YVNI_AZOVI	P40431 azotobacter
763	4	13.3	115	1	ANFC_TRISC	P55208 tritakis scy	836	4	13.3	128	1	RS9_THETH	P80374 thermus the

837	4	13.3	128	1	VATF_ARATH	Q9ZQX4 arabidopsis	910	4	13.3	137	1	ATPE_MERSA	Q9TKI6 medicago sa
838	4	13.3	128	1	V371_BUCAI	P57452 buchiera ap	911	4	13.3	137	1	ATPE_ORYSA	P12066 oryza sativ
839	4	13.3	128	1	YCDK_ECOLI	P75896 escherichia	912	4	13.3	137	1	ATPE_PEA	P05039 plasm sativ
840	4	13.3	129	1	COXE_YEAST	P32799 saccharomyc	913	4	13.3	137	1	ATPE_PICAB	Q47036 pices abies
841	4	13.3	129	1	HMFI_YEAST	P40037 saccharomyc	914	4	13.3	137	1	ATPE_PINTH	P41633 pins thunb
842	4	13.3	129	1	MINK_MOUSE	P23299 mus musculu	915	4	13.3	137	1	ATPE_WHEAT	P20859 triticum ae
843	4	13.3	129	1	RHCB_AGRKH	P81398 agkistrodon	916	4	13.3	137	1	CHH_PROCL	Q25663 procambus
844	4	13.3	129	1	RS9_ECOLI	P02363 escherichia	917	4	13.3	137	1	FLGB_ECOLI	P75954 escherichia
845	4	13.3	129	1	RS9_HAEBN	P44388 haemophilus	918	4	13.3	137	1	IGT_HUMAN	P01591 homo sapien
846	4	13.3	129	1	RS9_HAESO	P31782 haemophilus	919	4	13.3	137	1	URE2_STAXY	P12874 staphylococ
847	4	13.3	129	1	RS9_SALTY	Q8XFX5 salmonella	920	4	13.3	137	1	Y890_MENVA	Q58308 methanococ
848	4	13.3	129	1	RTI3_MAIZE	P08927 zea mays (m	921	4	13.3	137	1	YAB3_PSEPU	P45368 pseudomonas
849	4	13.3	129	1	TDCF_ECOLI	P42631 escherichia	922	4	13.3	138	1	ATPE_BUCAI	P57155 buchiera ap
850	4	13.3	129	1	YBAZ_ECOLI	P75707 escherichia	923	4	13.3	138	1	ATPE_BUCAP	P51871 buchiera ap
851	4	13.3	129	1	YD39_HABIN	P71378 haemophilus	924	4	13.3	138	1	FLGN_ECOLI	P43533 escherichia
852	4	13.3	129	1	YEB6_PASNU	Q91656 pasteurella	925	4	13.3	138	1	HUPG_RHCCA	Q03006 rhodobacter
853	4	13.3	130	1	DHSD_HALNI	Q9H652 halobacteri	926	4	13.3	138	1	NUSB_HELPU	Q9ZNS7 helicobacte
854	4	13.3	130	1	DHSD_NATPH	P72109 natriumona	927	4	13.3	138	1	NUSB_HELPU	Q24853 helicobacte
855	4	13.3	130	1	DSRE_CHRVT	Q87896 chironatium	928	4	13.3	138	1	SUFE_ECOLI	P76194 salmonella
856	4	13.3	130	1	MINK_PIG	Q9TUN9 sus scrofa	929	4	13.3	138	1	YTL1_SALTY	Q9FV42 petunia hyb
857	4	13.3	130	1	MINK_RABIT	Q28705 oryctolagus	930	4	13.3	139	1	ADP1_PETRY	Q41764 zea mays (m
858	4	13.3	130	1	MINK_RAT	P15383 rattus norv	931	4	13.3	139	1	ADP3_MAIZE	Q41764 zea mays (m
859	4	13.3	130	1	RS8_METTL	Q97788 methanococ	932	4	13.3	139	1	PABZ_CLOPE	Q8X158 clostridium
860	4	13.3	130	1	RS8_METVA	P14038 methanococ	933	4	13.3	139	1	RBS_C_ALCEU	P09658 alcaligenes
861	4	13.3	130	1	RS8_METVO	Q97789 methanococ	934	4	13.3	139	1	RBS_THANO	Q98948 thalassios
862	4	13.3	130	1	RS9_BUCAI	P57470 buchiera ap	935	4	13.3	139	1	RK16_PORPU	P51307 porphyra pu
863	4	13.3	130	1	RS9_PASNU	Q9CNB1 pasteurella	936	4	13.3	139	1	RL16_SYNY3	P73133 synechocyst
864	4	13.3	130	1	RS9_VIBCH	Q9KUF0 vibrio chol	937	4	13.3	139	1	Y252_AOUAE	Q66313 synechocyst
865	4	13.3	130	1	RS9_YERBE	Q8ZK62 yerersinia pe	938	4	13.3	140	1	EXB1_XANCP	Q34259 xanthomonas
866	4	13.3	130	1	Y075_NPPOP	Q10328 oryzaia pen	939	4	13.3	140	1	FLGN_SALTY	P37406 salmonella
867	4	13.3	130	1	YHM6_CABEL	Q43536 caenorhabdi	940	4	13.3	140	1	LCA_MACEU	Q06653 macropus eu
868	4	13.3	130	1	YUGF_HABIN	P23833 haemophilus	941	4	13.3	140	1	RS19_SULSO	Q06653 sulfobius
869	4	13.3	131	1	DFRA_MYXXA	Q52178 myxococcus	942	4	13.3	140	1	Y128_LISMO	P58702 listeria mo
870	4	13.3	131	1	HIS3_PYRAE	Q8ZV39 pyrobaculum	943	4	13.3	140	1	Y175_LISIN	Q92F61 listeria in
871	4	13.3	131	1	Y624_MYCTU	P96914 mycobacteri	944	4	13.3	140	1	YAB3_SCHPO	P00980 schistosac
872	4	13.3	132	1	AGSR_HUMAN	Q00253 homo sapien	945	4	13.3	140	1	YAB3_ECOLI	P40771 escherichia
873	4	13.3	132	1	ATPE_ARATH	P09468 arabidopsis	946	4	13.3	140	1	YEB6_MYCPN	P75317 mycoplasma
874	4	13.3	132	1	CYCP_PASPP	P00143 paracoccus	947	4	13.3	141	1	ATPE_PSEAE	Q9H421 pseudomonas
875	4	13.3	133	1	ACPS_CLOPE	Q8XNPI clostridium	948	4	13.3	141	1	HBA_TRLIN	P28325 thermoprote
876	4	13.3	133	1	AMPE_RAT	P50123 rattus norv	949	4	13.3	141	1	HBFI_URECA	P06148 urechis cau
877	4	13.3	133	1	ATPE_TROBA	P07138 ipomoea bat	950	4	13.3	141	1	NIFD_RHILT	P04645 rhizobium l
878	4	13.3	133	1	ATPE_OENHO	Q9MUC6 oenothera h	951	4	13.3	141	1	VE6_HPV17	P36805 human papil
879	4	13.3	133	1	ATPE_TOSAC	P00834 nicotiana t	952	4	13.3	141	1	YJEB_ECOLI	P21428 escherichia
880	4	13.3	133	1	YCGK_ECOLI	P87054 schizosacch	953	4	13.3	141	1	YORE_TTV1	P12929 thermoprote
881	4	13.3	133	1	YDUF_SCHPO	Q00247 plectonema	954	4	13.3	141	1	YROP_BACSU	P54122 bacillus su
882	4	13.3	133	1	YVU1_PLRBO	Q66398 aquifex aeo	955	4	13.3	142	1	AGNX_APLSP	P12284 aplysia sp.
883	4	13.3	133	1	ATPE_SPYOL	P00833 epinacia ol	956	4	13.3	142	1	ASPI_STRT	P80445 streptococ
884	4	13.3	134	1	D3_ONCVO	P74367 synechocyst	957	4	13.3	142	1	ASPI_STRT	Q30851 streptococ
885	4	13.3	134	1	PS11_SYNY3	P54188 onchocerca	958	4	13.3	142	1	CYTD_HUMAN	P28325 homo sapien
886	4	13.3	134	1	RK16_PINTH	P52767 pins thunb	959	4	13.3	142	1	LCA_BOVIN	P00711 bos taurus
887	4	13.3	134	1	YD89_MENVA	Q58784 methanococ	960	4	13.3	142	1	LCA_CAPII	P00712 capra hircu
888	4	13.3	134	1	YHCB_ECOLI	P39436 escherichia	961	4	13.3	142	1	LCA_HUMAN	P00709 homo sapien
889	4	13.3	134	1	ATPE_WARPO	P06285 marcantia	962	4	13.3	142	1	LCA_SHEEP	P09462 ovis aries
890	4	13.3	135	1	CHH1_ORCLI	Q25588 orconectes	963	4	13.3	142	1	PFDA_METAC	Q8116 methanosarc
891	4	13.3	135	1	CHH2_ORCLI	Q25588 orconectes	964	4	13.3	142	1	REXC_PSEPU	P37862 pseudomonas
892	4	13.3	135	1	LEG7_HUMAN	P47929 homo sapien	965	4	13.3	142	1	VE6_HPV60	Q80941 human papil
893	4	13.3	135	1	IGUL_ECOLI	Q59384 escherichia	966	4	13.3	142	1	Y742_CHLPP	P94703 chlamydia p
894	4	13.3	135	1	IGUL_ECOLI	Q60003 salmonella	967	4	13.3	142	1	Y742_CHLPP	P44055 haemophilus
895	4	13.3	135	1	IGUL_ECOLI	Q60003 salmonella	968	4	13.3	142	1	Y742_CHLPP	Q14155 schistosach
896	4	13.3	135	1	REV_EIAY9	P11305 equine infe	969	4	13.3	142	1	YKX5_YEAST	P50943 saccharomyc
897	4	13.3	135	1	REV_EIAY9	P11305 equine infe	970	4	13.3	142	1	SM16_SCHMA	Q00712 schistosoma
898	4	13.3	135	1	RK16_EUGGR	P25512 euglena gra	971	4	13.3	144	1	Y742_AOUAE	Q67162 aquifex aeo
899	4	13.3	135	1	YOHV_BACSU	P54519 bacillus su	972	4	13.3	145	1	COPY_ENTHR	Q47839 enterococu
900	4	13.3	136	1	ATPE_CUSRE	P30400 cuscutea ref	973	4	13.3	145	1	DUT_CHIMU	Q9PK82 chlamydia m
901	4	13.3	136	1	CALI_ARATH	P25854 arabidopsis	974	4	13.3	145	1	DUT_CHIMU	Q84294 chlamydia t
902	4	13.3	136	1	CALI_ONCKE	P01265 oncorhynch	975	4	13.3	145	1	MMF1_YEAST	P40185 saccharomyc
903	4	13.3	136	1	NNDI_ECOLI	Q47415 escherichia	976	4	13.3	145	1	VP3_BPCBP	P19194 bacteriophage
904	4	13.3	136	1	NNDI_SALTI	Q84466 salmonella	977	4	13.3	146	1	AROF_STRLI	P55911 streptomyce
905	4	13.3	136	1	NNDI_SALTY	Q56109 salmonella	978	4	13.3	146	1	PABZ_CAMJE	Q9P162 campylobact
906	4	13.3	136	1	RS9_BORBU	Q51313 borrelia bu	979	4	13.3	146	1	PABZ_PSEAE	Q9HX72 pseudomonas
907	4	13.3	136	1	UK14_RAT	P52759 rattus norv	980	4	13.3	146	1	HBBI_ANAMI	P83272 anarichias
908	4	13.3	137	1	ACTP_ACACA	P37167 acanthamoeb	981	4	13.3	146	1	HBBI_PAGBO	Q93348 pagothenia
909	4	13.3	137	1	ATPE_MAIZE	P00835 zea mays (m	982	4	13.3	146	1	HBBI_GADWO	Q13077 gadus morhu

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983 4 13.3 146 1 HBB_MELAE 009232 melanjogram
984 4 13.3 146 1 HBB_MERMR 013078 merlangius
985 4 13.3 146 1 MSRB_CLOAB 097100 clostridium
986 4 13.3 146 1 RL15_METHU 026133 methanobact
987 4 13.3 146 1 RL15_MYCTU 095071 mycobacteri
988 4 13.3 146 1 SMD1_YEAST 002260 saccharomyc
989 4 13.3 146 1 SP22_BACSV 010645 mycobacteri
990 4 13.3 146 1 YD34_MYCTU 094821 chlamydia p
991 4 13.3 147 1 ARGQ_CHLPP 030557 pseudomonas
992 4 13.3 147 1 CALM_PSEAE 039752 fagus eylva
993 4 13.3 147 1 CALM_PASST 039752 fagus eylva
994 4 13.3 147 1 ENPP_BPT3 010305 bacterioph
995 4 13.3 148 1 CAL1_PETRY 027162 petunia hyb
996 4 13.3 148 1 CAL2_ARATH 025069 arabidopsis
997 4 13.3 148 1 CAL4_ARATH 003510 arabidopsis
998 4 13.3 148 1 CAL6_ARATH 003509 arabidopsis
999 4 13.3 148 1 CALM_ACHTL 015094 achlya kleb
1000 4 13.3 148 1 CALM_BLAEM 09htfe blastoclad

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ALIGNMENTS

RESULT 1
SODM_CANAL STANDARD; PRT: 234 AA.

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AC 013401;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2.
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE=99177423; PubMed=10076057;
RA Rhee G.E., Huang C.S., Brady M.J., Kim S.T., Kim Y.R., Huh W.K.,
RA Beak Y.U., Lee B.H., Lee J.S., Kang S.O.;
RT "Manganese-containing superoxide dismutase and its gene from Candida
RT albicans."
RL Biochim. Biophys. Acta 1426:409-419(1999).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Manganese.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
CC -----
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CC -----
CC EMBL: AF031478; AAB86583.1; -.
CC HSSP: P04179; IABM.
CC InterPro: IPR001169; SODismutase.
CC Pfam: PF00081; sode1; 1.
CC PRODOM: PD000475; SODismutase; 1.
CC PROSITE: PS00088; SOD NM; 1.
CC Oxidoreductase; Manganese; Mitochondrion; Transit peptide.
FT TRANSIT 1 34 MITOCHONDRION.
FT CHAIN 35 234 SUPEROXIDE DISMUTASE [MN].
FT METAL 60 60 MANGANESE (BY SIMILARITY).
FT METAL 108 108 MANGANESE (BY SIMILARITY).

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FT METAL 198 198 MANGANESE (BY SIMILARITY).
FT METAL 202 202 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 234 AA; 26173 MW; EBFPC2D769C1D9C1 CRC64;
Query Match 83.3%; Score 25; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.9e-19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KYSLPELDYFSATPYISGOINEL 25
DB 35 KYSLPELDYFSATPYISGOINEL 59

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RESULT 2

SODM_YEAST STANDARD; PRT: 233 AA.

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AC P00447;
DT 21-JUL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2 OR YHR008C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=65127011; PubMed=3882422;
RA Mares C.A.M., van Loon A.P.G.M., Oudshoorn P., van Steeg H.,
RA Grivell L.A., Slater E.C.;
RT "Nucleotide sequence analysis of the nuclear gene coding for
RT manganese superoxide dismutase of yeast mitochondria, a gene
RT previously assumed to code for the Rieske iron-sulphur protein."
RL Eur. J. Biochem. 147:153-161(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288c / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favejlo A., Fulton L., Gattung S., Gelsel C., Kirsten J.,
RA Kucaba T., Hillier L., Jler M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Marais E., Meneses S., Mouser L.,
RA Nham M., Rifkin L., Riles L., St Peter H., Trevaaskis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterson R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VII."
RT Science 265:2077-2082(1994).
RN [3]
RP SEQUENCE OF 1-39 FROM N.A.
RX MEDLINE=89211942; PubMed=3072251;
RA Schrank I.S., Sims P.F., Oliver S.G.;
RT "Functional expression of the yeast Mn-superoxide dismutase gene in
RT Escherichia coli requires deletion of the signal peptide sequence."
RL Gene 73:121-130(1988).
RN [4]
RP SEQUENCE OF 27-233.
RA Ditlev C., Johansen J.T., Martin B.M., Svendsen I.;
RT "The complete amino acid sequence of manganese-superoxide dismutase
RT from Saccharomyces cerevisiae."
RL Carlsberg Res. Commun. 47:81-91(1982).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Manganese.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
CC -----
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CC
DR EMBL; X02156; CAA26092.1; -;
DR EMBL; U10400; AAB68939.1; -;
DR EMBL; M24079; AAA35065.1; -;
DR PIR; A00521; DSBYN.
DR PIR; S46785; S46785.
DR HSSP; P04179; 1ABM.
DR SGD; S0001050; SOD2.
DR InterPro; IPR01189; SODismutase.
DR Pfam; PF00081; sode; 1.
DR Pfam; PF02777; sode; C; 1.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
CC Oxidoreductase; Manganese; Mitochondrion; Transit peptide.
TRANSIT 1 26
CHAIN 27 233 SUPEROXIDE DISMUTASE [MN].
FT METAL 52 52 MANGANESE (BY SIMILARITY).
FT METAL 107 107 MANGANESE (BY SIMILARITY).
FT METAL 194 194 MANGANESE (BY SIMILARITY).
FT METAL 198 198 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 233 AA; 25774 MW; 88A9391FBB31D06B CRC64;

Query Match 33.3%; Score 10; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.0012; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 EPIYSGQINE 24
Db 41 EPIYSGQINE 50

RESULT 3
SODM_MYCAV STANDARD; PRT; 206 AA.
ID SODM_MYCAV
AC P47201;

DT 01-FEB-1996 (Rel. 33, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1).
GN SODA OR SOD.

OS Mycobacterium avium.
CC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
CC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
CC NCBI_TaxID=1764;

-RN
RP SEQUENCE FROM N.A.
RC STRAIN=TWC 724;
RX MEDLINE=96276149; PubMed=8692009;
RA Becuyer V.E., Haddad N., Frehel C., Berche P.;
RT "Molecular characterization of a surface-exposed superoxide dismutase
of Mycobacterium avium."
RL Microb. Pathog. 20:41-55(1996).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Manganese.
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.

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CC EMBL; U11550; AAB08770.1; -;

DR HSSP; P17670; 1IDS.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sode; 1.
DR Pfam; PF02777; sode; C; 1.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
CC Oxidoreductase; Manganese.

KW INIT MET 0
FT METAL 27 27 MANGANESE (BY SIMILARITY).
FT METAL 75 75 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 206 AA; 22912 MW; D6B49083AEBF3C98 CRC64;

Query Match 26.7%; Score 8; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 ISGQINEI 25
Db 19 ISGQINEI 26

RESULT 4
SODM_MYCLP STANDARD; PRT; 206 AA.
ID SODM_MYCLP
AC O66165;

DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1).
GN SODA OR SOD.

OS Mycobacterium lepraemurium.
CC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
CC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
CC NCBI_TaxID=64667;

-RN
RP SEQUENCE FROM N.A.
RC STRAIN=Hawaiian;
RA Nakamura M.;
RL Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Manganese (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.

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DR EMBL; D13288; BAA28850.1; -;
DR HSSP; P17670; 1IDS.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sode; 1.
DR Pfam; PF02777; sode; C; 1.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
CC Oxidoreductase; Manganese.

KW INIT MET 0
FT METAL 27 27 MANGANESE (BY SIMILARITY).
FT METAL 75 75 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 206 AA; 23031 MW; 92A063471FA9F22F CRC64;

Query Match 26.7%; Score 8; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.14;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 18 ISGQINEI 25
 |||||
 Db 19 ISGQINEI 26

RESULT 5

SODM_MYCFO STANDARD; PRT; 206 AA.

AC Q59519; (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Mn] (EC 1.15.1.1).
 GN SODA OR SOD.

OS Mycobacterium fortuitum.
 OC Bacteria; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1766;
 [1]

SEQUENCE FROM N.A.

CC STRAIN=ATCC 5841;
 CC MEDLINE=96102872; PubMed=8586279;
 CC RA Mendez M.C., Domenech P., Prieto J., Garcia M.J.;
 CC RT "Cloning and expression of the Mycobacterium fortuitum superoxide
 CC RT dismutase gene.";
 CC RL FEMS Microbiol. Lett. 134:273-278(1995).
 CC CC
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.

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CC EMBL; X70914; CAA50266.1; -.
 CC DR HSSP; P17670; 1IDS.
 CC DR InterPro; IPR001189; SODismutase.
 CC DR Pfam; PF02777; sodfe; 1.
 CC DR Pfam; PF02777; sodfe; 1.
 CC DR PROSITE; PS000475; SODismutase; 1.
 CC DR PROSITE; PS00088; SOD_MN; 1.
 CC DR Oxidoreductase; Manganese.

CC BY SIMILARITY.
 CC FT INIT MET 0
 CC FT METAL 27 27 MANGANESE (BY SIMILARITY).
 CC FT METAL 75 75 MANGANESE (BY SIMILARITY).
 CC FT METAL 159 159 MANGANESE (BY SIMILARITY).
 CC FT METAL 163 163 MANGANESE (BY SIMILARITY).
 CC SO SEQUENCE 206 AA; 22833 MW; 500625A8B9321246 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 18 ISGQINE 24
 |||||
 Db 19 ISGQINE 25

RESULT 6

SODM_MYCSM STANDARD; PRT; 206 AA.

AC P53649; Q8S612;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Mn] (EC 1.15.1.1).
 GN SODA OR SOD.
 OS Mycobacterium smegmatis.
 OC Bacteria; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1772;
 [1]

SEQUENCE FROM N.A., AND CHARACTERIZATION.

CC STRAIN=1-2C;
 CC MEDLINE=99134360; PubMed=9933629;
 CC RA Harth G., Horwitz M.A.;
 CC RT "Export of recombinant Mycobacterium tuberculosis superoxide dismutase
 CC RT is dependent upon both information in the protein and mycobacterial
 CC RT export machinery. A model for studying export of leaderless proteins
 CC RT by pathogenic mycobacteria.";
 CC RL J. Biol. Chem. 274:4281-4292(1999).
 CC [2]

CC REVISIONS TO 116 AND 201.
 CC RA Tullius M.V., Harth G., Horwitz M.A.;
 CC RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC [3]

CC SEQUENCE OF 27-164 FROM N.A.
 CC STRAIN=NCTC 10265 / ATCC 14468 / W-113;
 CC RA Bull T.J., Shannon D.C., Archard L.C.;
 CC RT "Rapid identification of mycobacteria from AIDS patients by capillary
 CC RT electrophoretic profiling of amplified SOD gene.";
 CC RL J. Clin. Pathol. Clin. Mol. Pathol. 48:124-133(1995).

CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese.
 CC -1- SUBUNIT: HOMOTETRAMER.

CC -1- SUBCELLULAR LOCATION: PARTIALLY SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.

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 CC -----

CC EMBL; AF061031; AAD15825.2; -.
 CC DR EMBL; Z48214; CAA88247.1; -.
 CC DR HSSP; P17670; 1IDS.
 CC DR InterPro; IPR001189; SODismutase.
 CC DR Pfam; PF02777; sodfe; 1.
 CC DR Pfam; PF02777; sodfe; 1.
 CC DR PROSITE; PS000475; SODismutase; 1.
 CC DR PROSITE; PS00088; SOD_MN; 1.
 CC DR Oxidoreductase; Manganese.

CC BY SIMILARITY.
 CC FT INIT MET 0
 CC FT METAL 27 27 MANGANESE (BY SIMILARITY).
 CC FT METAL 75 75 MANGANESE (BY SIMILARITY).
 CC FT METAL 159 159 MANGANESE (BY SIMILARITY).
 CC FT METAL 163 163 MANGANESE (BY SIMILARITY).
 CC SO SEQUENCE 206 AA; 22804 MW; B997A1AD0374AEC9 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 18 ISGQINE 24
 |||||
 Db 19 ISGQINE 25

RESULT 7

SODM_NOCAS STANDARD; PRT; 206 AA.

```

AC P53651;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1).
GN SODA OR SOD.
OS Nocardia asteroides.
OC Bacteria; Actinobacteria; Actinobacteriales (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Nocardia.
OX NCBI_TaxId=1824;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUH2;
RX MEDLINE=96060854; PubMed=7590304;
RA Alencor D.J., Chapman G.D., Beaman B.L.;
RT "Isolation, sequencing and expression of the superoxide dismutase-
RT encoding gene (sod) of Nocardia asteroides strain GUH-2.";
RL Gene 164143-147(1995).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Manganese (by similarity).
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
CC -----
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CC -----
DR EMBL: U02341; AAA91964.1; -.
DR HSSP: P17670; 1IDS.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF000081; sode; 1.
DR Pfam: PF02777; sode; C. 1.
DR ProDom: PD000475; SODismutase; 1.
DR PROSITE: PS00088; SOD_MN; 1.
DR Oxidoreductase; Manganese.
KM INIT_MET 0
FT METAL 27 27 BY SIMILARITY.
FT METAL 75 75 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
FT SEQUENCE 206 AA; 22823 MW; FA2BCFP27EB22CBDCD CRC64;
Query Match 23.3%; Score 7; DB 1; Length 206;
- Best Local Similarity 100.0%; Pred.No.1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 ISQIINE 24
Db 19 ISQIINE 25

```

```

RC SPECIES=M.tuberculosis; STRAIN=Erdmann;
RX MEDLINE=91251768; PubMed=1904126;
RA Zhang Y.;
RT "Genetic analysis of superoxide dismutase, the 23 kilodalton antigen
RT of Mycobacterium tuberculosis.";
RL Mol. Microbiol. 5:381-391(1991).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC SPECIES=M.tuberculosis; STRAIN=Erdmann;
RX MEDLINE=99134360; PubMed=9933629;
RA Harth G., Horwitz M.A.;
RT "Export of recombinant Mycobacterium tuberculosis superoxide dismutase
RT is dependent upon both information in the protein and mycobacterial
RT export machinery. A model for studying export of leaderless proteins
RT by pathogenic mycobacteria.";
RL J. Biol. Chem. 274:4281-4292(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=BCG / Pasteur;
RA Kimble E., Sanderson R.J., Gill R.E.;
RT "Superoxide dismutase of M. bovis BCG.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC SPECIES=M.tuberculosis;
RX MEDLINE=95182461; PubMed=7877174;
RA Cooper J.B., McIntyre K., Badasso M.O., Wood S.P., Zhang Y.,
RA Garbe T.R., Young D.;
RT "X-ray structure analysis of the iron-dependent superoxide dismutase
RT from Mycobacterium tuberculosis at 2.0-A resolution reveals novel
RT dimer-dimer interactions.";
RL J. Mol. Biol. 246:531-544(1995).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF MUTANT ALA-152.
RC SPECIES=M.tuberculosis;
RX MEDLINE=96244503; PubMed=8674528;
RA Cooper J.B., Seward S., Erskine P.T., Badasso M.O., Wood S.P.,
RA Zhang Y., Young D.;
RT "X-ray structure analysis of an engineered Fe-superoxide dismutase
RT Gly-Ala mutant with significantly reduced stability to denaturation.";
RL FEBS Lett. 387:105-108(1996).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Iron.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: Secreted.

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CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
CC -1- CAUTION: ALTHOUGH FOUND EXTRACELLULARLY, NO SIGNAL SEQUENCE IS
CC PRESENT. AN ALTERNATIVE SECRETORY PATHWAY MAY BE USED.
CC -----
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CC -----
DR EMBL; X52861; CAA37042.1; -
DR EMBL; AF061030; AAD15824.1; -
DR EMBL; Z83864; CAB06220.1; -
DR EMBL; AE007188; AAA48327.1; -
DR EMBL; AF077406; AAC27527.1; -
DR PIR; S10908; S10908.
DR PIR; S15205; S15205.
DR PDB; 1IDS; 20-DEC-94.
DR TIGR; MT3960; -
DR Tubercular; Rv3946; -
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sode; 1.
DR Pfam; PF02777; sode; 1.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00089; SOD_NM; 1.
DR Oxidoreductase; Iron; 3D-structure; Complete proteome.
FT METAL 28 28 IRON.
FT METAL 76 76 IRON.
FT METAL 160 160 IRON.
FT METAL 164 164 IRON.
SQ SEQUENCE 207 AA; 23034 MW; DE8F5921DABE54A CRC64;
Query Match 23.3%; Score 7; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 ISGQINE 24
Db 20 ISGQINE 26
RESULT 9
GCS2_BACSU
AC P54377;
ID_GCS2_BACSU STANDARD; PRT; 488 AA.
RT 01-OCT-1996 (Rel. 34, Created)
RT 01-OCT-1996 (Rel. 34, Last sequence update)
RT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable glycine dehydrogenase [decarboxylating] subunit 2
DE (EC 1.4.4.2) (Glycine decarboxylase) (Glycine cleavage system P-
DE protein).
GN YOHK.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / JH642;
RX MEDLINE=97124195; PubMed=8969508;
RA Minato M., Mesuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
RA Kobayashi Y.;
RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
RT the Bacillus subtilis genome containing the skin element and many
RT sporulation genes."
RL Microbiology 142:3103-3111(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunet F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Beesieres P., Bojotin A., Borchert S.,
RA Borrias R., Bourcier L., Brans A., Braun M., Briqnell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codant J.J., Connerton I.F., Connerton N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Enlian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gilm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halesch J., Harwood C.R., Henaut A.,
RA Hilbert H., Holappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Kamata D., Kasahara Y., Klier-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Patro V., Pohl T.M., Portetelle D., Portwollik S., Prescott A.M.,
RA Prescecian E., Puig P., Punnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Serron S.J., Serron P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpetre P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vamler F., Vassarotti A.,
RA Viari A., Wambolt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumestein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis".
RL Nature 350:249-256(1997).
CC -1- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYZES THE DEGRADATION OF
CC GLYCINE. THE P PROTEIN BINDS THE ALPHA-AMINO GROUP OF GLYCINE
CC THROUGH ITS PYRIDOXAL PHOSPHATE COFACTOR. CO(2) IS RELEASED AND
CC THE REMAINING METHYLAMINE MOIETY IS THEN TRANSFERRED TO THE
CC LIPONAMIDE COFACTOR OF THE H PROTEIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Glycine + lipoylprotein = S-
CC anthionemethylolipoylprotein + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SUBUNIT: THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS:
CC P, T, L, AND H.
CC -1- SIMILARITY: TO THE C-TERMINAL OF OTHER GLYCINE CLEAVAGE SYSTEM P-
CC PROTEIN.
CC -----
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CC -----
DR EMBL; D84432; BAA12548.1; -
DR EMBL; Z99116; CAB14386.1; -
DR Subtilisin; Bg11511; YQHK.
DR InterPro; IPR003437; GDC-P.
DR Pfam; PF02347; GDC-P; 1.
KW Hypothetical protein; Oxidoreductase; Pyridoxal phosphate;
KW Complete proteome.
FT BINDING 273 273 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 488 AA; 54427 MW; 0B9C7DAD75E657C CRC64;
Query Match 23.3%; Score 7; DB 1; Length 488;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 YSLPDL 8
Db 20 YSLPDL 26
RESULT 10
CAPP_SYNY3
ID_CAPP_SYNY3 STANDARD; PRT; 1034 AA.

```

AC P74299;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCASE) (PEPC).
GN PGC OR SLL0320.
OS Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=9905231.
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugitara M., Sasamoto S., Kikuta T.,
RA Hosouchi T., Matsuo A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synchocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
DNA Res. 3:109-136(1996).
CC -1- FUNCTION: TO FORM OXALACETATE, A FOUR-CARBON DICARBOXYLIC ACID
CC -1- SOURCE FOR THE TRICARBOXYLIC ACID CYCLE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
CC -1- PHOSPHOENOLPYRUVATE + CO(2).
CC -1- PATHWAY: Tricarboxylic acid cycle.
CC -1- SIMILARITY: BELONGS TO THE PEPCASE FAMILY.
CC -----
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CC -----
DR EMBL; D90914; BAI8393.1; -.
DR HSSP; P00864; IFY.
DR InterPro; IPR001449; PEPCase.
DR Pfam; PF00311; PEPCase; 1.
DR PRINTS; PR00150; PEPCARBLASE.
DR PROSITE; PS00393; PEPCASE_2; 1.
DR PROSITE; PS00781; PEPCASE_1; 1.
DR Lyase; Carbon dioxide fixation; Allosteric enzyme;
KM Tricarboxylic acid cycle; Complete proteome.
FT ACT_SITE 203 203 BY SIMILARITY.
FT ACT_SITE 680 680 BY SIMILARITY.
FT ACT_SITE 1034 AA; 118940 MM; 76DF6061BAB7235D CRC64;
CC -----
Query Match 23.3%; Score 7; DB 1; Length 1034;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 KYSLPEL 7
Db 754 KYSLPEL 760

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CC -1- SIMILARITY: BELONGS TO THE UPF0076 (UK114) FAMILY.
CC -----
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CC -----
DR EMBL; U50749; AAB48552.1; -.
DR HSSP; P37552; 10D9.
DR InterPro; IPR000543; YjgF-like.
DR Pfam; PF01042; UPF0076; 1.
DR TIGRFAMs; TIGR00004; YER057c_YjgF_UK114; 1.
DR PROSITE; PS01094; UPF0076; 1.
KM Hypothetical protein.
SQ SEQUENCE 130 AA; 14232 MW; 74531BAD1F2CA525 CRC64;
CC -----
Query Match 20.0%; Score 6; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 17 YISGQI 22
Db 29 YISGQI 34

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RESULT 12

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UK14_HUMAN
ID UK14_HUMAN STANDARD; PRT; 137 AA.
AC P52758;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 14.5 kDa translational inhibitor protein (p14.5) (UK114 antigen
DE homolog).
DR P5P.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 14-28; 30-43; 68-78 AND 98-113.
RC TISSUE=Liver;
RX MEDLINE=97129113; PubMed=8973653;
RA Schmiedeknecht G., Kerkhoff C., Orso E., Stoehr J., Aslanidis C.,
RA Nagy G.M., Khuechel R., Schmitz G.;
RT "Isolation and characterization of a 14.5-kDa trichloroacetic-acid-
RT soluble translational inhibitor protein from human monocytes that is
RT upregulated upon cellular differentiation.";
RL Eur. J. Biochem. 242:339-351(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Pozniakovaite N., Popenikyte V., Naktinis V.;
RT "Genomic structure of the human translational inhibitor protein
RT p14.5.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Tissue=Bone marrow, Brain, and Cervix;
RA Strauberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITS PROTEIN SYNTHESIS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: MOSTLY CYTOPLASMIC BUT IN LESS
CC DIFFERENTIATED CELLS OCCASIONALLY NUCLEAR.
CC -1- TISSUE SPECIFICITY: HEPATOCYTES AND RENAL DISTAL TUBULAR
CC EPITHELIAL CELLS. ONLY WEAK EXPRESSION IN OTHER TISSUES.
CC -1- DEVELOPMENTAL STAGE: UPREGULATED DURING CELLULAR DIFFERENTIATION.
CC -1- SIMILARITY: BELONGS TO THE UPF0076 (UK114) FAMILY.
CC -----
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DR EMBL; X95384; CAA64670.1; -
DR EMBL; AY026764; AAK01939.1; -
DR EMBL; BC008418; AAH08418.1; -
DR EMBL; BC010280; AAH10280.1; -
DR EMBL; BC012592; AAH12592.1; -
DR HSSP; P39330; 1009.
DR MIM; 602487; -
DR InterPro; IPR000543; YjGF-like.
DR Pfam; PF01042; UPF0076.1.
DR TIGRPFAM; TIGR00004; YER05C_YjGF_UK114; 1.
DR PROSITE; PS01094; UPF0076; 1.
KW Nuclear protein.
SQ SEQUENCE 137 AA; 14494 MW; DD0740621E8B6AD CRC64;
```

Query Match 20.0%; Score 6; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 YISGQI 22
| | | | |
Db 32 YISGQI 37

RESULT 13
SODM_PROFR STANDARD; PRT; 201 AA.
ID_P80293;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn/Fe] (EC 1.15.1.1).
GN SODA.
OS Propionibacterium freudenreichii shermanii.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Propionibacteriaceae; Propionibacteriaceae;
OC Propionibacterium.
OC NCBI_TaxID=1752;
CX [1]
RN SEQUENCE.
RP STRAIN=PE23;
RC MEDLINE=94139724; PubMed=8307013;
RA Meier B., Sehn A.P., Schinina M.E., Barra D.;
RA "In vivo incorporation of copper into the iron-exchangeable and
manganese-exchangeable superoxide dismutase from Propionibacterium
shermanii. Amino acid sequence and identity of the protein
molecules."; Eur. J. Biochem. 219:463-468 (1994).
RL Eur. J. Biochem. 219:463-468 (1994).
RL [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RA Schmidt M., Meier B., Parak F.;
RT "X-ray structure of the cambialistic superoxide dismutase from
Propionibacterium shermanii active with Fe or Mn."; J.
RL J. Biol. Inorg. Chem. 1:533-541 (1996).
RL [3]
RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).
RA Schmidt M., Scherk C., Iakovleva O., Nolting H.F., Meier B., Parak F.;
RL Submitted (SEP-1997) to the PDB data bank.
RL [4]
RP X-RAY CRYSTALLOGRAPHY (1.35 ANGSTROMS).
RX MEDLINE=99248073; PubMed=10233372;
RA Schmidt M.;
RT "Manipulating the coordination number of the ferric iron within the
RT cambialistic superoxide dismutase of Propionibacterium shermanii by
RT changing the pH-value. A crystallographic analysis."; Eur. J. Biochem.
262:117-127 (1999).
CC -1- FUNCTION: Destroys radicals which are normally produced within the

```
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: ACTIVE WITH EITHER MANGANESE OR IRON.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
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DR PIR; S41106; S41106.
DR PDB; 1AR4; 12-NOV-97.
DR PDB; 1AR5; 12-NOV-97.
DR PDB; 1AVM; 18-MAR-98.
DR PDB; 1BS3; 15-JUN-99.
DR PDB; 1BSW; 15-JUN-99.
DR PDB; 1BT8; 15-JUN-99.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sode; 1.
DR Pfam; PF02777; sodeC; 1.
DR PROSITE; PD000475; SODismutase; 1.
DR PROSITE; PS00086; SOD_MN; 1.
KW Oxidoreductase; Manganese; Iron; 3D-structure.
FT METAL 27 27 MANGANESE OR IRON.
FT METAL 75 75 MANGANESE OR IRON.
FT METAL 161 161 MANGANESE OR IRON.
FT METAL 165 165 MANGANESE OR IRON.
SQ SEQUENCE 201 AA; 22633 MW; 5BF8F424C7B32E00 CRC64;
```

Query Match 20.0%; Score 6; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 EPIYSG 20
| | | | |
Db 16 EPIYSG 21

RESULT 14
3MGH_LISTMO STANDARD; PRT; 207 AA.
ID_P58621;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative 3-methyladenine DNA glycosylase (EC 3.2.2.-).
GN LMO00928.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OC NCBI_TaxID=1639;
CX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Ruenick C., Amend A.,
RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA Charbit A., Cherouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Duran L., Dueset O.,
RA Eutian K.-D., Fehli H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapat G.,
RA Madueno E., Maitournan A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tietze A.,
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RT "Comparative genomics of Listeria species."; Science 294:849-852 (2001).
RL Science 294:849-852 (2001).
CC -1- SIMILARITY: BELONGS TO THE DNA GLYCOSYLASE MFG FAMILY.

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DR EMBL; AL591977; CAC99006.1; -.
 DR Listitisc; LMO00928; -.
 DR InterPro; IPR003180; Pair DNA_glyco.
 DR TIGRPFAMS; TIGR00567; 3mg; 1.
 KM Hydrophobic protein; DNA repair; Hydrolyase; Complete proteome.
 SQ SEQUENCE 207 AA; 23372 MW; 8066CCF45E1807D CRC64;

Query Match 20.0%; Score 6; DB 1; Length 207;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 PYISGQ 21
 Db 191 PYISGQ 196

RESULT 15

SODM_CHLPPN STANDARD; PRT; 207 AA.

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Mn] (EC 1.15.1.1).
 GN SODA OR SODM OR CPN0057 OR CP0718.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EWL029;
 RX MEDLINE=9206606; PubMed=10192388;
 RA Kilmann S., Mitchell W., Marathe C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
 RN Nat. Genet. 21:385-389(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=2015025; PubMed=10684935;
 RA Read T.D., Brumham R.C., Shen C., Gyll S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Uetzerback T., Berry K., Baas S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gilm M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis Mohn and Chlamydia
 pneumoniae AR39";
 RN Nucleic Acids Res. 28:1397-1406(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 from Japan and CML029 from USA";
 RN Nucleic Acids Res. 28:2311-2314(2000).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Manganese (By similarity).
 CC -!- SUBUNIT: HOMODIMER (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.

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DR EMBL; AE001591; AAD18210.1; -.
 DR EMBL; AE002230; AAF38524.1; -.
 DR EMBL; AP002545; BAA98268.1; -.
 DR HSSP; P04179; IAP6.
 DR PHCI-2DPAGE; Q929C4; -.
 DR TIGR; CP0718; -.
 DR InterPro; IPR001189; SODismutase.

DR Pfam; PF00081; sode; 1.
 DR Pfam; PF02777; sode; 1.
 DR Prodom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD MN; 1.

KM Oxidoreductase; Manganese; Complete proteome.
 FT METAL 31 31 MANGANESE (BY SIMILARITY).
 FT METAL 78 78 MANGANESE (BY SIMILARITY).
 FT METAL 166 166 MANGANESE (BY SIMILARITY).
 FT METAL 170 170 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 207 AA; 23541 MW; 45A4A6FF096F8934 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 207;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSLPEL 7
 Db 6 YSLPEL 11

RESULT 16

PURU_HAEN STANDARD; PRT; 278 AA.

DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Formyltetrahydrofolate deformylase (EC 3.5.1.10) (Formyl-FH(4)
 DE hydrolyase).
 GN PURU OR H11588.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uetzerback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Frichman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd.";
 RN Science 269:496-512(1995).
 RN [2]
 RP SEQUENCE OF 64-278 FROM N.A.
 RC STRAIN=RM 7004 / Serotype B;
 RX MEDLINE=93328119; PubMed=8335255;
 RA Maskell D.J.;
 RT "Cloning and sequencing of the Haemophilus influenzae ara gene";
 RN Gene 129:155-156(1993).

CC -!- FUNCTION: PRODUCES FORMATE FROM FORMYL-TETRAHYDROFOLATE. PROVIDES
 CC THE MAJOR SOURCE OF FORMATE FOR THE PURT-DEPENDENT SYNTHESIS OF
 CC 5'-PHOSPHORIBOSYL-N-FORMYLGLYCINAMIDE (FGAR) DURING AEROBIC
 CC GROWTH. HAS A ROLE IN REGULATING THE ONE-CARBON POOL
 CC (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: 10-formyltetrahydrofolate + H(2)O = formate +
 CC tetrahydrofolate.
 CC -!- ENZYME REGULATION: ACTIVATED BY METHIONINE, INHIBITED BY GLYCINE
 CC (BY SIMILARITY).

CC

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CC -1- PATHWAY: De novo purine biosynthesis.
CC -1- SUBUNIT: HOMOMEXAMER (BY SIMILARITY).
CC -1- SIMILARITY: SOME, TO GAR TRANSFORMYLASE (PURN).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U32833; AAC2336.1; -.
CC EMBL: L04686; AAA24942.1; -.
CC PIR: P06060; P06060.
CC HSP: P08179; IGRC.
CC TIGR: H1588; -.
CC InterPro: IPR002912; ACT.
CC InterPro: IPR004810; PURU.
CC InterPro: IPR002376; formyl transferase.
CC Pfam: PF00551; formyl transferase; 1.
CC ORFam: PF01842; ACT; 1.
CC TIGRfam: TIGR00555; PURU; 1.
CC Purine biosynthesis; Hydrolyase; One-carbon metabolism;
CC Complete proteome.
CC ACT SITE 223 BY SIMILARITY.
CC CONFLICT 115 117 VIG -> RNR (IN REF. 2).
CC CONFLICT 138 140 HEN -> PK (IN REF. 2).
CC CONFLICT 205 205 K -> E (IN REF. 2).
CC SEQUENCE 278 AA; 32173 MW; 7F375AB3C4225C4B CRC64;

Query Match 20.0%; Score 6; DB 1; Length 278;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYSLPE 6
Db 66 KYSLPE 71

RESULT 17
MENC_MYCLE STANDARD; PRT; 334 AA.
ID MENC_MYCLE
AC Q9CBB2;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable O-succinylbenzoate-CoA synthase (EC 4.2.1.-) (OSB synthase)
DE (OSBS) (4-(2-carboxyphenyl)-4-oxobutylric acid synthase) (O-
succinylbenzoyl-CoA synthase).
DE MENC OR ML2268.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeyer K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltham T., Fraser A., Hamlin N.,
RA Holtroyd S., Hornby T., Jegerle K., Jancic C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrett B.G.;
RA "Massive gene decay in the leprosy bacillus.";
RA Nature 409:1007-1011 (2001).
RL -1- FUNCTION: Converts SHHC to OSB (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-
carboxylate + O-succinylbenzoate + H(2)O.

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CC -1- COFACTOR: Requires a divalent metal ion (By similarity).
CC -1- PATHWAY: Menaguinone biosynthesis.
CC -1- SUBUNIT: BELONGS TO THE MANDULATE RACEMASE / MUONATE
CC LACTONIZING ENZYME FAMILY. MENC SUBFAMILY 1.
CC -----
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CC -----
CC EMBL: AL583925; CAC31784.1; -.
CC EMBL: ML2268; -.
CC InterPro: IPR001354; MR_MLE.
CC Pfam: PF01188; MR_MLE; 1.
CC Menaguinone biosynthesis; Lyase; Complete proteome.
CC ACT_SITE 107 107 BY SIMILARITY.
CC ACT_SITE 209 209 BY SIMILARITY.
CC SEQUENCE 334 AA; 35310 MW; 9590196DACF93145 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 334;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LPELDY 9
Db 252 LPELDY 257

RESULT 18
UTR2_YEAST STANDARD; PRT; 347 AA.
ID UTR2_YEAST
AC P32623;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE UTR2 protein (Unknown transcript 2 protein).
DE UTR2 OR YEL040W OR SYGP-ORF18.
GN Saccharomyces cerevisiae (Baker's yeast).
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., Komp C.,
RA Wei Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
RA Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RX [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Arujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Huntke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Moseedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petrel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RA Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RX [3]
RP SEQUENCE FROM N.A.
RC STRAIN=B-6441;
RX MEDLINE=94016558; PubMed=8411151;
RA Melnick L., Sherman F.;
RA "The gene clusters AKC and COR on chromosomes 5 and 10, respectively,
RA of Saccharomyces cerevisiae share a common ancestry.";
RA J. Mol. Biol. 233:372-388 (1993).
RL -1- SIMILARITY: SOME, TO YEAST YGR189C.
CC -1- SIMILARITY: SOME, TO YEAST YGR189C.
CC -----
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DR EMBL; U18779; AAB65002.1; ALT_INIT.
DR EMBL; L22173; AAA34941.1; -
DR EMBL; S65964; AAD13975.1; -
DR EMBL; S66130; AAB28444.1; -
DR PIR; S30839; S30839.
DR HSSP; P23904; 1A0.
DR SGD; S0000766; UMR2.
DR InterPro; IPR000757; Glyco_hydro_16.
DR Pfam; PF00722; Glyco_hydro_16; 1.
FT DOMAIN 234 322 SER-RICH.
FT DOMAIN 269 283 POLY-SER.
FT CONFLICT 10 10 L -> V (IN REF. 3).
FT CONFLICT 171 171 A -> R (IN REF. 3).
FT CONFLICT 234 234 S -> C (IN REF. 3).
SEQUENCE 347 AA; 36692 MW; 188AFB862C4BB328 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ELDYEF 11
|||||
DB 46 ELDYEF 51

RESULT 19
ID ID12 HALN1 STANDARD; PRT; 360 AA.
AC OSHHE4; O54623;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE (Isopentenyl)-diphosphate delta-isomerase (EC 5.3.3.2) (IPP isomerase)
DE (Isopentenyl) pyrophosphate isomerase.
GN (FNI1 OR VNG5084G OR H0660) AND (FNI2 OR VNG5233G OR H1696) AND
GN (FNI3 OR VNG6081G) AND (FNI4 OR VNG6445G).
OS Halobacterium sp. (Strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteriales;
OC Archaea; Euryarchaeota; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_Taxid=64091;
[1]
SEQUENCE FROM N.A.
PLASMID=PNRC100;
MEDLINE=99063795; PubMed=9847077;
RA Ng W.V., Cifuentes S.A., Smith T.M., Bungarner R.E., Baskin D., Faust J.,
RA Hall B., Loretz C., Sero J., Slagel J., Hood L., Dasarma S.,
RT "Snapshot of a large dynamic replicon in a halophilic archaeon:
RT megaplasmid or minichromosome";
RL Genome Res. 8:1131-1141(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC PLASMID=PNRC200;
RX MEDLINE=20504483; PubMed=11016950;
RA Shukla H.D., Kennedy S.P., Mahatras G.G., Bergquist B., Pan M.,
RA Shukla H.D., Laeky S.R., Ballya N.S., Thorson V., Strydom J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Weir R., Goo Y.A.,
RA Lettner B., Keller K., Cruz R., Hanson M.J., Hough D.W.,
RA Maddocks D.G., Jabloncki P.E., Krebs M.P., Angewine C.M., Dale H.,
RA Isenberger T.A., Peck R.F., Fehlechner M., Spudich J.L., Jung K.-H.,
RA Alam M., Freltas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Edhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dasarma S.,
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC -1- FUNCTION: CATALYZES THE 1,3-ALLYLIC REARRANGEMENT OF THE
CC HOMOMALYLIC SUBSTRATE ISOPENTENYL (IPP) TO ITS ALLYLIC ISOMER,
CC DIMETHYLLALLYL DIPHOSPHATE (DMAPP) (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl

CC diphosphate.
CC -1- COFACTOR: FMN AND NADPH (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IPP ISOMERASE TYPE 2 FAMILY.
CC
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DR EMBL; AF016485; AAC82844.1; ALT_INIT.
DR EMBL; AF016485; AAC82933.1; ALT_INIT.
DR EMBL; AE005145; AAG20768.1; -
DR EMBL; AE005145; AAG21040.1; -
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR000262; FMN_hydryac_dh.
DR Pfam; PF01070; FMN_dh; 1.
KM Isomerase; Isoprene biosynthesis; Flavoprotein; FMN; NADP; Plasmid;
KM Complete proteome.
SQ SEQUENCE 360 AA; 38342 MW; 67B14178071D3164 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LPELDY 9
|||||
DB 42 LPELDY 47

RESULT 20
ID HEMT HAEIN STANDARD; PRT; 428 AA.
AC P44772;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hemt protein homolog.
GN HEMT OR H10602.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
OC Haemophilus.
OX NCBI_Taxid=727;
[1]
SEQUENCE FROM N.A.
RC STRAIN=Rd / KM20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kervatage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uetereback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fritchman J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: INVOLVED IN A LATE STEP OF PROTOHEME IX SYNTHESIS
CC (BY SIMILARITY).
CC -1- PATHWAY: Porphyrin biosynthesis.
CC
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CC -----
 DR EMBL; U32742; AAC22260.1; -
 DR TIGR; H10602; -
 DR InterPro; IPR005254; Heme_bio.
 DR TIGRPRMS; TIGR00540; hemy_coll; 1.
 DR Porphylin biosynthesis; Complete proteome.
 KW SEQUENCE 428 AA; 48776 MW; 8654FAC94689CB5C CRC64;

Query Match 20.0%; Score 6; DB 1; Length 428;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 PFISQ 21
 |||||
 Db 19 PFISQ 24

RESULT 21
 TC21_AVEA STANDARD; PRT; 535 AA.

01-FEB-1995 (Rel. 31, Created)
 01-FEB-1995 (Rel. 31, Last sequence update)
 01-OCT-1996 (Rel. 34, Last annotation update)
 DE T-complex protein 1, epsilon subunit (TCP-1-epsilon) (CCT-epsilon)
 (TCP-K19).
 OS Avena sativa (Oat).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Avenae; Avena.
 OX NCBI_TaxID=4498;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=cv. Dewi; TISSUE=Mesocotyl, and Coleoptile;
 RX MEDLINE=94085629; PubMed=7903257;
 RA Elmann B., Krenz W., Mummert E., Schaefer E.;
 RT "Two Tcp-1-related but highly divergent gene families exist in oat
 encoding proteins of assumed chaperone function."
 FEBS Lett. 336:313-316(1993).
 CC -1- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON
 ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF
 ACTIN AND TUBULIN.

CC -1- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 kDa THAT
 FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.

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CC EMBL; X75777; CA53396.1; -
 DR PIR; S39319; S39319.
 DR PIR; S40461; S40461.
 DR HSP; P48424; 1A6D.

DR InterPro; IPR002194; Chaperonin_TCP-1.
 DR InterPro; IPR002423; Cpn60/TCP-1.
 DR Pfam; PF00118; Cpn60_TCP1.1.
 DR PRINTS; PR00304; TCOMPLEXTCP1.
 DR PROSITE; PS00750; TCP1_1; 1.
 DR PROSITE; PS00751; TCP1_2; 1.
 DR PROSITE; PS00951; TCP1_3; 1.
 DR Chaperone; ATP-binding; Multigene family.
 KW SEQUENCE 535 AA; 58899 MW; 6AFAF847CA891BC32 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 535;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YFSAT 14
 |||||
 Db 151 YFSAT 156

RESULT 22
 TC22_AVEA STANDARD; PRT; 535 AA.

AC P54411;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE T-complex protein 1, epsilon subunit (TCP-1-epsilon) (CCT-epsilon)
 (TCP-K36).
 OS Avena sativa (Oat).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Avenae; Avena.
 OX NCBI_TaxID=4498;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=cv. Dewi; TISSUE=Mesocotyl, and Coleoptile;
 RX MEDLINE=94085629; PubMed=7903257;
 RA Elmann B., Krenz W., Mummert E., Schaefer E.;
 RT "Two Tcp-1-related but highly divergent gene families exist in oat
 encoding proteins of assumed chaperone function."
 FEBS Lett. 336:313-316(1993).
 CC -1- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON
 ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF
 ACTIN AND TUBULIN.

CC -1- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 kDa THAT
 FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.

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CC EMBL; X75778; CA53397.1; -
 DR HSP; P48424; 1A6D.

DR InterPro; IPR002194; Chaperonin_TCP-1.
 DR InterPro; IPR002423; Cpn60/TCP-1.

DR Pfam; PF00118; Cpn60_TCP1.1.
 DR PRINTS; PR00304; TCOMPLEXTCP1.

DR PROSITE; PS00750; TCP1_1; 1.
 DR PROSITE; PS00751; TCP1_2; 1.
 DR PROSITE; PS00951; TCP1_3; 1.
 KW Chaperone; ATP-binding; Multigene family.
 KW SEQUENCE 535 AA; 59034 MW; 02761226F5F17B81 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 535;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YFSAT 14
 |||||
 Db 151 YFSAT 156

RESULT 23
 YD23_AVEA STANDARD; PRT; 561 AA.

AC P31826; P76133; P76876;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical ABC transporter ATP-binding protein ydda (CDS102).
 GN YD23 OR B1496.

OC Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_Taxid=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=9742617; PubMed=9278503;
 RA Blatner F.R., Plunkett G. II, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
 RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,
 RA Oshima T., Saito N., Sampei G., Seki Y., Sivasubraman S.,
 RA Tengan H., Takeeda J., Takemoto K., Takeuchi Y., Wada C.,
 RA Yamamoto Y., Horiiuchi T.;
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 28.0-40.1 min region on the linkage map";
 RL DNA Res. 3:363-377(1996).
 RN [3]
 RP SEQUENCE OF 306-561 FROM N.A.
 RC STRAIN=K12;
 RA Thirlin E., Gasser F., Bienville F.;
 RT "Sequence and functional analysis of an Escherichia coli DNA fragment
 able to complement pggE and pggF from Methylobacterium organophilum";
 RL Submitted (May-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
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 CC -----
 DR EMBL: A600246; AAC74569.1; -;
 DR EMBL: X71917; CAAS0732.1; ALT_INIT.
 DR EMBL: D90791; BAA15167.1; ALT_INIT.
 DR EMBL: D90792; BAA15170.1; -;
 DR PIR: S33468; S33468.
 DR EcoGene: EG11742; Ydda.
 DR InterPro: IPR003439; ABC_transportr.
 DR Pfam: PF00005; ABC_tran; 1.
 DR ProDom: PD000006; ABC_transportr; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KM Hypothetical protein; ATP-binding; Transport; Transmembrane;
 KM Complete proteome.
 FT TRANSMEM 4 24 POTENTIAL.
 FT TRANSMEM 32 52 POTENTIAL.
 FT TRANSMEM 71 91 POTENTIAL.
 FT TRANSMEM 152 172 POTENTIAL.
 FT TRANSMEM 188 208 POTENTIAL.
 FT TRANSMEM 291 311 POTENTIAL.
 FT NP BIND 400 407 ATP (POTENTIAL).
 SQ SEQUENCE 561 AA; 64984 MW; 92847426294413P5 CRC64;
 QY Query Match 20.0%; Score 6; DB 1; Length 561;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 18 ISGQIN 23
 |||||

DB 302 ISGQIN 307
 RESULT 24
 EMBL_MOUSE
 ID EMBL_MOUSE STANDARD; PRT; 879 AA.
 AC Q922H5;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Band 4.1-like protein 1 (Neuronal protein 4.1) (4.1N).
 GN EPB41L1 OR EPB4.1L1 OR EPB4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99343811; PubMed=10414974;
 RA Palensky L.D., Blackshaw S., Liao D., Mackins C.C., Weier H.-U.G.,
 RA Parra M., Hagan R.L., Conboy J.G., Mohandas N., Snyder S.H.;
 RT "A novel neuron-enriched homolog of the erythrocyte membrane
 cytoskeletal protein 4.1";
 RL J. Neurosci. 19:6457-6467(1999).
 CC -1- FUNCTION: May function to confer stability and plasticity to
 CC neuronal membrane via multiple interactions, including the
 CC spectrin-actin-based cytoskeleton, integral membrane channels and
 CC membrane-associated guanylate kinases.
 CC -1- TISSUE SPECIFICITY: Highest expression in brain, also present in
 CC kidney, olfactory epithelium, retina, sensory ganglia,
 CC gastrointestinal tract (only enteric neurons) and lung.
 CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: AF061283; AAC68583.1; -;
 DR MGD: MGI:103010; Epp4.111.
 DR InterPro: IPR000299; Band_4.1.
 DR Pfam: PF00373; Band_41; 1.
 DR PRINTS: PR00935; BAND41.
 DR SMART: SM00295; B41; 1.
 DR PROSITE: PS00660; BAND_41_1; 1.
 DR PROSITE: PS00661; BAND_41_2; 1.
 DR PROSITE: PS00657; BAND_41_3; 1.
 KM Structural protein; Cytoskeleton.
 FT DOMAIN 94 308 BAND_4.1-LIKE.
 FT DOMAIN 375 482 HYDROPHILIC.
 FT DOMAIN 483 541 SPECTRIN--ACTIN-BINDING.
 FT DOMAIN 743 879 CARBOXYL--TERMINAL (CTD).
 SQ SEQUENCE 879 AA; 98314 MW; 2E8501A4BDCA325 CRC64;
 QY Query Match 20.0%; Score 6; DB 1; Length 879;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 3 SLEPDL 8
 |||||
 DB 639 SLEPDL 644
 RESULT 25
 EMBL_HUMAN
 ID EMBL_HUMAN STANDARD; PRT; 881 AA.
 AC Q9H4G0; O15046;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Band 4.1-like protein 1 (Neuronal protein 4.1) (4.1N).
 GN EPB41.1 OR KIAA0338.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain.
 RX MEDLINE=97349984; PubMed=9205841;
 RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. VII.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro."
 RL Dna Res. 4:141-150(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stuvrider G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Collier R.E., Connor R.E., Corby N.R.,
 RA Cragg S., Copley V.E., Collier R.E., Dhami P.D., Dunn M.,
 RA Coulson A., Coville G.J., Deadman R., Frankland J.A., French L., Garner P.,
 RA Ellington A.G., Frankland J.A., Frazer A., Griffiths M.N.D., Hall R.E.,
 RA Griffith D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird D.M., Lawlor S.,
 RA Levevaev M.H., Leverish M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McComachie L.J., McElay K., McMurtry A.A.,
 RA Oliver S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T.,
 RA Oline K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuse C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilmberg L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20."
 RL Nature 414:865-871(2001).
 CC -1- FUNCTION: May function to confer stability and plasticity to
 CC neuronal membrane via multiple interactions, including the
 CC spectrin-actin-based cytoskeleton, integral membrane channels and
 CC membrane-associated guanylate kinases.
 CC -1- TISSUE SPECIFICITY: Highest expression in brain, lower in heart,
 CC kidney, pancreas, placenta, lung and skeletal muscle.
 CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
 CC -----
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 CC -----
 CC EMBL; AB002336; BAA20796.1; ALT_INIT.
 CC EMBL; AL121895; CAC09920.1; --
 CC GenBank; HGNC:3378; EPB41.1.
 CC MIM; 602879; --
 CC InterPro; IPR000299; Band 4.1.
 CC Pfam; PF00373; Band 41; 1.
 CC PRINTS; PR00935; BAND41.
 CC SMART; SM00295; B41; 1.
 CC PROSITE; PS00660; BAND_41_1; 1.
 CC PROSITE; PS00661; BAND_41_2; 1.

DR PROSITE; PSS0057; BAND_41_3; 1.
 KW Structural protein; Cytoskeleton.
 FT DOMAIN 94 308 BAND 4.1-LIKE.
 FT DOMAIN 483 541 SPECTRIN-ACTIN-BINDING.
 FT DOMAIN 746 881 CARBOXYL-TERMINAL (CTD).
 FT CONFLICT 484 484 MISSING (IN REF. 2).
 FT CONFLICT 729 729 MISSING (IN REF. 2).
 SQ SEQUENCE 881 AA; 98502 MW; D923CF554EDB41D3 CRC64;
 Query Match 20.0%; Score 6; DB 1; Length 881;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SLPEID 8
 DB 639 SLPEID 644
 RESULT 26
 UVRA NEIMA STANDARD; PRT; 948 AA.
 ID UVRA NEIMA
 AC Q9JUS4;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Excinuclease ABC subunit A.
 GN UVRA OR NMA1159.
 OS Neisseria meningitidis (serogroup A).
 CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 CC NCBI_TaxID=55699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22491 / Serogroup A / Serotype 4A;
 RX MEDLINE=20222556; PubMed=10761919;
 RA Pakhilli U., Achtman M., James K.D., Bentley S.D., Churcher C.,
 RA Klee S.R., Morelli G., Baeham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holtroyd S.,
 RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
 RA Randeram M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 RT meningitidis 22491."
 RL Nature 404:502-506(2000).
 CC -1- FUNCTION: The ABC excision nuclease is a DNA repair enzyme that
 CC catalyzes the excision reaction of UV-damaged nucleotide segments
 CC producing oligomers having the modified base(S). Uvra is an ATPase
 CC and a DNA-binding protein that preferentially binds single-
 CC stranded or UV-irradiated double-stranded DNA (by similarity).
 CC -1- SUBUNIT: Consists of three subunits; uvra, uvrb and uvrc.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AL162755; CAB84421.1; --
 CC InterPro; IPR003439; ABC_transportr.
 CC InterPro; IPR004602; UVRA.
 CC Pfam; PF00005; ABC_tran; 2.
 CC ProDom; PD000006; ABC_transportr; 1.
 CC TIGRfam; TIGR00630; uvra; 1.
 CC PROSITE; PS00211; ABC_TRANSPORTER; 2.
 CC SOS response; Excision nuclease; DNA repair; ATP-binding; Repeat;
 CC DNA-binding; Zinc-finger; Complete proteome.
 FT NP_BIND 42 49 ATP (POTENTIAL).
 FT NP_BIND 649 656 ATP (POTENTIAL).
 FT ZN_FING 262 289 C4-TYPE.
 FT ZN_FING 748 774 C4-TYPE.

SEQ SEQUENCE 948 AA; 105191 MW; E98717DF62B9A0D CRC64;

Query Match 20.0%; Score 6; DB 1; Length 948;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLEP 7

DB 267 YSLEP 272

RESULT 27

UVRA_NEIMB

ID UVRA_NEIMB STANDARD; PRT; 949 AA.

AC Q9JZP1;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

EXCINUCLEASE ABC subunit A.

UVRA OR NMB0962.

OS Neisseria meningitidis (serogroup B).

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=491;

[1]

SEQUENCE FROM N.A.

RC STRAIN=MC58 / Serogroup B;

MDLINE=20175755; PubMed=10710307;

RA Tettein H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

Eisen J.A., Ketchum K.A., Hood D.W., Feden J.F., Dodson R.U.,

Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,

Hait D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

Mason T., Clecko A., Parksey D.S., Blair E., Cifton H., Clark E.B.,

Cotton M.D., Uterback T.R., Khouri H., Qin H., Vamathavan J.,

Gill J., Scarlato V., Maignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Frazer C.M., Moxon E.R., Rappuoli R., Venter J.C.,

"Complete genome sequence of Neisseria meningitidis serogroup B strain

MC58."

RT Science 287:1809-1815 (2000).

CC -1- FUNCTION: The ABC excision nuclease is a DNA repair enzyme that

catalyzes the excision reaction of UV-damaged nucleotide segments

producing oligomers having the modified base(s). UVRA is an ATPase

and a DNA-binding protein that preferentially binds single-

stranded or UV-irradiated double-stranded DNA (by similarity).

CC -1- SUBUNIT: Consists of three subunits, uvra, uvrb and uvrc.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).

CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.

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CC EMBL; AE002447; AAF41368.1; -.

DR TIGR; NMB0962; -.

DR InterPro; IPR003439; ABC_transportr.

DR InterPro; IPR004602; UVRA.

DR Pfam; PF00005; ABC_tran; 2.

DR ProDom; PD000006; ABC_transportr; 1.

DR TIGRFAMs; TIGR00630; uvra; 1.

DR PROSITE; PS00211; ABC_TRANSPORTER; 2.

SOS response; Excision nuclease; DNA repair; ATP-binding; Repeat;

KM DNA-binding; Zinc-finger; Complete proteome.

FT NP_BIND 42 49 ATP (POTENTIAL).

FT NP_BIND 649 656 ATP (POTENTIAL).

FT ZN_FING 262 289 C4-TYPE.

FT ZN_FING 748 774 C4-TYPE.

SEQ SEQUENCE 949 AA; 105536 MW; 153F5AE2D48CD035 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 949;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLEP 7

DB 267 YSLEP 272

RESULT 28

UVRA_NEIGO

ID UVRA_NEIGO STANDARD; PRT; 950 AA.

AC O50968;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Excinuclease ABC subunit A.

GN UVRA.

OS Neisseria gonorrhoeae.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=485;

[1]

SEQUENCE FROM N.A.

RC MEDLINE=97340932; PubMed=9197406;

RA Black C.G., Pyfe J.A.M., Davies J.K.;

"Cloning, nucleotide sequence and transcriptional analysis of the

uvra gene from Neisseria gonorrhoeae."

RL Mol. Genet. 254:479-485 (1997).

CC -1- FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT

CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS

PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN ATPASE

AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-

STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).

CC -1- SUBUNIT: CONSISTS OF THREE SUBUNITS; UVRA, UVRB AND UVRC.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).

CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.

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CC EMBL; U34760; AAA84885.1; -.

DR InterPro; IPR003439; ABC_transportr.

DR InterPro; IPR004602; UVRA.

DR Pfam; PF00005; ABC_tran; 2.

DR ProDom; PD000006; ABC_transportr; 1.

DR TIGRFAMs; TIGR00630; uvra; 1.

DR PROSITE; PS00211; ABC_TRANSPORTER; 2.

SOS response; Excision nuclease; DNA repair; ATP-binding; Repeat;

KM DNA-binding; Zinc-finger.

FT NP_BIND 42 49 ATP (POTENTIAL).

FT NP_BIND 649 656 ATP (POTENTIAL).

FT ZN_FING 262 289 C4-TYPE.

FT ZN_FING 748 774 C4-TYPE.

SEQ SEQUENCE 950 AA; 105552 MW; 359806240AAD6F1 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 950;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLEP 7

DB 267 YSLEP 272

RESULT 29

BCG3_ACEXY

ID BCG3_ACEXY STANDARD; PRT; 1325 AA.

AC Q9WK63;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

```

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellulose synthase 1 operon protein C precursor.
GN BCSCI.
OS Acetobacter xylinus.
OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
OC Gluconacetobacter.
OX NCBI_TaxID=28448;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 7664 / IFO 13693;
RX PubMed=10382968;
RA Umeda Y., Hirano A., Teshibashi M., Akiyama H., Onizuka T., Ikeuchi M.,
RA Inoue Y.;
RT "Cloning of cellulose synthase genes from Acetobacter xylinum JCM
RT 7664: implication of a novel set of cellulose synthase genes.";
RL DNA Res. 6:109-115(1999).
CC -1- FUNCTION: Required for maximal bacterial cellulose synthesis. It
CC may be involved in the formation of a membrane complex for
CC extrusion of the cellulose product (By similarity).
CC -1- PATHWAY: Bacterial cellulose biosynthesis.
CC -1- SUBCELLULAR LOCATION: Outer membrane (Potential).
CC -1- SIMILARITY: BELONGS TO THE ACSC/BCSC FAMILY.
CC -1- SIMILARITY: CONTRAINS 8 TPR REPEATS.
-----
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-----
DR EMBL; AB015802; BAA77587.1; -.
DR InterPro; IPR003921; Cellsynth_C.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 4.
DR PRINTS; PR01441; CELL5THSEC.
DR KEGG; Cellulose biosynthesis; Repeat; TPR repeat; Membrane; Outer membrane;
KW Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 1 1325 CELLULOSE SYNTHASE 1 OPERON PROTEIN C.
FT REPEAT 50 83 TPR 1.
FT REPEAT 85 117 TPR 2.
FT REPEAT 292 325 TPR 3.
FT REPEAT 326 359 TPR 4.
FT REPEAT 406 439 TPR 5.
FT REPEAT 558 591 TPR 6.
FT REPEAT 702 735 TPR 7.
FT REPEAT 737 769 TPR 8.
FT SEQUENCE 1325 AA; 142541 MW; DA4EEECFADEDED74D CRC64;
-----
Query Match 20.0%; Score 6; DB 1; Length 1325;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
-----
Oy 18 ISGQIN 23
Db 900 ISGQIN 905
-----
RESULT 30
ID V194 FOMPV STANDARD; PRT; 74 AA.
AC Q95539;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein FV194.
GN FV194.
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;

```

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RA Alfonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831(2000).
CC -1- SIMILARITY: BELONGS TO THE POXVIRUSES A30 FAMILY.
-----
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-----
DR EMBL; AF198100; AAF4538.1; -.
DR SEQUENCE 74 AA; 8580 MW; E41581447F94752C CRC64;
-----
Query Match 16.7%; Score 5; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
-----
Oy 10 EFSAT 14
Db 29 EFSAT 33
-----
RESULT 31
ID YKK2 CAEEL STANDARD; PRT; 85 AA.
AC P34279;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C02F5.2 in chromosome III.
GN C02F5.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2; PubMed=7906398;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Frazer A.,
RA Johnston L., Jones M., Kersey J., Kirschen J., Laiseter N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smailson N., Smith A., Smith M., Sonhammer B., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Wellstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
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-----
DR EMBL; L14745; AAA27917.1; -.
DR PIR; S44604; S44604.
DR Wormpep; C02F5.2; CE00038.
KW Hypothetical protein.
SEQUENCE 85 AA; 9425 MW; 10D565D051A2CCC CRC64;

```


Query Match 16.7%; Score 5; DB 1; Length 85;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FSATE 15
Db 60 FSATE 64

RESULT 32
YCK5_CHIRE STANDARD; PRT; 101 AA.
ID YCK5_CHIRE
AC P37825;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 11.4 kDa protein in TRNR-CHLB intergenic region (ORF101).
OS Chlamydomonas reinhardtii.
GC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
ON NCBI_TaxID=3055;
RX STRAIN=137C / CC-125;
RX MEDLINE=9403309; PubMed=8219066;
RA Liu X.-Q., Xu H., Huang C.;
RT "Chloroplast chl b gene is required for light-independent chlorophyll
RT accumulation in Chlamydomonas reinhardtii."
RL Plant Mol. Biol. 23:297-308(1993).
KM Chloroplast; Hypothetical protein.
SQ SEQUENCE 101 AA; 11437 MW; D6B871B65FB3065C CRC64;

Query Match 16.7%; Score 5; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 ISGOI 22
Db 26 ISGOI 30

RESULT 33
Y265_UREPA STANDARD; PRT; 109 AA.
ID Y265_UREPA
AC Q9P0G6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein UY265.
GN UY265
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
ON NCBI_TaxID=134831;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serovar 3;
RX MEDLINE=20500219; PubMed=11048724;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Casseil G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
RT urealyticum."
RL Nature 407:757-762(2000).

CC -1- SIMILARITY: BELONGS TO THE UPF0154 FAMILY.

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CC -----
DR EMBL; A6002123; AAF30674.1; -.
DR InterPro; IPR005359; UPF0154.
DR Pfam; PF03672; UPF0154; 1.
KM Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 42 62
SQ SEQUENCE 109 AA; 12223 MW; 00EE24A524356823 CRC64;

Query Match 16.7%; Score 5; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QINEL 25
Db 97 QINEL 101

RESULT 34
ANFC_SCYCA STANDARD; PRT; 115 AA.
ID ANFC_SCYCA
AC P23259;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-type natriuretic peptide (CNP-115).
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeidae; Carcharhiniformes;
OC Scyliorhinidae; Scyllorhinus.
ON NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart atrium, and Heart ventricle;
RX MEDLINE=91243822; PubMed=1828036;
RA Suzuki R., Takahashi A., Hazon N., Takei Y.;
RT "Isolation of high-molecular-weight C-type natriuretic peptide from
RT the heart of a cartilaginous fish (European dogfish, Scyllorhinus
RT canicula)."
RL FEBS Lett. 282:321-325(1991).
RL -1- FUNCTION: VASORELAXANT ACTIVITY. HAS A GMP-STIMULATING ACTIVITY
CC -1- (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: CNP-115 IS DIFFERENTIALLY PROCESSED TO
CC PRODUCE CNP-38 AND CNP-39 IN THE HEART AND CNP-22 IN THE BRAIN.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
DR InterPro; IPR002406; C_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; C_natriurtcep; 1.
DR SMART; SM00183; NAT_pep; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KM Vasoactive.
FT PEPTIDE 77 115
FT PEPTIDE 78 115
FT PEPTIDE 94 115
FT DISULFD 99 115
SQ SEQUENCE 115 AA; 12885 MW; 49AE7200BE4C7F8A CRC64;

Query Match 16.7%; Score 5; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SLPEL 7
Db 40 SLPEL 44

RESULT 35
SMD2_SCHPO STANDARD; PRT; 115 AA.
ID SMD2_SCHPO
AC O14036;

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DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable small nuclear ribonucleoprotein Sm D2 (snRNP core protein D2)
DE (Sm-D2).
GN SMD2 OR SPAC2C4.03C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
CX NCBI_TaxID=4896;
RX MEDLINE=972;
RX STRAIN=972;
RA MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooke K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Welfens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesti D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leinbach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Weiler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleu V., Motier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: REQUIRED FOR PRE-MRNA SPLICING. REQUIRED FOR SNRNP
CC -!- BIOGENESIS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SNRNP CORE PROTEIN FAMILY.
CC -----
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CC -----
CC EMBL; Z99259; CAB16363.1; -.
CC DR InterPro; IPR001163; snRNP_Sm.
CC DR Pfam; PF01423; Sm; 1.
CC KM Nuclear protein; Ribonucleoprotein; mRNA splicing; mRNA processing.
CC SEQUENCE 115 AA; 13095 MW; EF39B5ID94356C33 CRC64;

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Query Match 16.7%; Score 5; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 YEFSA 13
DB 23 YEFSA 27

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RESULT 36
REV_STVCZ STANDARD; PRT; 124 AA.
ID_REV_STVCZ
AC P17280;

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DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE REV protein (Anti-repression transactivator protein) (ART/TRS).
DE REV.
GN Chimpanzee immunodeficiency virus (SIVcpz) (CIV).
OS Viruses; Retroid viruses; Retroviridae; Lentiviruses.
CX NCBI_TaxID=11723;
RX MEDLINE=90259077; PubMed=2188136;
RA Hueb T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
RT "Genetic Organization of a chimpanzee lentivirus related to HIV-1.";
RL Nature 345:356-359(1990).
CC -!- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE
CC NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
CC -!- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleol.
CC -!- PTM: PHOSPHOPROTEIN WHOSE STATE OF PHOSPHORYLATION IS MEDIATED
CC BY A SPECIFIC SERINE KINASE ACTIVITY PRESENT IN THE NUCLEUS.
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CC -----
CC EMBL; X52154; CAJ36405.1; -.
CC DR PIR; S09988; VKLJST.
CC DR HIV; X52154; REVSCP2.
CC DR InterPro; IPR000625; REV_protein.
CC DR Pfam; PF00424; REV; 1.
CC KM Transcription regulation; AIDS; Phosphorylation; Nuclear protein.
CC SEQUENCE 124 AA; 13701 MW; F5877D1BD65A7B2 CRC64;

```

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Query Match 16.7%; Score 5; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LPELD 8
DB 76 LPELD 80

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RESULT 37
Y364.AQUB STANDARD; PRT; 125 AA.
ID Y364.AQUB
AC 06689;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AQ_364.
GN AQ_364.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
CX NCBI_TaxID=63363;
RX MEDLINE=98196666; PubMed=9537320;
RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -!- SIMILARITY: BELONGS TO THE UPF0076 (UKL14) FAMILY.
CC -----
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DR EMBL; AB000686; AAC06655.1; -
DR HSSP; P37552.10D9.
DR InterPro; IPR000543; YjGF-like.
DR Pfam; PF01042; UPF0076.1.
DR TrEMBL; TIGR00004; YER057C YjGF_UK14; 1.
DR PROSITE; PS01094; UPF0076.1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 125 AA; 14004 MW; 945D559A5C71E819 CRC64;

Query Match 16.7%; Score 5; DB 1; Length 125;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

18 ISGQ1 22
|||||
28 ISGQ1 32

RESULT 38
Y026_NPVOP
ID Y026_NPVOP STANDARD; PRT; 127 AA.
AC O10297;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 14.4 kDa protein (ORF42).
OS Orygia pseudotsugata multicaudata polyhedrosis virus (OpnMPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=164623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97271300; PubMed=9126251;
RA Atkins C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
RA Rohrmann G.F.;
RT "The sequence of the Orygia pseudotsugata multicaudata nuclear
RT polyhedrosis virus genome.";
RL Virology 229:381-399(1997).
CC -1- SIMILARITY: TO CORRESPONDING ORF IN ACNMPV.
CC -----
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CC or send an email to license@isb-sib.ch).

DR EMBL; U75930; AAC59041.1; -
DR KW Hypothetical protein.
SQ SEQUENCE 127 AA; 14389 MW; 0771366D98517399 CRC64;

Query Match 16.7%; Score 5; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LDYEF 11
|||||
Db 79 LDYEF 83

RESULT 39
VAL2_ABMVW
ID VAL2_ABMVW STANDARD; PRT; 129 AA.
AC P21944;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE AL2 protein.
GN AC2.
OS Abutilon mosaic virus (isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9102094; PubMed=2219703;
RA Frischmuth T., Zimmet G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features.";
RL Virology 178:461-468(1990).
RN [2]
RP REVISIONS.
RA Jeske H.;
RL Submitted (NOV-1990) to GEMINIVIRUSES AL2 PROTEIN FAMILY.
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.
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DR EMBL; X15983; CAA34112.1; -
DR PIR; D36214; OOCVW4.
DR InterPro; IPR000942; Gemin1 AL2.
DR Pfam; PF01440; Gemin1 AL2; 1.
DR PRINTS; PR00230; GEMCONVAL2.
DR ProDom; PD001117; Gemin1 AL2; 1.
SQ SEQUENCE 129 AA; 14628 MW; 89C4E4DA563B9F CRC64;

Query Match 16.7%; Score 5; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SLPEL 7
|||||
Db 109 SLPEL 113

RESULT 40
VAL2_TM0V
ID VAL2_TM0V STANDARD; PRT; 129 AA.
AC Q06658;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL2 protein.
GN AL2.
OS Tomato mottle virus (isolate Florida) (TM0V).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36449;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93107858; PubMed=1469361;
RA Abouzid A.M., Polston J.E., Hiebert E.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
RT isolated from tomatoes in Florida.";
RL J. Gen. Virol. 73:3225-3229(1992).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.
CC -----
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DR EMBL; L14460; AAC32417.1; -

DR PIR; J01871; J01871.
DR InterPro; IPR000942; Gemini AL2.
DR Pfam; PF01440; Gemini AL2; 1.
DR PRINTS; PR00230; GEMCOATP12
DR ProDom; PD001117; Gemini_AL2; 1.
SQ SEQUENCE 129 AA; 14503 MW; AS1FA123739C9D9 CRC64;

Query Match 16.7%; Score 5; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 SLPEL 7
|||
Db 109 SLPEL 113

Search completed: April 9, 2003, 14:14:55
Job time : 30.9908 secs

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: April 9, 2003, 14:09:35 ; Search time 14.8624 Seconds
(without alignments)
415.910 Million cell updates/sec

Title: US-09-987-190-2
Perfect score: 30
Sequence: 1 KYSLELDYEFSAFEPYISQINEIXYTX 30

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues
Word size: 0

Total number of hits satisfying chosen parameters: 671580
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database:

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26.7	8	207	2 Q9F9R1	Q9F9R1 mycobacteri
2	26.7	8	210	2 Q9AM00	Q9AM00 mycobacteri
3	26.7	8	227	3 P79022	P79022 candida sp.
4	23.3	7	226	10 Q93X78	Q93X78 vitis vinif
5	23.3	7	23.3	10 Q9CSH7	Q9CSH7 arabidopsis
6	23.3	7	462	10 Q94ZJ1	Q94ZJ1 oryza sativ
7	23.3	7	495	10 Q91V34	Q91V34 arabidopsis
8	23.3	7	23.3	10 Q42975	Q42975 oryza sativ
9	23.3	7	507	10 Q24524	Q24524 manihot esc
10	23.3	7	512	10 Q91V33	Q91V33 arabidopsis
11	23.3	7	514	10 Q8VWL8	Q8VWL8 lycopersico
12	23.3	7	531	10 Q41172	Q41172 manihot esc
13	23.3	7	541	10 Q40283	Q40283 manihot esc
14	23.3	7	620	5 Q8SVR3	Q8SVR3 encephalito
15	23.3	7	807	5 Q9U275	Q9U275 caenorhabdi
16	23.3	7	936	2 Q9AMT5	Q9AMT5 bradyrhizob

17	23.3	7	1011	8	Q94QB2	Q94QB2 synechococ
18	20.0	6	57	17	Q97AN6	Q97AN6 thermoplas
19	20.0	6	91	16	Q8Z0Y8	Q8Z0Y8 salmoneila
20	20.0	6	100	15	Q97776	Q97776 human immun
21	20.0	6	150	2	Q9K590	Q9K590 halomonas e
22	20.0	6	153	11	Q9CJ39	Q9CJ39 muscicula
23	20.0	6	156	5	Q9BPW2	Q9BPW2 metagonimus
24	20.0	6	163	16	Q992V3	Q992V3 streptococ
25	20.0	6	184	1	Q06112	Q06112 methanococ
26	20.0	6	189	2	Q59673	Q59673 propionibac
27	20.0	6	193	15	Q90LU8	Q90LU8 human immun
28	20.0	6	200	2	Q9APV3	Q9APV3 corynebacte
29	20.0	6	200	15	Q9YV92	Q9YV92 human immun
30	20.0	6	200	15	Q90009	Q90009 human immun
31	20.0	6	202	15	Q70722	Q70722 human immun
32	20.0	6	202	15	Q70723	Q70723 human immun
33	20.0	6	202	15	Q71823	Q71823 human immun
34	20.0	6	202	15	Q71824	Q71824 human immun
35	20.0	6	202	15	Q71827	Q71827 human immun
36	20.0	6	203	15	Q90010	Q90010 human immun
37	20.0	6	203	15	Q9YV91	Q9YV91 human immun
38	20.0	6	203	15	Q9YV90	Q9YV90 human immun
39	20.0	6	203	15	Q70724	Q70724 human immun
40	20.0	6	203	15	Q70725	Q70725 human immun
41	20.0	6	203	15	Q70726	Q70726 human immun
42	20.0	6	203	15	Q71825	Q71825 human immun
43	20.0	6	203	15	Q71826	Q71826 human immun
44	20.0	6	205	11	Q91V37	Q91V37 mus musculi
45	20.0	6	206	15	Q70842	Q70842 human immun
46	20.0	6	206	15	Q12256	Q12256 human immun
47	20.0	6	206	15	Q12260	Q12260 human immun
48	20.0	6	206	15	Q12262	Q12262 human immun
49	20.0	6	207	15	Q70835	Q70835 human immun
50	20.0	6	209	12	Q91B19	Q91B19 rice black
51	20.0	6	209	12	Q913E1	Q913E1 rice black
52	20.0	6	209	12	Q910K4	Q910K4 rice black
53	20.0	6	209	12	Q913E3	Q913E3 rice black
54	20.0	6	221	4	Q96T08	Q96T08 homo sapien
55	20.0	6	223	5	Q8SGV7	Q8SGV7 encephalito
56	20.0	6	234	16	Q91656	Q91656 pseudomonas
57	20.0	6	264	15	Q9WPK4	Q9WPK4 human immun
58	20.0	6	264	15	Q9WB86	Q9WB86 human immun
59	20.0	6	264	15	Q9WBQ0	Q9WBQ0 human immun
60	20.0	6	266	15	Q9J4Q5	Q9J4Q5 human immun
61	20.0	6	283	2	Q31291	Q31291 buchnera ap
62	20.0	6	293	15	Q9J4P0	Q9J4P0 human immun
63	20.0	6	313	16	Q9CTU2	Q9CTU2 pasteurella
64	20.0	6	318	5	Q95YH4	Q95YH4 pseudotrich
65	20.0	6	318	5	Q95YH3	Q95YH3 pseudotrich
66	20.0	6	318	5	Q95NK6	Q95NK6 pseudotrich
67	20.0	6	326	5	Q95P29	Q95P29 holomastigo
68	20.0	6	328	5	Q95P32	Q95P32 pseudotrich
69	20.0	6	338	16	Q9CFP4	Q9CFP4 lactococcus
70	20.0	6	340	2	Q68186	Q68186 lactococcus
71	20.0	6	342	16	Q83329	Q83329 treponema f
72	20.0	6	345	5	Q22846	Q22846 caenorhabdi
73	20.0	6	352	17	Q9HP70	Q9HP70 halobacteri
74	20.0	6	354	10	Q9C5W2	Q9C5W2 arabidopsis
75	20.0	6	355	16	Q9HU37	Q9HU37 pseudomonas
76	20.0	6	361	17	Q82XN6	Q82XN6 pyrobaculum
77	20.0	6	366	10	Q9SXX9	Q9SXX9 arabidopsis
78	20.0	6	384	10	Q9SLA0	Q9SLA0 arabidopsis
79	20.0	6	385	16	Q9CCT5	Q9CCT5 mycobacteri
80	20.0	6	385	16	Q05881	Q05881 mycobacteri
81	20.0	6	398	15	Q11594	Q11594 human immun
82	20.0	6	405	2	Q66165	Q66165 agrobacteri
83	20.0	6	405	2	Q52225	Q52225 agrobacteri
84	20.0	6	411	16	Q8U691	Q8U691 agrobacteri
85	20.0	6	412	16	Q97M76	Q97M76 clostridium
86	20.0	6	429	3	Q9UCY9	Q9UCY9 schistosac
87	20.0	6	443	2	Q9ZHL4	Q9ZHL4 haemophilus
88	20.0	6	446	16	Q8UBH0	Q8UBH0 agrobacteri
89	20.0	6	448	12	Q91IL0	Q91IL0 white spot

90	6	20.0	448	12	Q8QTG4	Q8qtg4 white spot	163	5	16.7	67	16	Q8XP4	Q8xp4 clostridium
91	6	20.0	454	6	Q3BDE1	Q3bde1 micromycet	164	5	16.7	68	6	Q9N139	Q9n139 bos taurus
92	6	20.0	454	6	Q3BGC9	Q3bgc9 micromycet	165	5	16.7	68	15	Q97748	Q97748 human immun
93	6	20.0	455	15	Q92MW2	Q92mw2 rhizobium m	166	5	16.7	68	15	O40491	O40491 human immun
94	6	20.0	473	15	Q9WRJ3	Q9wrj3 human immun	167	5	16.7	69	2	O44536	O44536 azotobacter
95	6	20.0	477	17	Q9WRJ3	Q9wrj3 pyrobaculum	168	5	16.7	69	3	P87091	P87091 cyphonectr
96	6	20.0	482	16	Q97KK6	Q97kk6 clostridium	169	5	16.7	70	5	Q9NMS8	Q9nms8 leishmania
97	6	20.0	487	3	Q9P8R2	Q9p8r2 candida alb	170	5	16.7	70	16	Q9JUH7	Q9juh7 neisseria m
98	6	20.0	488	15	Q9K936	Q9k936 bacillus ha	171	5	16.7	75	6	Q9GMI9	Q9gmi9 macaca fasc
99	6	20.0	496	2	O69262	O69262 thermobacil	172	5	16.7	75	12	Q9OB61	Q9ob61 yaba monkey
100	6	20.0	506	10	O64879	O64879 arabadopsis	173	5	16.7	75	12	Q9DHJ3	Q9dhj3 yaba-like d
101	6	20.0	507	10	Q9FHO3	Q9fho3 arabadopsis	174	5	16.7	76	5	Q20092	Q20092 caenorhabdi
102	6	20.0	507	10	Q9LUD0	Q9lud0 arabadopsis	175	5	16.7	77	16	Q8REH7	Q8reh7 thermocnaer
103	6	20.0	508	16	O8Z194	O8z194 yersinia pe	176	5	16.7	79	5	Q9U0C4	Q9uoc4 plasmodium
104	6	20.0	509	2	Q93F40	Q93f40 shigella fl	177	5	16.7	80	5	Q9U0P8	Q9uop8 plasmodium
105	6	20.0	511	16	O8R949	O8r949 thermocnaer	178	5	16.7	80	5	Q9U0P8	Q9uop8 plasmodium
106	6	20.0	514	10	Q9M1D0	Q9m1d0 arabadopsis	179	5	16.7	80	5	Q9U0P7	Q9uop7 plasmodium
107	6	20.0	517	10	O64882	O64882 arabadopsis	180	5	16.7	80	5	Q9U0P3	Q9uop3 plasmodium
108	6	20.0	528	10	Q945G7	Q945g7 prunus sero	181	5	16.7	80	5	Q9U0P1	Q9uop1 plasmodium
109	6	20.0	545	10	Q9M3O9	Q9m3o9 arabadopsis	182	5	16.7	80	5	Q9TVP9	Q9tvp9 plasmodium
110	6	20.0	553	10	O40984	O40984 prunus sero	183	5	16.7	80	5	Q9TVN9	Q9tvn9 plasmodium
111	6	20.0	561	10	Q9FPW6	Q9fpw6 arabadopsis	184	5	16.7	82	9	O8SC60	O8sc60 plasmodium
112	6	20.0	561	16	O8XAW0	O8xaw0 escherichia	185	5	16.7	84	5	Q26111	Q26111 pratylenchu
113	6	20.0	569	8	Q9G401	Q9g401 lithobius f	186	5	16.7	85	16	O8Y2G9	O8y2g9 anabaena sp
114	6	20.0	588	16	O92X77	O92xc7 rhizobium m	187	5	16.7	86	2	O9ZEM1	O9zem1 lactobacill
115	6	20.0	593	2	O9EY32	O9ey32 xanthomonas	188	5	16.7	88	9	O8SC25	O8sc25 stx2 conver
116	6	20.0	603	8	Q9MR61	Q9mr61 ciconia boy	189	5	16.7	88	16	O8TWFL	O8twfl anabaena sp
117	6	20.0	617	2	O68077	O68077 rhodobacter	190	5	16.7	91	6	Q28857	Q28857 pan troglod
118	6	20.0	620	5	Q9VFS3	Q9vfs3 dirosophila	191	5	16.7	97	6	Q9TSB6	Q9tsb6 trichosurus
119	6	20.0	640	16	Q9C1U9	Q9c1u9 lactococcus	192	5	16.7	99	10	Q9FNC9	Q9fnc9 arabadopsis
120	6	20.0	647	16	O9WZE0	O9wze0 thermotoga	193	5	16.7	101	17	Q9YB57	Q9yb57 aeropyrum p
121	6	20.0	650	5	Q9V3X1	Q9v3x1 dirosophila	194	5	16.7	102	15	Q9QNB1	Q9qnb1 human immun
122	6	20.0	661	16	O31849	O31849 bacillus su	195	5	16.7	102	16	O8RE89	O8re89 fusobacteri
123	6	20.0	729	5	Q9VYU1	Q9vyu1 dirosophila	196	5	16.7	103	15	O7A883	O7a883 human immun
124	6	20.0	740	2	Q9F6Z9	Q9f6z9 streptococc	197	5	16.7	103	16	O8UKJ8	O8ukj8 agrobacteri
125	6	20.0	779	4	Q96CV5	Q96cv5 homo sapien	198	5	16.7	104	12	O8VAM3	O8vam3 white spot
126	6	20.0	785	16	Q9CNO5	Q9cno5 pasteurella	199	5	16.7	104	15	O69816	O69816 human immun
127	6	20.0	815	10	O9SXY0	O9sxy0 arabadopsis	200	5	16.7	104	15	O69817	O69817 human immun
128	6	20.0	855	15	O902H5	O902h5 human immun	201	5	16.7	106	5	Q9U6P2	Q9u6p2 plasmodium
129	6	20.0	872	4	O96165	O96165 homo sapien	202	5	16.7	106	10	O9M5V6	O9m5v6 glycine max
130	6	20.0	879	11	Q9WTP0	Q9wtp0 ratius norv	203	5	16.7	107	15	O78887	O78887 human immun
131	6	20.0	899	10	P93698	P93698 vigna ungu	204	5	16.7	107	17	Q9YAA9	Q9yaa9 aeropyrum p
132	6	20.0	948	16	Q9JUS4	Q9juz4 neisseria m	205	5	16.7	108	11	Q9QWD7	Q9qwd7 ratius sp.
133	6	20.0	949	16	O9JZP1	O9jzdp1 neisseria m	206	5	16.7	109	4	O9BY65	O9by65 homo sapien
134	6	20.0	954	16	O9Y2B6	O9y2b6 ralsconia s	207	5	16.7	109	4	Q9BT01	Q9bt01 homo sapien
135	6	20.0	965	16	O9PAR9	O9par9 xylolla fas	208	5	16.7	110	3	O9C1J6	O9c1j6 neuropept
136	6	20.0	1023	5	Q9XYD4	Q9xyd4 diacyosteli	209	5	16.7	110	9	O9AF61	O9af61 streptococc
137	6	20.0	1109	16	O8XMS8	O8xms8 clostridium	210	5	16.7	111	4	Q9H383	Q9h383 homo sapien
138	6	20.0	1146	3	O06685	O06685 saccharomyc	211	5	16.7	112	16	Q96318	Q96318 rhizobium 1
139	6	20.0	1190	17	O8TVN7	O8tvn7 methanopyru	212	5	16.7	114	15	O8O5P6	O8o5p6 maedi-virna
140	6	20.0	1277	3	O9C2D2	O9c2d2 neuropept	213	5	16.7	115	5	O25836	O25836 plasmodium
141	6	20.0	1280	2	O9P6X9	O9p6x9 chloroflexu	214	5	16.7	115	5	O9TVW7	O9tvw7 plasmodium
142	6	20.0	1325	2	O9WX63	O9wx63 acetobacter	215	5	16.7	115	11	O99LQ9	O99lq9 mus musculu
143	6	20.0	1379	17	Q9HLS5	Q9hls5 thermoplasma	216	5	16.7	116	4	Q9N293	Q9n293 mus sapien
144	6	20.0	1551	11	Q9WTP1	Q9wtp1 ratius norv	217	5	16.7	116	4	O8WVL9	O8wvl9 homo sapien
145	6	20.0	1679	3	O9P7H8	O9p7h8 schizosacch	218	5	16.7	116	10	Q9SE71	Q9se71 brassica na
146	6	20.0	1687	11	O35651	O35651 mus musculu	219	5	16.7	116	10	Q9SE70	Q9se70 brassica na
147	6	20.0	1706	11	P97780	P97780 mus musculu	220	5	16.7	116	10	Q9SE69	Q9se69 brassica ol
148	6	20.0	1719	11	P97789	P97789 mus musculu	221	5	16.7	116	10	Q9SE68	Q9se68 brassica ol
149	6	20.0	1823	5	O26638	O26638 paracentrot	222	5	16.7	117	5	Q25797	Q25797 plasmodium
150	6	20.0	2316	2	O9FDJ9	O9fdj9 bacteroides	223	5	16.7	119	4	Q9BWB3	Q9bwb3 homo sapien
151	6	20.0	3198	5	O26639	O26639 strongyloce	224	5	16.7	119	9	O9EFH0	O9efh0 homo sapien
152	6	20.0	25	6	O9N256	O9n256 pan troglod	225	5	16.7	119	9	O9XJY4	O9xjy4 bacteriopa
153	6	20.0	25	6	O9N255	O9n255 papio hamad	226	5	16.7	119	16	O8YKJ1	O8ykj1 anabaena sp
154	6	20.0	25	6	O9N254	O9n254 macaca fasc	227	5	16.7	119	16	O8XK37	O8xk37 escherichia
155	6	20.0	25	6	O9N253	O9n253 macaca mula	228	5	16.7	120	10	O49990	O49990 lycopersico
156	6	20.0	32	8	O9T2Q1	O9t2q1 pinus sylve	229	5	16.7	120	11	O9D6Y4	O9d6y4 mus musculu
157	6	20.0	47	16	O8XG94	O8xg94 salmonella	230	5	16.7	121	17	O8TIR6	O8tir6 melanosarc
158	6	20.0	49	2	O9RAU1	O9rau1 azotobacter	231	5	16.7	122	2	O05561	O05561 mycobacteri
159	6	20.0	61	16	O8Z0J5	O8z0j5 anabaena sp	232	5	16.7	122	4	O9BY22	O9by22 homo sapien
160	6	20.0	61	2	O57203	O57203 shigella fl	233	5	16.7	122	10	O9LMB3	O9lmb3 arabadopsis
161	6	20.0	61	12	O91GA0	O91ga0 columbid ci	234	5	16.7	122	16	P74159	P74159 synechocyst
162	6	20.0	61	12	O91G95	O91g95 columbid ci	235	5	16.7	124	12	Q9DMC7	Q9dmc7 rat cytomeg

236	5	16.7	124	16	Q9RTY7	Q9TEY7	deinococcus	309	5	16.7	149	16	Q8Y7B9	Q8Y7b9	listeria mo
237	5	16.7	124	16	Q8XX03	Q8xx03	ralseltona s	310	5	16.7	150	16	Q9PMT8	Q9pmt8	campylobact
238	5	16.7	125	10	Q9SE72	Q9se72	brassica ca	311	5	16.7	151	16	Q9CKH3	Q9ckh3	pasteurella
239	5	16.7	125	10	Q9SE73	Q9se73	brassica ol	312	5	16.7	152	16	Q55703	Q55703	synecocyst
240	5	16.7	125	16	Q9RSE4	Q9re4	deinococcus	313	5	16.7	154	2	Q51563	Q51563	pseudomonas
241	5	16.7	125	16	Q9ZMS2	Q9zms2	rhizobium m	314	5	16.7	154	16	Q9KEA5	Q9keas	bacillus ha
242	5	16.7	127	16	Q92M22	Q92m22	rhizobium m	315	5	16.7	154	16	Q9ZQ57	Q9zq57	rhizobium m
243	5	16.7	128	6	Q95KM9	Q95km9	ovis aries	316	5	16.7	155	11	Q9D354	Q9d354	mus muscicu
244	5	16.7	128	16	Q07771	Q07771	mycobacteri	317	5	16.7	157	16	Q8R9N1	Q8r9n1	thermoplaea
245	5	16.7	129	5	Q17876	Q17876	caenorhabdi	318	5	16.7	157	17	Q977A5	Q977a5	sulfolobus
246	5	16.7	129	12	Q36623	Q36623	taimo tomat	319	5	16.7	158	15	Q73097	Q73097	human immun
247	5	16.7	129	12	Q71962	Q71962	sida golden	320	5	16.7	158	15	Q73098	Q73098	human immun
248	5	16.7	129	12	Q67561	Q67561	bean dwarf	321	5	16.7	158	15	Q73099	Q73099	human immun
249	5	16.7	129	12	Q96611	Q96611	abutilon mo	322	5	16.7	158	15	Q73100	Q73100	human immun
250	5	16.7	129	12	Q89125	Q89125	sida golden	323	5	16.7	158	15	Q73101	Q73101	human immun
251	5	16.7	129	12	P89130	P89130	sida golden	324	5	16.7	158	15	Q73102	Q73102	human immun
252	5	16.7	129	12	Q41337	Q41337	tomato leaf	325	5	16.7	158	15	Q73103	Q73103	human immun
253	5	16.7	129	12	Q9YMW6	Q9ymw6	sida golden	326	5	16.7	158	15	Q73105	Q73105	human immun
254	5	16.7	129	12	Q9YNW0	Q9ynw0	sida golden	327	5	16.7	158	15	Q73106	Q73106	human immun
255	5	16.7	129	12	Q91198	Q91198	havana toma	328	5	16.7	158	15	Q73109	Q73109	human immun
256	5	16.7	129	12	Q91204	Q91204	potato Yell	329	5	16.7	158	15	Q73110	Q73110	human immun
257	5	16.7	129	12	Q9YL75	Q9yl75	tomato leaf	330	5	16.7	158	15	Q73111	Q73111	human immun
258	5	16.7	132	2	Q33019	Q33019	mycobacteri	331	5	16.7	158	15	Q73112	Q73112	human immun
259	5	16.7	132	12	Q913X7	Q913x7	pepper huas	332	5	16.7	158	15	Q73113	Q73113	human immun
260	5	16.7	134	16	Q98K58	Q98k58	rhizobium l	333	5	16.7	158	15	Q73114	Q73114	human immun
261	5	16.7	134	16	Q8YU00	Q8yuh0	anabaena sp	334	5	16.7	158	15	Q73116	Q73116	human immun
262	5	16.7	135	16	Q9FYX8	Q9fyx8	eucommia ul	335	5	16.7	158	15	Q73121	Q73121	human immun
263	5	16.7	135	16	Q9ACD6	Q9acd6	caulobacter	336	5	16.7	159	2	Q07466	Q07466	rhodospseudo
264	5	16.7	135	16	Q8VNA5	Q8vna5	listeria mo	337	5	16.7	159	15	Q9JBT1	Q9jbt1	human immun
265	5	16.7	136	2	Q9A112	Q9a112	photorhabdu	338	5	16.7	159	15	Q9JEBQ	Q9jebq	human immun
266	5	16.7	137	6	Q97509	Q97509	capra hircu	339	5	16.7	159	15	Q9JEBQ3	Q9jebq3	human immun
267	5	16.7	137	12	Q55581	Q55581	leucania se	340	5	16.7	159	16	Q53709	Q53709	mycobacteri
268	5	16.7	137	13	Q9YH66	Q9yh66	gnglymysto	341	5	16.7	160	12	Q8QTF4	Q8qtf4	white spot
269	5	16.7	137	16	Q06257	Q06257	strepptomyc	342	5	16.7	160	15	Q73104	Q73104	human immun
270	5	16.7	138	4	Q9NV55	Q9nv55	homo sapien	343	5	16.7	160	15	Q73107	Q73107	human immun
271	5	16.7	139	13	Q9YH08	Q9yhm8	gnglymysto	344	5	16.7	160	15	Q73108	Q73108	human immun
272	5	16.7	141	9	Q8SC44	Q8sc44	etx2 conyer	345	5	16.7	160	15	Q73115	Q73115	human immun
273	5	16.7	141	12	Q9QRZ9	Q9qrz9	human rotav	346	5	16.7	160	15	Q73118	Q73118	human immun
274	5	16.7	141	12	Q9QRZ8	Q9qrz8	human rotav	347	5	16.7	160	15	Q73122	Q73122	human immun
275	5	16.7	141	12	Q9QRZ6	Q9qrz6	human rotav	348	5	16.7	161	11	Q61430	Q61430	human immun
276	5	16.7	141	12	Q9QRZ5	Q9qrz5	human rotav	349	5	16.7	162	12	Q8YB83	Q8yb83	white spot
277	5	16.7	141	12	Q9QRZ4	Q9qrz4	human rotav	350	5	16.7	162	16	Q9C098	Q9c098	lactococcus
278	5	16.7	141	12	Q9QRZ3	Q9qrz3	human rotav	351	5	16.7	162	16	Q9C098	Q9c098	rhizobium m
279	5	16.7	141	12	Q9QRZ2	Q9qrz2	human rotav	352	5	16.7	164	2	Q9ZSE8	Q9zse8	rhodocyclus
280	5	16.7	141	12	Q9QRZ1	Q9qrz1	human rotav	353	5	16.7	164	5	Q9V7H5	Q9v7h5	drosophila
281	5	16.7	141	12	Q9QRZ0	Q9qrz0	human rotav	354	5	16.7	164	6	P79252	P79252	oryctolagus
282	5	16.7	141	12	Q9QRZ9	Q9qrz9	human rotav	355	5	16.7	165	2	Q45403	Q45403	bacillus su
283	5	16.7	141	12	Q9QRZ8	Q9qrz8	human rotav	356	5	16.7	165	16	P73153	P73153	synecocyst
284	5	16.7	141	12	Q9QRZ7	Q9qrz7	human rotav	357	5	16.7	165	16	Q8Y158	Q8y158	ralseltonia s
285	5	16.7	141	12	Q9QRZ6	Q9qrz6	human rotav	358	5	16.7	166	9	Q03915	Q03915	bacterioph
286	5	16.7	141	12	Q9QRZ5	Q9qrz5	human rotav	359	5	16.7	166	10	Q9L867	Q9l867	arabidopsis
287	5	16.7	141	12	Q9QRZ4	Q9qrz4	human rotav	360	5	16.7	168	10	Q9FY13	Q9fy13	arabidopsis
288	5	16.7	141	12	Q9QRZ3	Q9qrz3	human rotav	361	5	16.7	168	16	Q9RMQ0	Q9rmq0	delinococcus
289	5	16.7	141	12	Q9DKS3	Q9dkes3	human rotav	362	5	16.7	168	16	Q9K495	Q9k495	strepptomyc
290	5	16.7	141	16	Q8X5E2	Q8x5e2	escherichia	363	5	16.7	169	5	Q9NFM1	Q9nfm1	schistosoma
291	5	16.7	142	8	Q9TJ75	Q9tj75	gretum grem	364	5	16.7	169	11	Q9CRF9	Q9crf9	mus muscicu
292	5	16.7	142	12	Q9OS00	Q9ose0	human rotav	365	5	16.7	169	11	Q89060	Q89060	mus muscicu
293	5	16.7	142	12	Q9QRZ2	Q9qrz2	human rotav	366	5	16.7	169	15	Q9E2U6	Q9e2u6	human immun
294	5	16.7	142	12	Q9QRZ1	Q9qrz1	human rotav	367	5	16.7	169	16	Q9CK49	Q9ck49	pasteurella
295	5	16.7	142	12	Q9QRZ0	Q9qrz0	human rotav	368	5	16.7	169	17	Q29109	Q29109	archaeoglob
296	5	16.7	142	12	Q9QRX9	Q9qrx9	human rotav	369	5	16.7	170	4	Q8WYJ4	Q8wyj4	homo sapien
297	5	16.7	143	2	Q9AKY3	Q9aky3	legionella	370	5	16.7	170	5	Q95P81	Q95p81	bombux mori
298	5	16.7	143	10	Q9AMZ9	Q9amz9	guillardia	371	5	16.7	171	12	Q9QAU8	Q9qau8	human rotav
299	5	16.7	144	4	Q9N082	Q9n082	homo sapien	372	5	16.7	171	12	Q9QAU7	Q9qau7	human rotav
300	5	16.7	145	5	Q9N3V4	Q9n3v4	caenorhabdi	373	5	16.7	171	12	Q9QAU6	Q9qau6	human rotav
301	5	16.7	145	8	Q9MFB3	Q9mfb3	beta vulgar	374	5	16.7	171	12	Q9QAU4	Q9qau4	human rotav
302	5	16.7	145	13	Q9YH09	Q9yhg9	gnglymysto	375	5	16.7	171	12	Q9QAU3	Q9qau3	human rotav
303	5	16.7	147	16	Q8VKH8	Q8vkh8	mycobacteri	376	5	16.7	171	12	Q9QAU2	Q9qau2	human rotav
304	5	16.7	147	17	Q58828	Q58828	pyrococcus	377	5	16.7	171	12	Q9QAU0	Q9qau0	human rotav
305	5	16.7	147	17	Q9UZL1	Q9uzl1	pyrococcus	378	5	16.7	171	12	Q9QAT9	Q9qat9	human rotav
306	5	16.7	149	2	Q9ZEV1	Q9zev1	decillus st	379	5	16.7	171	12	Q9QAT9	Q9qat9	human rotav
307	5	16.7	149	5	Q8S286	Q8s286	drosophila	380	5	16.7	171	12	Q9QAT8	Q9qat8	human rotav
308	5	16.7	149	16	Q9ZBY8	Q9zby8	listeria in	381	5	16.7	171	12	Q9QAT7	Q9qat7	human rotav

382	5	16.7	171	12	Q9QAT6	Q9qat6 human rotav	455	5	16.7	198	15	Q9E4G7	Q9e4g7 human immun
383	5	16.7	172	8	Q959YE	Q959ye kaupichthys	456	5	16.7	198	15	Q9E4G8	Q9e4g8 human immun
384	5	16.7	173	2	Q8VVE3	Q8vve3 thermus the	457	5	16.7	199	6	Q95M01	Q95m01 bos taurus
385	5	16.7	173	4	Q961Z3	Q961z3 homo sapien	458	5	16.7	199	15	Q9JDM8	Q9jdm8 human immun
386	5	16.7	173	11	Q9D652	Q9d652 mus musculu	459	5	16.7	199	15	Q9JDM4	Q9jdm4 human immun
387	5	16.7	174	16	Q8YCC3	Q8ycc3 bruceia me	460	5	16.7	199	15	Q9JDM0	Q9jdm0 human immun
388	5	16.7	175	8	Q99605	Q99605 artibeus ja	461	5	16.7	199	15	Q9JDM8	Q9jdm8 human immun
389	5	16.7	175	16	Q9RM23	Q9rm23 deinococcus	462	5	16.7	199	15	Q9JDM7	Q9jdm7 human immun
390	5	16.7	176	17	Q9HK61	Q9hk61 thermoplasma	463	5	16.7	199	15	Q9JDM4	Q9jdm4 human immun
391	5	16.7	176	17	Q975U3	Q975u3 sulfobobus	464	5	16.7	199	15	Q9JDM2	Q9jdm2 human immun
392	5	16.7	178	12	Q9WNT3	Q9wnr3 trichoplusia	465	5	16.7	199	15	Q9JDM1	Q9jdm1 human immun
393	5	16.7	178	15	Q70610	Q70610 human immun	466	5	16.7	199	15	Q9JDM6	Q9jdm6 human immun
394	5	16.7	178	15	Q70611	Q70611 human immun	467	5	16.7	199	15	Q9JDM5	Q9jdm5 human immun
395	5	16.7	178	17	Q980M5	Q980m5 sulfobobus	468	5	16.7	199	15	Q9JDM0	Q9jdm0 human immun
396	5	16.7	179	16	Q92JH6	Q92jnh rickettsia	469	5	16.7	199	15	Q9JDM9	Q9jdm9 human immun
397	5	16.7	181	5	Q8SMCI	Q8smci encephalito	470	5	16.7	199	15	Q9JDM1	Q9jdm1 human immun
398	5	16.7	181	11	Q921W1	Q921w1 mus musculu	471	5	16.7	199	15	Q9JDM5	Q9jdm5 human immun
399	5	16.7	183	5	Q16043	Q16043 drosophila	472	5	16.7	199	15	Q9JDM9	Q9jdm9 human immun
400	5	16.7	183	15	Q70609	Q70609 human immun	473	5	16.7	199	15	Q9JDM8	Q9jdm8 human immun
401	5	16.7	183	15	Q70614	Q70614 human immun	474	5	16.7	199	15	Q9JDM6	Q9jdm6 human immun
402	5	16.7	183	15	Q70616	Q70616 human immun	475	5	16.7	199	15	Q9JDM5	Q9jdm5 human immun
403	5	16.7	183	15	Q70617	Q70617 human immun	476	5	16.7	199	15	Q9JDM4	Q9jdm4 human immun
404	5	16.7	183	15	Q70621	Q70621 human immun	477	5	16.7	199	15	Q9JDM3	Q9jdm3 human immun
405	5	16.7	183	15	Q8UQ86	Q8uq86 human immun	478	5	16.7	199	15	Q9JDM2	Q9jdm2 human immun
406	5	16.7	183	15	Q8UQ84	Q8uq84 human immun	479	5	16.7	199	15	Q9JDM1	Q9jdm1 human immun
407	5	16.7	183	15	Q8UQ83	Q8uq83 human immun	480	5	16.7	199	15	Q9JDM0	Q9jdm0 human immun
408	5	16.7	183	15	Q8UQ82	Q8uq82 human immun	481	5	16.7	199	15	Q9JDM9	Q9jdm9 human immun
409	5	16.7	183	15	Q8UQ81	Q8uq81 human immun	482	5	16.7	199	15	Q9JDM4	Q9jdm4 human immun
410	5	16.7	183	15	Q8UQ80	Q8uq80 human immun	483	5	16.7	199	15	Q9JDM3	Q9jdm3 human immun
411	5	16.7	183	15	Q8UQ79	Q8uq79 human immun	484	5	16.7	199	15	Q9JDM2	Q9jdm2 human immun
412	5	16.7	183	15	Q8UQ78	Q8uq78 human immun	485	5	16.7	199	15	Q9JBM7	Q9jbm7 human immun
413	5	16.7	183	15	Q8UQ77	Q8uq77 human immun	486	5	16.7	199	15	Q8UQ94	Q8uq94 human immun
414	5	16.7	183	15	Q8UQ76	Q8uq76 human immun	487	5	16.7	200	10	Q80711	Q80711 arabidopsis
415	5	16.7	183	15	Q8UQ75	Q8uq75 human immun	488	5	16.7	200	15	Q90008	Q90008 human immun
416	5	16.7	183	15	Q8UQ74	Q8uq74 human immun	489	5	16.7	200	15	Q9YV86	Q9yv86 human immun
417	5	16.7	183	15	Q8UQ73	Q8uq73 human immun	490	5	16.7	200	15	Q9JDM6	Q9jdm6 human immun
418	5	16.7	183	15	Q8UQ72	Q8uq72 human immun	491	5	16.7	200	15	Q9JDM5	Q9jdm5 human immun
419	5	16.7	183	15	Q8UQ70	Q8uq70 human immun	492	5	16.7	200	15	Q9JDM3	Q9jdm3 human immun
420	5	16.7	183	15	Q8UQ69	Q8uq69 human immun	493	5	16.7	200	15	Q9JDM2	Q9jdm2 human immun
421	5	16.7	183	15	Q8UQ68	Q8uq68 human immun	494	5	16.7	200	15	Q9JDM0	Q9jdm0 human immun
422	5	16.7	183	15	Q8UQ67	Q8uq67 human immun	495	5	16.7	200	15	Q9JDM9	Q9jdm9 human immun
423	5	16.7	183	15	Q8UQ65	Q8uq65 human immun	496	5	16.7	201	3	Q9P418	Q9p418 coccidioid
424	5	16.7	183	15	Q8UQ64	Q8uq64 human immun	497	5	16.7	201	15	Q90031	Q90031 human immun
425	5	16.7	183	15	Q8UQ63	Q8uq63 human immun	498	5	16.7	201	15	Q9YRW7	Q9yrw7 human immun
426	5	16.7	183	17	Q29155	Q29155 archaeoglob	499	5	16.7	201	15	Q9YRW3	Q9yrw3 human immun
427	5	16.7	185	2	Q44518	Q44518 anabaena va	500	5	16.7	201	15	Q9JDM8	Q9jdm8 human immun
428	5	16.7	185	16	Q8YV89	Q8yv89 anabaena sp	501	5	16.7	201	15	Q9JDM7	Q9jdm7 human immun
429	5	16.7	186	2	Q52994	Q52994 escherichia	502	5	16.7	201	15	Q9JDM6	Q9jdm6 human immun
430	5	16.7	187	16	Q8YQ61	Q8yq61 ralteconia s	503	5	16.7	201	15	Q9JDM4	Q9jdm4 human immun
431	5	16.7	188	4	Q96J67	Q96j67 homo sapien	504	5	16.7	201	15	Q9JDM2	Q9jdm2 human immun
432	5	16.7	188	12	Q9QF44	Q9qff4 avian pneum	505	5	16.7	201	15	Q9JDM0	Q9jdm0 human immun
433	5	16.7	189	3	Q94694	Q94694 schizosacch	506	5	16.7	201	15	Q8UQ47	Q8uq47 human immun
434	5	16.7	189	16	Q8Y1A0	Q8y1a0 ralteconia s	507	5	16.7	201	15	Q8UQ45	Q8uq45 human immun
435	5	16.7	192	16	Q8RH38	Q8rh38 fubobacteri	508	5	16.7	201	15	Q8UQ44	Q8uq44 human immun
436	5	16.7	193	2	Q92GN1	Q92gn1 azotobacter	509	5	16.7	201	15	Q8UQ43	Q8uq43 human immun
437	5	16.7	193	5	Q9VKQ8	Q9vkq8 drosophila	510	5	16.7	201	15	Q8UQ42	Q8uq42 human immun
440	5	16.7	195	11	Q8R512	Q8r512 mus musculu	513	5	16.7	201	15	Q8UQ39	Q8uq39 human immun
441	5	16.7	195	16	Q51524	Q51524 borelia bu	514	5	16.7	201	15	Q8UQ98	Q8uq98 human immun
442	5	16.7	195	16	P73665	P73665 synechocyst	515	5	16.7	201	15	Q8UQ97	Q8uq97 human immun
443	5	16.7	196	15	Q8QDC7	Q8qdc7 human immun	516	5	16.7	201	15	Q8UQ96	Q8uq96 human immun
444	5	16.7	196	16	Q99T18	Q99t18 staphylococ	517	5	16.7	201	15	Q8UQ95	Q8uq95 human immun
445	5	16.7	196	16	Q8YQ49	Q8yq49 anabaena sp	518	5	16.7	201	15	Q8UQ92	Q8uq92 human immun
446	5	16.7	197	10	Q93WS2	Q93ws2 davidia inv	519	5	16.7	201	15	Q8UQ91	Q8uq91 human immun
447	5	16.7	197	15	Q9JDM1	Q9jdm1 human immun	520	5	16.7	201	15	Q8UQ89	Q8uq89 human immun
448	5	16.7	197	15	Q9JDM7	Q9jdm7 human immun	521	5	16.7	201	15	Q8UQ88	Q8uq88 human immun
449	5	16.7	197	15	Q9JDM8	Q9jdm8 human immun	522	5	16.7	201	15	Q8UQ87	Q8uq87 human immun
450	5	16.7	197	15	Q9JDM7	Q9jdm7 human immun	523	5	16.7	201	15	Q8QD75	Q8qd75 human immun
451	5	16.7	198	15	Q9JDM1	Q9jdm1 human immun	524	5	16.7	202	8	Q47094	Q47094 striga asia
452	5	16.7	198	15	Q71835	Q71835 human immun	525	5	16.7	202	15	Q89996	Q89996 human immun
453	5	16.7	198	15	Q904U9	Q904u9 human immun	526	5	16.7	202	15	Q90003	Q90003 human immun
454	5	16.7	198	15	Q9E4G2	Q9e4g2 human immun	527	5	16.7	202	15	Q90024	Q90024 human immun

528	5	16.7	202	15	090030	090030 human	immun	601	5	16.7	204	15	090408	090408 human	immun
529	5	16.7	202	15	090032	090032 human	immun	602	5	16.7	204	15	090409	090409 human	immun
530	5	16.7	202	15	090033	090033 human	immun	603	5	16.7	204	15	090410	090410 human	immun
531	5	16.7	202	15	090034	090034 human	immun	604	5	16.7	204	15	090411	090411 human	immun
532	5	16.7	202	15	090035	090035 human	immun	605	5	16.7	204	15	090412	090412 human	immun
533	5	16.7	202	15	090036	090036 human	immun	606	5	16.7	205	5	085810	085810 human	immun
534	5	16.7	202	15	090037	090037 human	immun	607	5	16.7	205	8	047093	047093 human	immun
535	5	16.7	202	15	090038	090038 human	immun	608	5	16.7	205	15	090413	090413 human	immun
536	5	16.7	202	15	090039	090039 human	immun	609	5	16.7	205	15	090414	090414 human	immun
537	5	16.7	202	15	090040	090040 human	immun	610	5	16.7	205	15	090415	090415 human	immun
538	5	16.7	202	15	090041	090041 human	immun	611	5	16.7	205	16	090416	090416 human	immun
539	5	16.7	202	15	090042	090042 human	immun	612	5	16.7	205	16	090417	090417 human	immun
540	5	16.7	202	15	090043	090043 human	immun	613	5	16.7	206	2	085811	085811 human	immun
541	5	16.7	202	15	090044	090044 human	immun	614	5	16.7	206	3	090418	090418 human	immun
542	5	16.7	202	15	090045	090045 human	immun	615	5	16.7	206	15	090419	090419 human	immun
543	5	16.7	202	15	090046	090046 human	immun	616	5	16.7	206	15	090420	090420 human	immun
544	5	16.7	202	15	090047	090047 human	immun	617	5	16.7	206	15	090421	090421 human	immun
545	5	16.7	202	15	090048	090048 human	immun	618	5	16.7	206	15	090422	090422 human	immun
546	5	16.7	202	15	090049	090049 human	immun	619	5	16.7	206	15	090423	090423 human	immun
547	5	16.7	202	15	090050	090050 human	immun	620	5	16.7	206	15	090424	090424 human	immun
548	5	16.7	202	15	090051	090051 human	immun	621	5	16.7	206	15	090425	090425 human	immun
549	5	16.7	202	15	090052	090052 human	immun	622	5	16.7	207	8	021512	021512 human	immun
550	5	16.7	202	15	090053	090053 human	immun	623	5	16.7	207	15	090426	090426 human	immun
551	5	16.7	202	15	090054	090054 human	immun	624	5	16.7	207	15	090427	090427 human	immun
552	5	16.7	202	15	090055	090055 human	immun	625	5	16.7	207	15	090428	090428 human	immun
553	5	16.7	202	15	090056	090056 human	immun	626	5	16.7	207	15	090429	090429 human	immun
554	5	16.7	202	15	090057	090057 human	immun	627	5	16.7	207	15	090430	090430 human	immun
555	5	16.7	202	15	090058	090058 human	immun	628	5	16.7	207	15	090431	090431 human	immun
556	5	16.7	202	15	090059	090059 human	immun	629	5	16.7	207	15	090432	090432 human	immun
557	5	16.7	202	15	090060	090060 human	immun	630	5	16.7	207	15	090433	090433 human	immun
558	5	16.7	202	15	090061	090061 human	immun	631	5	16.7	207	15	090434	090434 human	immun
559	5	16.7	202	15	090062	090062 human	immun	632	5	16.7	207	15	090435	090435 human	immun
560	5	16.7	202	15	090063	090063 human	immun	633	5	16.7	207	15	090436	090436 human	immun
561	5	16.7	202	15	090064	090064 human	immun	634	5	16.7	207	15	090437	090437 human	immun
562	5	16.7	202	15	090065	090065 human	immun	635	5	16.7	207	15	090438	090438 human	immun
563	5	16.7	202	15	090066	090066 human	immun	636	5	16.7	207	15	090439	090439 human	immun
564	5	16.7	202	15	090067	090067 human	immun	637	5	16.7	207	15	090440	090440 human	immun
565	5	16.7	202	15	090068	090068 human	immun	638	5	16.7	207	15	090441	090441 human	immun
566	5	16.7	202	15	090069	090069 human	immun	639	5	16.7	207	15	090442	090442 human	immun
567	5	16.7	202	15	090070	090070 human	immun	640	5	16.7	207	15	090443	090443 human	immun
568	5	16.7	202	15	090071	090071 human	immun	641	5	16.7	207	15	090444	090444 human	immun
569	5	16.7	202	15	090072	090072 human	immun	642	5	16.7	207	15	090445	090445 human	immun
570	5	16.7	202	15	090073	090073 human	immun	643	5	16.7	207	15	090446	090446 human	immun
571	5	16.7	202	15	090074	090074 human	immun	644	5	16.7	207	15	090447	090447 human	immun
572	5	16.7	202	15	090075	090075 human	immun	645	5	16.7	207	15	090448	090448 human	immun
573	5	16.7	202	15	090076	090076 human	immun	646	5	16.7	207	15	090449	090449 human	immun
574	5	16.7	202	15	090077	090077 human	immun	647	5	16.7	207	15	090450	090450 human	immun
575	5	16.7	202	15	090078	090078 human	immun	648	5	16.7	207	15	090451	090451 human	immun
576	5	16.7	202	15	090079	090079 human	immun	649	5	16.7	207	15	090452	090452 human	immun
577	5	16.7	202	15	090080	090080 human	immun	650	5	16.7	207	15	090453	090453 human	immun
578	5	16.7	202	15	090081	090081 human	immun	651	5	16.7	207	15	090454	090454 human	immun
579	5	16.7	202	15	090082	090082 human	immun	652	5	16.7	207	15	090455	090455 human	immun
580	5	16.7	202	15	090083	090083 human	immun	653	5	16.7	207	15	090456	090456 human	immun
581	5	16.7	202	15	090084	090084 human	immun	654	5	16.7	207	15	090457	090457 human	immun
582	5	16.7	202	15	090085	090085 human	immun	655	5	16.7	207	16	031588	031588 human	immun
583	5	16.7	202	15	090086	090086 human	immun	656	5	16.7	207	17	087894	087894 human	immun
584	5	16.7	202	15	090087	090087 human	immun	657	5	16.7	207	17	087895	087895 human	immun
585	5	16.7	202	15	090088	090088 human	immun	658	5	16.7	208	4	096815	096815 human	immun
586	5	16.7	202	15	090089	090089 human	immun	659	5	16.7	208	6	097739	097739 human	immun
587	5	16.7	202	15	090090	090090 human	immun	660	5	16.7	208	8	021506	021506 human	immun
588	5	16.7	202	15	090091	090091 human	immun	661	5	16.7	208	15	090092	090092 human	immun
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590	5	16.7	202	15	090093	090093 human	immun	663	5	16.7	208	15	090094	090094 human	immun
591	5	16.7	202	15	090094	090094 human	immun	664	5	16.7	208	15	090095	090095 human	immun
592	5	16.7	202	15	090095	090095 human	immun	665	5	16.7	208	15	090096	090096 human	immun
593	5	16.7	202	15	090096	090096 human	immun	666	5	16.7	208	15	090097	090097 human	immun
594	5	16.7	202	15	090097	090097 human	immun	667	5	16.7	208	17	028099	028099 human	immun
595	5	16.7	202	15	090098	090098 human	immun	668	5	16.7	209	12	085650	085650 human	immun
596	5	16.7	202	15	090099	090099 human	immun	669	5	16.7	209	15	080003	080003 human	immun
597	5	16.7	202	15	090100	090100 human	immun	670	5	16.7	209	15	080004	080004 human	immun
598	5	16.7	202	15	090101	090101 human	immun	671	5	16.7	209	15	080005	080005 human	immun
599	5	16.7	202	15	090102	090102 human	immun	672	5	16.7	209	15	080006	080006 human	immun
600	5	16.7	202	15	090103	090103 human	immun	673	5	16.7	209	15	080007	080007 human	immun

674	5	16.7	209	16	Q97KW0	Q97kw0 clostridium	747	5	16.7	222	16	Q54191	Q54191 streptomyces
675	5	16.7	209	17	Q8TOG9	Q8tcg9 methanosarc	748	5	16.7	223	16	Q9HUS1	Q9hus1 pseudomonas
676	5	16.7	210	6	Q62813	Q62813 papio hamad	749	5	16.7	223	17	Q8TM30	Q8tm30 methanosarc
677	5	16.7	210	6	Q28273	Q28273 canis famli	750	5	16.7	224	2	Q46369	Q46369 chlorobium
678	5	16.7	210	15	Q9JDR7	Q9jdr7 human immun	751	5	16.7	224	2	Q8RJ77	Q8rj77 nitrosococc
679	5	16.7	210	15	Q8QAU4	Q8qau4 human immun	752	5	16.7	224	4	Q00617	Q00617 homo sapien
680	5	16.7	210	15	Q8QAU1	Q8qau1 human immun	753	5	16.7	224	4	Q28848	Q28848 smintropsis
681	5	16.7	210	16	Q9KN12	Q9kn12 vibrio chol	754	5	16.7	225	6	Q9BRQ7	Q9brq7 homo sapien
682	5	16.7	210	17	Q97UG8	Q97ug8 sulfolobus	755	5	16.7	225	5	Q17715	Q17715 caenorhabdi
683	5	16.7	211	11	Q9DIW6	Q9diw6 mus musculu	756	5	16.7	225	5	Q8STN5	Q8stn5 encephalito
684	5	16.7	211	12	Q39300	Q39300 equine hepr	757	5	16.7	225	10	Q8RYW7	Q8ryw7 oryza sativ
685	5	16.7	211	15	Q8Q7K1	Q8q7k1 human immun	758	5	16.7	225	12	Q9PYW4	Q9pyw4 xestia c-ni
686	5	16.7	211	15	Q9HYZ4	Q9hyz4 pseudomonas	759	5	16.7	225	15	Q8QAT3	Q8qat3 human immun
687	5	16.7	211	17	Q96Y84	Q96y84 sulfolobus	760	5	16.7	226	17	Q9UZP3	Q9uzp3 mytilus edu
688	5	16.7	212	6	Q28512	Q28512 macaca mula	761	5	16.7	226	5	Q9NH33	Q9nhb3 mytilus edu
689	5	16.7	212	6	Q28567	Q28567 ovis aries	762	5	16.7	226	16	Q8YXV7	Q8yxv7 anaabaena sp
690	5	16.7	212	10	Q9ZW80	Q9zw80 arabidopsis	763	5	16.7	227	2	Q9S503	Q9s503 myxococcus
691	5	16.7	213	15	Q77609	Q77609 human immun	764	5	16.7	227	11	P70103	P70103 cynomys lud
692	5	16.7	213	15	Q77616	Q77616 human immun	765	5	16.7	228	15	Q89550	Q89550 human immun
693	5	16.7	213	15	Q77629	Q77629 human immun	766	5	16.7	228	16	Q97DC0	Q97dc0 clostridium
694	5	16.7	213	15	Q77630	Q77630 human immun	767	5	16.7	229	16	Q8Y2R4	Q8y2r4 ralsstonia s
695	5	16.7	213	15	Q77651	Q77651 human immun	768	5	16.7	229	16	Q93MA2	Q93ma2 clostridium
696	5	16.7	213	15	Q77653	Q77653 human immun	769	5	16.7	230	2	Q9K570	Q9k570 lactococcus
697	5	16.7	213	15	Q77675	Q77675 human immun	770	5	16.7	230	15	Q9E052	Q9e052 human immun
698	5	16.7	213	15	Q8QDC6	Q8qdc6 human immun	771	5	16.7	230	16	P74631	P74631 synechocyst
699	5	16.7	214	15	Q77620	Q77620 human immun	772	5	16.7	230	16	Q9CF87	Q9cf87 lactococcus
700	5	16.7	214	15	Q77685	Q77685 human immun	773	5	16.7	231	11	Q9D4Q8	Q9d4q8 mus musculu
701	5	16.7	214	15	Q79367	Q79367 human immun	774	5	16.7	231	15	Q56309	Q56309 wallaye. epi
702	5	16.7	214	15	Q79372	Q79372 human immun	775	5	16.7	231	15	Q9RV00	Q9rv00 delnococtus
703	5	16.7	214	15	Q79375	Q79375 human immun	776	5	16.7	231	16	Q8X8L2	Q8x8l2 escherichia
704	5	16.7	214	15	Q79376	Q79376 human immun	777	5	16.7	231	16	Q8UBZ0	Q8ube0 agrobacteri
705	5	16.7	214	15	Q79380	Q79380 human immun	778	5	16.7	231	16	Q92PB8	Q92pb8 rhizobium m
706	5	16.7	214	15	Q79381	Q79381 human immun	779	5	16.7	232	11	Q99P51	Q99p51 mus musculu
707	5	16.7	214	15	Q79382	Q79382 human immun	780	5	16.7	232	16	Q8XIU6	Q8xiu6 clostridium
708	5	16.7	214	15	Q79386	Q79386 human immun	781	5	16.7	233	2	Q9ATV1	Q9atv1 pseudomonas
709	5	16.7	214	15	Q79387	Q79387 human immun	782	5	16.7	233	9	Q9ZXM2	Q9zxm2 bacterioph
710	5	16.7	214	15	Q79399	Q79399 human immun	783	5	16.7	234	16	P74626	P74626 synechocyst
711	5	16.7	214	15	Q79402	Q79402 human immun	784	5	16.7	235	2	Q9AGR7	Q9agr7 streptococc
712	5	16.7	214	15	Q79407	Q79407 human immun	785	5	16.7	235	2	Q93MY4	Q93my4 streptococc
713	5	16.7	214	15	Q79412	Q79412 human immun	786	5	16.7	236	10	Q9ZV06	Q9zv06 arabidopsis
714	5	16.7	214	16	Q8YTB4	Q8ytb4 anaabaena sp	787	5	16.7	236	16	Q9A108	Q9a108 streptococc
715	5	16.7	215	12	Q8QRV1	Q8qrv1 chimpanzee	788	5	16.7	237	5	Q20955	Q20955 caenorhabdi
716	5	16.7	215	15	Q77617	Q77617 human immun	789	5	16.7	237	10	Q9FHR2	Q9fhr2 arabidopsis
717	5	16.7	215	15	Q77619	Q77619 human immun	790	5	16.7	237	16	Q92G43	Q92g43 ticketsia
718	5	16.7	215	15	Q77621	Q77621 human immun	791	5	16.7	237	16	Q8YVC3	Q8yvc3 anaabaena sp
719	5	16.7	215	15	Q77626	Q77626 human immun	792	5	16.7	238	2	Q9ZHV6	Q9zhv6 nostoc punc
720	5	16.7	215	15	Q77655	Q77655 human immun	793	5	16.7	238	5	Q9W1M4	Q9w1m4 drosophi
721	5	16.7	215	15	Q71405	Q71405 human immun	794	5	16.7	238	16	Q8YV87	Q8yv87 anaabaena sp
722	5	16.7	215	17	Q9YEL2	Q9yel2 aetopyrum p	795	5	16.7	239	2	Q9RCL1	Q9rc11 streptococc
723	5	16.7	217	15	Q97088	Q97088 human immun	796	5	16.7	239	15	Q8URQ9	Q8urg9 human immun
724	5	16.7	217	15	Q97085	Q97085 human immun	797	5	16.7	239	15	Q8URQ8	Q8urg8 human immun
725	5	16.7	217	15	Q8OAT8	Q8oat8 human immun	798	5	16.7	239	15	Q8URQ7	Q8urg7 human immun
726	5	16.7	218	15	Q90M04	Q90m04 human immun	799	5	16.7	239	15	Q8URQ6	Q8urg6 human immun
727	5	16.7	218	16	Q91470	Q91470 pseudomonas	800	5	16.7	239	15	Q8URQ5	Q8urg5 human immun
728	5	16.7	218	16	Q8ZNB3	Q8znb3 salmonella	801	5	16.7	239	15	Q8URQ4	Q8urg4 human immun
729	5	16.7	219	15	Q8Z424	Q8z424 salmonella	802	5	16.7	239	15	Q8URQ3	Q8urg3 human immun
730	5	16.7	219	15	Q71074	Q71074 human immun	803	5	16.7	239	15	Q8URQ2	Q8urg2 human immun
731	5	16.7	219	15	Q97087	Q97087 human immun	804	5	16.7	239	15	Q8URQ1	Q8urg1 human immun
732	5	16.7	219	16	Q9JXY9	Q9jxy9 neisseria m	805	5	16.7	239	15	Q8URQ0	Q8urg0 human immun
733	5	16.7	220	11	Q8VE86	Q8ve86 mus musculu	806	5	16.7	239	15	Q8URP9	Q8urp9 human immun
734	5	16.7	220	15	Q71073	Q71073 human immun	807	5	16.7	239	15	Q8URP8	Q8urp8 human immun
735	5	16.7	220	15	Q73287	Q73287 human immun	808	5	16.7	239	15	Q8URP7	Q8urp7 human immun
736	5	16.7	220	16	Q06346	Q06346 mycobacteri	809	5	16.7	239	15	Q8URP6	Q8urp6 human immun
737	5	16.7	220	17	Q9HJ46	Q9hj46 thermoplas	810	5	16.7	239	15	Q8URP5	Q8urp5 human immun
738	5	16.7	221	5	Q76328	Q76328 dtrosophila	811	5	16.7	239	15	Q8URP4	Q8urp4 human immun
739	5	16.7	221	10	Q9LFF1	Q9lff1 arabidopsis	812	5	16.7	239	15	Q8URP3	Q8urp3 human immun
740	5	16.7	221	15	Q9YRX3	Q9yrx3 human immun	813	5	16.7	239	15	Q8URP2	Q8urp2 human immun
741	5	16.7	221	15	Q9YRX2	Q9yrx2 human immun	814	5	16.7	239	15	Q8URP1	Q8urp1 human immun
742	5	16.7	221	15	Q9YRX1	Q9yrx1 human immun	815	5	16.7	239	15	Q8URP0	Q8urp0 human immun
743	5	16.7	221	15	Q9YRY0	Q9yry0 human immun	816	5	16.7	239	15	Q8URN9	Q8urn9 human immun
744	5	16.7	221	15	Q9YTB5	Q9ytb5 human immun	817	5	16.7	239	15	Q8URN8	Q8urn8 human immun
745	5	16.7	221	15	Q9YIX7	Q9yix7 human immun	818	5	16.7	239	15	Q8URN7	Q8urn7 human immun
746	5	16.7	221	10	Q9LVV4	Q9lvv4 arabidopsis	819	5	16.7	239	15	Q8URN6	Q8urn6 human immun

820	5	16.7	239	15	Q8URN5	Q8urn5 human	immun	893	5	16.7	243	15	Q9E020	Q9e020 human	immun
821	5	16.7	239	15	Q8URN4	Q8urn4 human	immun	894	5	16.7	243	15	Q9E019	Q9e019 human	immun
822	5	16.7	239	15	Q8URN3	Q8urn3 human	immun	895	5	16.7	243	15	Q9E018	Q9e018 human	immun
823	5	16.7	239	15	Q8URN2	Q8urn2 human	immun	896	5	16.7	243	15	Q9E017	Q9e017 human	immun
824	5	16.7	239	15	Q8URN1	Q8urn1 human	immun	897	5	16.7	243	15	Q9E016	Q9e016 human	immun
825	5	16.7	239	15	Q8URN0	Q8urn0 human	immun	898	5	16.7	243	15	Q9E015	Q9e015 human	immun
826	5	16.7	239	15	Q8URN9	Q8urn9 human	immun	899	5	16.7	243	15	Q9E014	Q9e014 human	immun
827	5	16.7	239	15	Q8URN8	Q8urn8 human	immun	900	5	16.7	243	15	Q9E013	Q9e013 human	immun
828	5	16.7	239	15	Q8URN7	Q8urn7 human	immun	901	5	16.7	243	15	Q9E012	Q9e012 human	immun
829	5	16.7	239	16	Q8URN6	Q8urn6 human	immun	902	5	16.7	243	15	Q9E011	Q9e011 human	immun
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833	5	16.7	240	11	Q9CUL6	Q9cul6 mus musculi	906	5	16.7	243	17	Q8X7Y5	Q8x7y5 escherichia		
834	5	16.7	241	5	Q9XWMS	Q9xwms caenorhabdi	907	5	16.7	243	16	Q9H1F1	Q9h1f1 thermoplasma		
835	5	16.7	241	5	001464	001464 caenorhabdi	908	5	16.7	244	4	Q13784	Q13784 homo sapien		
836	5	16.7	241	12	011309	011309 molluscum c	909	5	16.7	244	5	Q20804	Q20804 caenorhabdi		
837	5	16.7	242	2	Q9ZA27	Q9za27 streptomyces	910	5	16.7	245	2	Q9X7K5	Q9x7k5 rhizobium g		
838	5	16.7	242	2	050391	050391 mycobacteri	911	5	16.7	245	4	Q9NYC4	Q9nyc4 homo sapien		
839	5	16.7	242	10	Q91GB9	Q91gb9 oryza sativ	912	5	16.7	245	16	Q67870	Q67870 aquifex aeo		
840	5	16.7	242	16	Q9BJ89	Q9bj89 rhizobium l	913	5	16.7	246	2	Q9EUM7	Q9eum7 listeria in		
841	5	16.7	243	10	Q919U2	Q919u2 lagopus lag	914	5	16.7	246	11	061435	061435 mus musculi		
842	5	16.7	243	15	Q9E072	Q9e072 human	immun	915	5	16.7	246	16	Q8Y7Q1	Q8y7q1 anabaena sp	
843	5	16.7	243	15	Q9E071	Q9e071 human	immun	916	5	16.7	247	2	Q32546	Q32546 escherichia	
844	5	16.7	243	15	Q9E070	Q9e070 human	immun	917	5	16.7	247	10	Q9F1X5	Q9f1x5 arabidopsis	
845	5	16.7	243	15	Q9E069	Q9e069 human	immun	918	5	16.7	247	16	Q8Z1Z8	Q8z1z8 salmonella	
846	5	16.7	243	15	Q9E068	Q9e068 human	immun	919	5	16.7	247	16	Q8Z1J5	Q8z1j5 salmonella	
847	5	16.7	243	15	Q9E067	Q9e067 human	immun	920	5	16.7	247	16	Q9Z1R4	Q9z1r4 rhizobium m	
848	5	16.7	243	15	Q9E066	Q9e066 human	immun	921	5	16.7	248	2	Q9AG70	Q9agr0 staphylococ	
849	5	16.7	243	15	Q9E065	Q9e065 human	immun	922	5	16.7	248	5	Q25676	Q25676 plasmodium	
850	5	16.7	243	15	Q9E064	Q9e064 human	immun	923	5	16.7	248	16	Q99W72	Q99w72 staphylococ	
851	5	16.7	243	15	Q9E063	Q9e063 human	immun	924	5	16.7	248	16	Q8UGK3	Q8ugk3 agrobacteri	
852	5	16.7	243	15	Q9E062	Q9e062 human	immun	925	5	16.7	248	17	Q26833	Q26833 methanobact	
853	5	16.7	243	15	Q9E061	Q9e061 human	immun	926	5	16.7	249	10	Q8W5R4	Q8w5r4 oryza sativ	
854	5	16.7	243	15	Q9E060	Q9e060 human	immun	927	5	16.7	249	16	Q93GM5	Q93gm5 salmonella	
855	5	16.7	243	15	Q9E059	Q9e059 human	immun	928	5	16.7	250	10	Q9LE11	Q9le11 hordeum vul	
856	5	16.7	243	15	Q9E058	Q9e058 human	immun	929	5	16.7	250	10	Q9ASV8	Q9asv8 arabidopsis	
857	5	16.7	243	15	Q9E057	Q9e057 human	immun	930	5	16.7	251	2	Q9AP86	Q9ap86 uncultured	
858	5	16.7	243	15	Q9E056	Q9e056 human	immun	931	5	16.7	251	2	Q9APN9	Q9apn9 uncultured	
859	5	16.7	243	15	Q9E055	Q9e055 human	immun	932	5	16.7	251	16	Q8ZC06	Q8zcg6 salmonella	
860	5	16.7	243	15	Q9E054	Q9e054 human	immun	933	5	16.7	251	16	Q8Z891	Q8z891 salmonella	
861	5	16.7	243	15	Q9E053	Q9e053 human	immun	934	5	16.7	251	16	Q8X822	Q8x822 escherichia	
862	5	16.7	243	15	Q9E051	Q9e051 human	immun	935	5	16.7	252	5	Q9N3G8	Q9n3g8 caenorhabdi	
863	5	16.7	243	15	Q9E050	Q9e050 human	immun	936	5	16.7	252	10	Q94167	Q94167 potentilla	
864	5	16.7	243	15	Q9E049	Q9e049 human	immun	937	5	16.7	252	16	Q8YEW2	Q8yew2 brucella me	
865	5	16.7	243	15	Q9E048	Q9e048 human	immun	938	5	16.7	253	2	Q9WTC0	Q9wtc0 escherichia	
866	5	16.7	243	15	Q9E047	Q9e047 human	immun	939	5	16.7	253	2	Q937T4	Q937t4 acinetobact	
867	5	16.7	243	15	Q9E046	Q9e046 human	immun	940	5	16.7	254	5	Q9NSX6	Q9n5x6 caenorhabdi	
868	5	16.7	243	15	Q9E045	Q9e045 human	immun	941	5	16.7	254	17	Q59523	Q59523 pyrococcus	
869	5	16.7	243	15	Q9E044	Q9e044 human	immun	942	5	16.7	255	10	Q9ZWM8	Q9zwm8 oryza sativ	
870	5	16.7	243	15	Q9E043	Q9e043 human	immun	943	5	16.7	255	13	Q91911	Q91911 oncorhynch	
871	5	16.7	243	15	Q9E042	Q9e042 human	immun	944	5	16.7	256	10	Q96326	Q96326 arabidopsis	
872	5	16.7	243	15	Q9E041	Q9e041 human	immun	945	5	16.7	256	12	Q9UG85	Q9ug85 ct virus. o	
873	5	16.7	243	15	Q9E040	Q9e040 human	immun	946	5	16.7	257	3	Q94322	Q94322 schizosacch	
874	5	16.7	243	15	Q9E039	Q9e039 human	immun	947	5	16.7	257	16	Q9ZAN0	Q9zan0 listeria in	
875	5	16.7	243	15	Q9E038	Q9e038 human	immun	948	5	16.7	257	16	Q8YGB3	Q8ygb3 listeria mo	
876	5	16.7	243	15	Q9E037	Q9e037 human	immun	949	5	16.7	258	10	Q80714	Q80714 arabidopsis	
877	5	16.7	243	15	Q9E036	Q9e036 human	immun	950	5	16.7	258	16	Q8ZRB4	Q8zrb4 salmonella	
878	5	16.7	243	15	Q9E035	Q9e035 human	immun	951	5	16.7	258	16	Q8ZBR0	Q8zbr0 salmonella	
879	5	16.7	243	15	Q9E034	Q9e034 human	immun	952	5	16.7	259	2	Q9S3U5	Q9s3u5 bacteroides	
880	5	16.7	243	15	Q9E033	Q9e033 human	immun	953	5	16.7	259	10	Q9SNO0	Q9sno0 oryza sativ	
881	5	16.7	243	15	Q9E032	Q9e032 human	immun	954	5	16.7	259	17	Q8TXX2	Q8txx2 pyrococcus	
882	5	16.7	243	15	Q9E031	Q9e031 human	immun	955	5	16.7	260	4	Q8TCH6	Q8tch6 homo sapien	
883	5	16.7	243	15	Q9E030	Q9e030 human	immun	956	5	16.7	260	12	Q8UZ53	Q8uz53 indian cass	
884	5	16.7	243	15	Q9E029	Q9e029 human	immun	957	5	16.7	260	16	Q8YLU2	Q8ylu2 anabaena sp	
885	5	16.7	243	15	Q9E028	Q9e028 human	immun	958	5	16.7	261	4	Q9BSG5	Q9bsg5 homo sapien	
886	5	16.7	243	15	Q9E027	Q9e027 human	immun	959	5	16.7	261	16	Q98CP4	Q98cp4 rhizobium l	
887	5	16.7	243	15	Q9E026	Q9e026 human	immun	960	5	16.7	262	16	Q8YL53	Q8yl53 anabaena sp	
888	5	16.7	243	15	Q9E025	Q9e025 human	immun	961	5	16.7	263	4	Q96MW1	Q96mw1 homo sapien	
889	5	16.7	243	15	Q9E024	Q9e024 human	immun	962	5	16.7	263	15	Q9WDM7	Q9wdm7 human	immun
890	5	16.7	243	15	Q9E023	Q9e023 human	immun	963	5	16.7	263	15	Q9WDM3	Q9wdm3 human	immun
891	5	16.7	243	15	Q9E022	Q9e022 human	immun	964	5	16.7	263	15	Q9WDM5	Q9wdm5 human	immun
892	5	16.7	243	15	Q9E021	Q9e021 human	immun	965	5	16.7	263	15	Q9WDM8	Q9wdm8 human	immun

966	5	16.7	263	15	Q9WDV0	Q9wdv0 human immun
967	5	16.7	263	15	Q9WDV6	Q9wdv6 human immun
968	5	16.7	263	15	Q9WDV8	Q9wdv8 human immun
969	5	16.7	263	15	Q9WDW0	Q9wdw0 human immun
970	5	16.7	263	15	Q9WDW3	Q9wdw3 human immun
971	5	16.7	263	15	Q9WDW5	Q9wdw5 human immun
972	5	16.7	263	15	Q9WDW7	Q9wdw7 human immun
973	5	16.7	263	15	Q9WDW8	Q9wdw8 human immun
974	5	16.7	263	15	Q9WDW9	Q9wdw9 human immun
975	5	16.7	263	15	Q9WDX0	Q9wdx0 human immun
976	5	16.7	263	15	Q9WDX5	Q9wdx5 human immun
977	5	16.7	263	15	Q9WDX6	Q9wdx6 human immun
978	5	16.7	263	15	Q9WE18	Q9we18 human immun
979	5	16.7	263	15	Q9WE19	Q9we19 human immun
980	5	16.7	263	15	Q9WEJ0	Q9wej0 human immun
981	5	16.7	263	15	Q9WEJ1	Q9wej1 human immun
982	5	16.7	263	15	Q9WEJ2	Q9wej2 human immun
983	5	16.7	263	15	Q9WEJ4	Q9wej4 human immun
984	5	16.7	263	15	Q9WEJ5	Q9wej5 human immun
985	5	16.7	263	15	Q9WEJ7	Q9wej7 human immun
986	5	16.7	263	15	Q9WEJ8	Q9wej8 human immun
987	5	16.7	263	15	Q9WEJ9	Q9wej9 human immun
988	5	16.7	263	15	Q9WEJ3	Q9wej3 human immun
989	5	16.7	263	15	Q9WE17	Q9we17 human immun
990	5	16.7	263	15	Q9WEM0	Q9wem0 human immun
991	5	16.7	263	15	Q9WEM1	Q9wem1 human immun
992	5	16.7	263	15	Q9WEM4	Q9wem4 human immun
993	5	16.7	263	15	Q9WEM7	Q9wem7 human immun
994	5	16.7	263	15	Q9WEM8	Q9wem8 human immun
995	5	16.7	263	16	Q8YK11	Q8yK11 arabidena sp
996	5	16.7	264	4	Q9B9Q2	Q9b9q2 homo sapien
997	5	16.7	264	4	Q9B8Z8	Q9b8z8 mus musculu
998	5	16.7	264	11	Q88547	Q88547 mus musculu
999	5	16.7	264	11	Q92JG4	Q92jg4 mus musculu
1000	5	16.7	264	15	Q9WDM2	Q9wdm2 human immun

ALIGNMENTS

RESULT 1

Q9F9R1 PRELIMINARY; PRT; 207 AA.

AC Q9F9R1;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Superoxide dismutase.

EN SOD.

OS Mycobacterium paratuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1770;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-10;
 RA Liu X., Peng Z., Cirillo J., Barletta R.G.;
 RT "Mycobacterium paratuberculosis manganese superoxide dismutase.";
 RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 FAMILY.

DR HSSP; AF180816; AAG09425.1; -.
 DR HSSP; P17670; IIDS.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe_1.
 DR Pfam; PF02777; sodfe_C_1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 DR Oxidoreductase.
 KW SEQUENCE 207 AA; 23030 MW; EDA8C2EB40ED428D CRC64;

Query Match 26.7%; Score 8; DB 2; Length 207;
 Best Local Similarity 100.0%; Pred. No. 0.68;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ISGQNEI 25
 |||||
 Db 20 ISGQNEI 27

RESULT 2

Q9AM00 PRELIMINARY; PRT; 210 AA.

AC Q9AM00;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Superoxide dismutase.

OS Mycobacterium paratuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1770;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Dheenadhayalan V., Chang Y.F.;
 RT "Mycobacterium avium subsp. paratuberculosis superoxide dismutase
 gene.";

CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 FAMILY.

DR EMBL; AF33434; AAG50084.1; -.
 DR HSSP; P17670; IIDS.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe_1.
 DR Pfam; PF02777; sodfe_C_1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 DR Oxidoreductase.
 KW SEQUENCE 210 AA; 23357 MW; E492E313352B2E20 CRC64;

Query Match 26.7%; Score 8; DB 2; Length 210;
 Best Local Similarity 100.0%; Pred. No. 0.69;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ISGQNEI 25
 |||||
 Db 20 ISGQNEI 27

RESULT 3

P79022 PRELIMINARY; PRT; 227 AA.

AC P79022;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Superoxide dismutase (EC 1.15.1.1) precursor.

EN MMSOD.

OS Candida sp. H995.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; microspor Saccharomycetales; Candida.
 OX NCBI_TaxID=159257;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Choi S.-Y., Nam Y.-S., Hong Y.M.;
 RT "Molecular cloning and characterization of Mn-superoxide dismutase
 gene from Candida sp.";

RL Korean J. Microbiol. 35:309-314(1997).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL: Y11598; CAA72335.1; -.
 DR HSSP: P04179; IAP6.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sode, 1.
 DR Pfam: PF02777; sode C, 1.
 DR ProDom: PD000475; SODismutase; 1.
 DR PROSITE: PS00088; SOD MN; 1.
 KM Oxidoreductase; Signal.
 FT SIGNAL 1 30
 FT CHAIN 1 227 SUPEROXIDE DISMUTASE.
 SQ SEQUENCE 227 AA; 25227 MW; 29E7F6E3C7743DB0 CRC64;

Query Match 26.7%; Score 8; DB 3; Length 227;
 Best Local Similarity 100.0%; Pred. No. 0.74;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 18 ISGQINEI 25
 |||||
 Db 46 ISGQINEI 53

RESULT 4
 ID Q93X78 PRELIMINARY; PRT; 226 AA.
 AC Q93X78;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Beta-glucosidase (EC 3.2.1.21) (Fragment).
 OS Vitis vinifera (Grape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
 OC Vitif.
 OX NCBI_TaxID=29760;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. SHIRAZ; TISSUE=FRUIT;
 RA Sarry J.-E., Romieu C., Terrier N.;
 RT "Beta-glucosidase hydrolyse from grape berries."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY039034; AAK72100.1; -.
 DR InterPro: IPR001360; GH 1.
 DR Pfam: PF00232; Glyco_hydro_1; 1.
 DR ProDom: PD000650; GH_1; 1.
 DR Glycosidase; Hydrolase.
 FT NON_TER 1 1
 FT NON_TER 226 226
 SQ SEQUENCE 226 AA; 25610 MW; 2153960F27E61432 CRC64;

Query Match 23.3%; Score 7; DB 10; Length 226;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SATEPYI 18
 |||||
 Db 83 SATEPYI 89

RESULT 5
 ID Q9CSH7 PRELIMINARY; PRT; 312 AA.
 AC Q9CSH7;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative beta-glucosidase protein.
 GN MRC8.6/AT3G18080.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shim P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RT "Full Length cDNA of gene MRC8.6/AT3G18080 (GI:9294063).";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M.,
 RA Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P.,
 RA Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shim P., Southwick A., Tracy S.E.,
 RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full Length cDNA of gene MRC8.6/AT3G18080 (GI:9294063).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF360240; AAK25950.1; -.
 DR EMBL: AY040038; AAK64096.1; -.
 DR HSSP: P26205; 1CBG.
 DR InterPro: IPR001360; GH 1.
 DR Pfam: PF00232; Glyco_hydro_1; 1.
 DR PRINTS: PR00131; GHYDRLASE1.
 DR ProDom: PD000650; GH_1; 1.
 SQ SEQUENCE 312 AA; 36162 MW; 908D8E22553489F CRC64;

Query Match 23.3%; Score 7; DB 10; Length 312;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SATEPYI 18
 |||||
 Db 36 SATEPYI 42

RESULT 6
 ID Q942J1 PRELIMINARY; PRT; 462 AA.
 AC Q942J1;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative beta-glucosidase.
 GN P045H0310.1.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriarthoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nippobare(GAS) genomic DNA, chromosome 1, PAC
 RT clone: P045H0310.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP003435; BAB68015.1; -.
 DR InterPro: IPR001360; GH 1.
 DR Pfam: PF00232; Glyco_hydro_1; 1.
 DR ProDom: PD000650; GH_1; 1.
 SQ SEQUENCE 462 AA; 53007 MW; A4FBA6AE25AF052 CRC64;

Query Match 23.3%; Score 7; DB 10; Length 462;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SATEPYI 18
 |||||
 Db 153 SATEPYI 159

RESULT 7

Q9LV34 PRELIMINARY; PRT; 495 AA.

AC Q9LV34.
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Beta-glucosidase.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20363099; PubMed=10907853;

RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
 RT TAC and BAC clones.";
 RL DNA Res. 7:217-221(2000).
 DR EMBL; AB020749; BAB02019.1; -.
 DR HSSP; P26205; ICBG.
 DR InterPro; IPR001360; GH_1.
 DR Pfam; PF00232; Glyco_hydro_1; 1.
 DR PRINTS; PR00131; GLHYDRLASE1.
 DR ProDom; PD000650; GH_1; 1.
 SQ SEQUENCE 495 AA; 56496 MW; 85D92F613B79C22 CRC64;

Query Match 23.3%; Score 7; DB 10; Length 495;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SATEPYI 18
 |||||
 Db 219 SATEPYI 225

RESULT 8

Q42975 PRELIMINARY; PRT; 504 AA.

AC Q42975.
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Beta-glucosidase (EC 3.2.1.21).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE OF 1-123 FROM N.A.
 RC STRAIN=NIPPONBARE; TISSUE=ROOT;
 RA Yuzo M., Takuji S.;
 RT "Oryza sativa beta-glucosidase mRNA sequence."
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIPPONBARE; TISSUE=ROOT;
 RA Eesen A., Opasiri R., Ketudat Cairns J., Akiyama T.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U28047; AAA84906.2; -.
 RX Hydrolase; Glycosidase.
 SQ SEQUENCE 504 AA; 56906 MW; 5D93BF0605E43257 CRC64;

Query Match 23.3%; Score 7; DB 10; Length 504;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SATEPYI 18
 |||||
 Db 232 SATEPYI 238

RESULT 9

Q24524 PRELIMINARY; PRT; 507 AA.

AC Q24524.
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Linamarase (EC 3.2.1.21).
 GN PLIN-GEN.
 OS Manihot esculenta (Cassava) (Manioc).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Malpighiales; Euphorbiaceae; Manihot.
 OX NCBI_TaxID=3983;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McMahon J.M., Sayre R.T.;
 RT "Genomic sequence for a linamarase gene from cassava (Manihot
 RT esculenta Crantz).";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U95298; AAB71381.1; -.
 DR HSSP; P26205; ICBG.
 DR InterPro; IPR001360; GH_1.
 DR Pfam; PF00232; Glyco_hydro_1; 1.
 DR PRINTS; PR00131; GLHYDRLASE1.
 DR ProDom; PD000650; GH_1; 1.
 KW Glycosidase; Hydrolase.
 SQ SEQUENCE 507 AA; 59324 MW; 9CF33AD8755A7AF CRC64;

Query Match 23.3%; Score 7; DB 10; Length 507;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SATEPYI 18
 |||||
 Db 206 SATEPYI 212

RESULT 10

Q9LV33 PRELIMINARY; PRT; 512 AA.

AC Q9LV33.
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Beta-glucosidase.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;

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RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AB020749; BAB02020.1; -.
DR HSSP; P26205; ICBG.
DR InterPro; IPR001360; GH_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR PRODOM; PD000650; GH_1; 1.
SQ SEQUENCE 512 AA; 58983 MW; A870F9BB20C342E7 CRC64;

Query Match 23.3%; Score 7; DB 10; Length 512;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SATEPYI 18
    |||||
    236 SATEPYI 242

RESULT 11
O8VWL8 PRELIMINARY; PRT; 514 AA.
ID O8VWL8;
AC O8VWL8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-mannosidase (beta-mannosidase enzyme).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasteridae I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=CV; GLAMOUR;
RA Mo B.; Bewley D.;
RT "Beta-mannosidase gene from tomato (lewside 2).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV; GLAMOUR; TISSUE=SEED;
RA Mo B.; Bewley J.;
RT "Lycopersicon esculentum beta-mannosidase (lewside) gene encoding
RT beta-mannosidase enzyme, complete sequence.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF413204; AL137719.1; -.
DR EMBL; AF413204; AL137719.1; -.
DR InterPro; IPR001360; GH_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR PRODOM; PD000650; GH_1; 1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; UNKNOWN 1.
SQ SEQUENCE 514 AA; 59288 MW; 0A3855084EDA1971 CRC64;

Query Match 23.3%; Score 7; DB 10; Length 514;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SATEPYI 18
    |||||
    239 SATEPYI 245

RESULT 12
O41172 PRELIMINARY; PRT; 531 AA.
ID O41172;
AC O41172;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

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DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Linamarase.
GN LINAMARASE.
OS Manihot esculenta (Cassava) (Manioc).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Malpighiales; Euphorbiaceae; Manihot.
OX NCBI_TaxID=3983;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92264724; PubMed=1586156;
RA Hughes M.A., Brown K., Pancoro A., Murray B.S., Oxtoby E., Hughes J.;
RT "A molecular and biochemical analysis of the structure of the
RT cyanogenic beta-glucosidase (linamarase) from cassava (Manihot
RT esculenta Cranz).";
RL Arch. Biochem. Biophys. 295:273-279(1992).
DR EMBL; S35175; AAB22162.1; -.
DR HSSP; P26205; ICBG.
DR InterPro; IPR001360; GH_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR PRODOM; PD000650; GH_1; 1.
SQ SEQUENCE 531 AA; 61373 MW; 4FE14D39FBA0F17 CRC64;

Query Match 23.3%; Score 7; DB 10; Length 531;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SATEPYI 18
    |||||
    230 SATEPYI 236

RESULT 13
O40283 PRELIMINARY; PRT; 541 AA.
ID O40283;
AC O40283;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta glucosidase precursor.
GN BGLA.
OS Manihot esculenta (Cassava) (Manioc).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Malpighiales; Euphorbiaceae; Manihot.
OX NCBI_TaxID=3983;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBG3;
RA Liddle S.; Kereszteszy Z.; Hughes J.; Hughes M.A.;
RT "A genomic cyanogenic beta-glucosidase gene from Cassava (Accession
RT No. X94986). (PGR98-148).";
RL Plant Physiol. 117:1526-1526(1998).
DR EMBL; X94986; CA64442.1; -.
DR HSSP; P26205; ICBG.
DR InterPro; IPR001360; GH_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR PRODOM; PD000650; GH_1; 1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
KW SIGNAL.
FT CHAIN 1 28 POTENTIAL.
FT CHAIN 29 541 BETA GLUCOSIDASE.
SQ SEQUENCE 541 AA; 63095 MW; 01735B5D4429EDA CRC64;

Query Match 23.3%; Score 7; DB 10; Length 541;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SATEPYI 18
    |||||
    241 SATEPYI 247

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RESULT 14

Q9SVR3 PRELIMINARY; PRT; 620 AA.
AC Q9SVR3;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
GN Hypothetical protein ECU04_1410.
OS Encephalitozoon cuniculi.
OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
SQ SEQUENCE FROM N.A.
STRAIN=GB-M1;
MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat P.,
RA Prenster G., Barthe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL; AL590444; CAD25330.1; -.
KW Hypothetical protein.
SQ SEQUENCE 620 AA; 69120 MW; CED63EACF52191 CRC64;

Query Match 23.3%; Score 7; DB 5; Length 620;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYSLPEL 7
Db 264 KYSLPEL 270

RESULT 15

Q9U275 PRELIMINARY; PRT; 807 AA.
AC Q9U275;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
GN Y50E8A.16 protein.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peioderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Steward C.A.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
SQ SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AL117200; CAB60586.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABC_transporter.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 1.

DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport.
SQ SEQUENCE 807 AA; 91163 MW; B9ABC598966DF1EF CRC64;

Query Match 23.3%; Score 7; DB 5; Length 807;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PELDYEF 11
Db 532 PELDYEF 538

RESULT 16

Q9AMT5 PRELIMINARY; PRT; 936 AA.
AC Q9AMT5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
GN ID880.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=110SPC4;
RX MEDLINE=21101824; PubMed=1157954;
RA Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R.,
RA Hennecke H.;
RT "Potential symbiosis-specific genes uncovered by sequencing a 410-kb
RT DNA region of the Bradyrhizobium japonicum chromosome.";
RL J. Bacteriol. 183:1405-1412(2001).
DR EMBL; AF322013; AAC61062.1; -.
SQ SEQUENCE 936 AA; 104325 MW; 9AD94C465044F904 CRC64;

Query Match 23.3%; Score 7; DB 2; Length 936;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EFSATEP 16
Db 393 EFSATEP 399

RESULT 17

Q94QB2 PRELIMINARY; PRT; 1011 AA.
AC Q94QB2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
GN Phosphoenolpyruvate carboxylase (EC 4.1.1.31).
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
OG Nucleomorph.
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32053;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen L.M., Omiya T., Hata S., Inoue Y., Iwai K.;
RT "Molecular characterization of Synechococcus vulcanus
RT phosphoenolpyruvate carboxylase.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB057454; BAB64533.1; -.
DR InterPro; IPR001449; PEPcase.
DR Pfam; PF00311; PEPcase; 1.
DR PROSITE; PS00393; PEPcase_2; UNKNOWN_1.

KW Lyase; Pyruvate.
SQ SEQUENCE 1011 AA; 116426 MW; 0A11D4D01FE9E7FE CRC64;

Query Match 23.3%; Score 7; DB 8; Length 1011;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYSLPEL 7
|||||
Db 732 KYSLPEL 738

RESULT 18

Q97AN6 PRELIMINARY; PRT; 57 AA.

AC Q97AN6;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DT Hypothetical protein TV0774.
TV0774 OR TVG0779096.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Munoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
sequence of Thermoplasma volcanium";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262 (2000).
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 57 AA; 6709 MW; 8EACD1FAAE3A02FB CRC64;

Query Match 20.0%; Score 6; DB 17; Length 57;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYSLPE 6
|||||
Db 51 KYSLPE 56

RESULT 19

Q8Z0Y8 PRELIMINARY; PRT; 91 AA.

AC Q8Z0Y8;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical protein STR4854.
GN STR4854.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Baaham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Hogue A., Hien T.T., Holroyd S., Jajale K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;

RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852 (2001).
DR EMBL; AL627283; CAD06973.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 91 AA; 10657 MW; CB4D4D357F68FB CRC64;

Query Match 20.0%; Score 6; DB 16; Length 91;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 YISQOI 22
|||||
Db 79 YISQOI 84

RESULT 20

Q97776 PRELIMINARY; PRT; 100 AA.

AC Q97776;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2188188; PubMed=1546316;
RA Wolinsky S.M., Wike C.M., Korber B.T., Hutto C., Parks W.P.,
RA Rosenblum L.L., Kunstman K.J., Furuta M.R., Munoz U.L.;
RT "Selection transmission of human immunodeficiency virus type-1
variants from mothers to infants";
RL Science 255:1134-1137 (1992).
DR EMBL; M76911; AAB09342.1; -;
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1 100
FT NON_TER 1 100
SQ SEQUENCE 100 AA; 11073 MW; 7FB3DA98C9E89B0 CRC64;

Query Match 20.0%; Score 6; DB 15; Length 100;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 ISQGIN 23
|||||
Db 64 ISQGIN 69

RESULT 21

Q9K590 PRELIMINARY; PRT; 150 AA.

AC Q9K590;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MobB protein.
GN MOBB.
OS Halomonas elongata.
OC Plasmid PHE1.
OC Bacteria; Proteobacteria; gamma subdivision; Halomonadaceae;
OC Halomonas.
OX NCBI_TaxID=2746;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33174;
RX MEDLINE=20252113; PubMed=10794139;
RA Vargas C., Tegos G., Vartolomatos G., Draines C., Ventosa A.,
RA Nieto J.J.;

RT "Genetic organization of the mobilization region of the plasmid pHE1
 from *Halomonas elongata*.";
 RL Syst. Appl. Microbiol. 22:520-529(1999).
 DR EMBL; AJ243735; CAB96960.1; -.
 KW Plasmid.
 SQ SEQUENCE 150 AA; 16460 MW; 77B7631EF76DBE93 CRC64;

Query Match 20.0%; Score 6; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 GOINEI 25
 |||||
 DB 94 GOINEI 99

RESULT 22

O9CTJ9 PRELIMINARY; PRT; 153 AA.

O9CTJ9; 01-JUN-2001 (TREMBlrel. 17, Created)
 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE 18 days embryo cDNA, RIKEN full-length enriched library,
 clone:110002121, full insert sequence (fragment).
 GN 2210412X09RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kanakawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kuhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gurelitch S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereis P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.
 RA "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK003313; BAB22709.1; -.
 DR MGD; MGI:1924209; 2210412X09RIK.
 FT NON TER 1
 SQ SEQUENCE 153 AA; 16332 MW; E780CE2347A4C3B2 CRC64;

Query Match 20.0%; Score 6; DB 11; Length 153;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SLPELD 8
 |||||
 DB 59 SLPELD 64

RESULT 23

O9BPM2 PRELIMINARY; PRT; 156 AA.

ID O9BPM2
 AC O9BPM2
 DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Cysteine proteinase (Fragment).
 GN Cpl.
 OS Metagonimus yokogawai.

OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Opisthorchiida; Opisthorchiata; Opisthorchiidae; Heterophyidae;
 CC Metagonimus.
 CX NCBI_TaxID=84529;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Park H., Yun H.C., Kim K.Y., Park S.Y., Park S.K.;
 RT "Metagonimus yokogawai cysteine proteinase (Cpl) mRNA."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF121840; AAC52658.1; -.
 DR HSSP; P07711; 1CS8.

DR MEROPS; C01.032; -.
 DR InterPro; IPR000668; Peptidase_C1.
 DR InterPro; IPR000169; SHprot_acsite.
 DR InterPro; IPR000834; Zn_cardoPept.
 DR Pfam; PF00112; Peptidase_C1; 1.
 DR ProDom; PD000158; Peptidase_C1; 1.
 DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.

FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 156 AA; 16938 MW; 26ED60FE5F315E15 CRC64;

Query Match 20.0%; Score 6; DB 5; Length 156;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 PYISQ 21
 |||||
 DB 63 PYISQ 68

RESULT 24

O99ZV3 PRELIMINARY; PRT; 163 AA.

O99ZV3; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Spv-like phosphotransferase system (PTS), enzyme II component B.
 GN Spv1058.

OS Streptococcus pyogenes.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 CC Streptococcaceae; Streptococcus.

OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 Primeaux C., Sezate S., Suvorov A.N., Kenyon S., Lai H.S., Lin S.P.,
 Qian Y., Jia H.G., Najjar F.Z., Ren O., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RT "Complete genome sequence of an M1 strain of *Streptococcus pyogenes*."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 DR EMBL; AE006550; AAK33945.1; -.
 KW Transferase; Complete proteome.

SQ SEQUENCE 163 AA; 17934 MW; B1ABB69B4C263262 CRC64;

Query Match 20.0%; Score 6; DB 16; Length 163;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SLPELD 8
 |||||
 DB 139 SLPELD 144

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RESULT 25
006112 PRELIMINARY; PRT; 184 AA.
AC 006112;
DT 01-JUN-1997 (TREMBlrel. 04, Created)
DT 01-JUN-1997 (TREMBlrel. 04, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE Hypothetical 21.5 kDa protein.
OS Methanococcus maripaludis.
OC Plasmid PUR8500.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=39152;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS;
RX MEDLINE=97284503; PubMed=9139917;
RA Tumbula D.L., Bowen T.L., Whitman W.B.;
RT "Characterization of PUR8500 from the archaeon Methanococcus
maripaludis and construction of a shuttle vector.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CS;
RA Tumbula D.L., Whitman W.B.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U47023; AAC45262.1; -.
KM Hypothetical protein; Plasmid.
SQ SEQUENCE 184 AA; 21492 MW; 481963C2F1BCC08 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLPEL 7
DB 108 YSLPEL 113

RESULT 26
059673 PRELIMINARY; PRT; 189 AA.
AC 059673;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Superoxide dismutase (EC 1.15.1.1) (Fragment).
OS SOD.
OS Propionibacterium freudenreichii.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Propionibacteriaceae; Propionibacteriaceae;
OC Propionibacterium.
OX NCBI_TaxID=1744;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P23;
RX MEDLINE=96074560; PubMed=7488202;
RA Gabblanelli R., Battistoni A., Polizio F., Carri M.T., De Martino A.,
Meier B., Desideri A., Rocillo G.;
RT "Metal uptake of recombinant cambialistic superoxide dismutase from
Propionibacterium shermanii is affected by growth conditions of host
Escherichia coli cells.";
RL Biochem. Biophys. Res. Commun. 216:841-847(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=P23;
RA Gabblanelli R.;
RT Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.

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DR EMBL; X91650; CAAG2838.1; -.
DR EMBL; Y09012; CAAT0215.1; -.
DR HSSP; P80293; IAVM.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe_C1.
DR Pfam; PF02777; sodfe_C1.
DR PROSITE; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KM Oxidoreductase.
FT NON_TER 189
SQ SEQUENCE 189 AA; 21334 MW; 1971419C716FF651 CRC64;

Query Match 20.0%; Score 6; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EPTSG 20
DB 17 EPTSG 22

RESULT 27
090LUB PRELIMINARY; PRT; 193 AA.
AC 090LUB;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Envelope glycoprotein (Fragment).
OS ENV.
OS Human immunodeficiency virus type 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1016;
RA Delwart E.L.;
RT "Homogeneous quasispecies in 16/17 individuals during very early HIV-1
RT primary infection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF403533; AAK95241.1; -.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KM AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 193 AA; 21366 MW; 1CD5BA0920228B5 CRC64;

Query Match 20.0%; Score 6; DB 15; Length 193;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 ISGOIN 23
DB 155 ISGOIN 160

RESULT 28
09APY3 PRELIMINARY; PRT; 200 AA.
AC 09APY3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Manganese superoxide dismutase (EC 1.15.1.1).
OS SODA.
OS Corynebacterium melassecola, and
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Corynebacteriaceae;
OC Corynebacterium.
OX NCBI_TaxID=41643, 1718;
RN [1]

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RP SEQUENCE FROM N.A.
RC SPECIES=C.melasecola; STRAIN=ATCC17965;
RX MEDLINE=21101811; PubMed=11157941;
RA Merkum M., Guyonvarch A.;
RT "Cloning of the SODA Gene from *Corynebacterium melasecola* and Role of Superoxide Dismutase in Cellular Viability."; J. Bacteriol. 183:1284-1295(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=C.glutamicum; STRAIN=ATCC 13032;
RA Nakagawa S., Mizoguchi H., Ando S., Hayashi M., Hattori M., Shiba T., Sakaki Y., Yokoi H., Ozaki A.;
RT "SOD of *Corynebacterium glutamicum* ATCC 13032.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
DR EMBL; AF236111; AK01490.1; -
DR EMBL; AB055218; BAB62412.1; -
DR HSSP; P17670; 1IDS
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sode; 1.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00089; SOD_MN; 1.
KW Oxidoreductase.
SQ SEQUENCE 200 AA; 22101 MW; D236A2C3F291CE13 CRC64;

Query Match 20.0%; Score 6; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LPELDY 9
DB 6 LPELDY 11

RESULT 29
ID Q9YV92 PRELIMINARY; PRT; 200 AA.
AC Q9YV92;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=08-121V4;
RX MEDLINE=98248614; PubMed=9582120;
RA Frenkel L.M., Mullins J.I., Learn G.H., Manns-Arcuino L., Herring B.L., Kalish M.L., Steksee R.W., Thea D.M., Nichols J.E., Liu S.-L., Harmache A., He X., Muthui D., Madan A., Hood L., Haase A.T., Zupanic M., Steakus K., Wolinsky S.M., Krogstad P., Zhao J.-Q., Chen I., Koup R., Ho D.D., Korber B.T., Apple R.J.;
RA Coombs R.W., Pahwa S., Roberts N.J. Jr.;
RT "Genetic evaluation of suspected cases of transient HIV-1 infection of infants.";
RL Science 280:1073-1077(1998).
DR EMBL; AF065540; AAC21503.1; -
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 200 AA; 22373 MW; 1844CAFA07BDA8F6 CRC64;

Query Match 20.0%; Score 6; DB 15; Length 200;

Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 ISGOIN 23
DB 168 ISGOIN 173

RESULT 30
ID Q90009 PRELIMINARY; PRT; 200 AA.
AC Q90009;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=08-121V4;
RX MEDLINE=98248614; PubMed=9582120;
RA Frenkel L.M., Mullins J.I., Learn G.H., Manns-Arcuino L., Herring B.L., Kalish M.L., Steksee R.W., Thea D.M., Nichols J.E., Liu S.-L., Harmache A., He X., Muthui D., Madan A., Hood L., Haase A.T., Zupanic M., Steakus K., Wolinsky S.M., Krogstad P., Zhao J.-Q., Chen I., Koup R., Ho D.D., Korber B.T., Apple R.J., Coombs R.W., Pahwa S., Roberts N.J. Jr.;
RT "Genetic evaluation of suspected cases of transient HIV-1 infection of infants.";
RL Science 280:1073-1077(1998).
DR EMBL; AF065542; AAC21505.1; -
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 200 AA; 22363 MW; 008F570236B1AC77 CRC64;

Query Match 20.0%; Score 6; DB 15; Length 200;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 ISGOIN 23
DB 168 ISGOIN 173

RESULT 31
ID Q70722 PRELIMINARY; PRT; 202 AA.
AC Q70722;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Surface envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=91NE537;
RX MEDLINE=94365971; PubMed=8084001;
RA Delwart E.L., Sheppard H.W., Walker B.D., Goudsmic J., Mullins J.I.;
RT "Human immunodeficiency virus type 1 evolution in vivo tracked by DNA heteroduplex mobility assays.";
RL J. Virol. 68:6672-6683(1994).
DR EMBL; U13243; AAA61888.1; -
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.

KM AIDS; Coat protein; Envelope protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 202
SQ SEQUENCE 202 AA; 22474 MW; 9D2A8004C9B93D75 CRC64;
Query Match 20.0%; Score 6; DB 15; Length 202;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 18 ISGQIN 23
Db 167 ISGQIN 172
RESULT 32
Q70723 PRELIMINARY; PRT; 202 AA.
AC Q70723;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
RT "Human immunodeficiency virus type 1 evolution in vivo tracked by DNA heteroduplex mobility assays."
RL J. Virol. 68:6672-6683(1994).
DR EMBL: U13244; AAA61889.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DE AIDS; Coat protein; Envelope protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 202
SQ SEQUENCE 202 AA; 22399 MW; 83CB929A3F6AA88F CRC64;
Query Match 20.0%; Score 6; DB 15; Length 202;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 18 ISGQIN 23
Db 167 ISGQIN 172
RESULT 33
Q71823 PRELIMINARY; PRT; 202 AA.
AC Q71823;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
RT "Human immunodeficiency virus type 1."
RL AIDS Res. Hum. Retroviruses 10:1679-1684(1994).
DE Envelope glycoprotein, V3-V5 region (Fragment).
FT NON_TER 1
FT NON_TER 202
SQ SEQUENCE 202 AA; 22399 MW; 83CB929A3F6AA88F CRC64;
Query Match 20.0%; Score 6; DB 15; Length 202;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 18 ISGQIN 23
Db 167 ISGQIN 172

RP SEQUENCE FROM N.A.
RC STRAIN=537 SAMPLE 1991;
RX MEDLINE=96089215; PubMed=8554905;
RA Delwart E.L., Busch M.P., Kalish M.L., Mosley J.W., Mullins J.I.;
RT "Rapid molecular epidemiology of human immunodeficiency virus transmission."
RL AIDS Res. Hum. Retroviruses 11:1081-1093(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=537 SAMPLE 1991;
RA Shpaer E.G.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U23653; AAB0636.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KM AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 202
SQ SEQUENCE 202 AA; 22474 MW; 9D2A8004C9B93D75 CRC64;
Query Match 20.0%; Score 6; DB 15; Length 202;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 18 ISGQIN 23
Db 167 ISGQIN 172
RESULT 34
Q71824 PRELIMINARY; PRT; 202 AA.
AC Q71824;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
RT "Human immunodeficiency virus type 1 evolution in vivo tracked by DNA heteroduplex mobility assays."
RL J. Virol. 68:6672-6683(1994).
DR EMBL: U13244; AAA61889.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DE AIDS; Coat protein; Envelope protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 202
SQ SEQUENCE 202 AA; 22399 MW; 83CB929A3F6AA88F CRC64;
Query Match 20.0%; Score 6; DB 15; Length 202;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 18 ISGQIN 23
Db 167 ISGQIN 172

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 18 ISGQIN 23
 |||||
 Db 167 ISGQIN 172

RESULT 35

ID 071827 PRELIMINARY; PRT; 202 AA.

AC 071827;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Envelope glycoprotein, V3-V5 region (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;

SEQUENCE FROM N.A.

STRAIN=537 SAMPLE 1991;

RA Shpaer E.G., Delwart E.L., Kuiken C.L., Goudsmit J., Bachmann M.H.,

RA Mullins J.I.;

RT "Conserved V3 loop sequences and transmission of human

RT immunodeficiency virus type 1."

RL AIDS Res. Hum. Retroviruses 10:1679-1684(1994).

RP SEQUENCE FROM N.A.

RC STRAIN=537 SAMPLE 1991;

RC MEDLINE=96089215; PubMed=8554905;

RA Delwart E.L., Busch M.P., Kallish M.L., Mosley J.W., Mullins J.I.;

RT "Rapid molecular epidemiology of human immunodeficiency virus

RT transmission."

RL AIDS Res. Hum. Retroviruses 11:1081-1093(1995).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

SEQUENCE FROM N.A.

STRAIN=537 SAMPLE 1991;

RA Shpaer E.G.;

RA Submittet (MAR-1995) to the EMBL/GenBank/DBJ databases.

RA EMBL; U23657; AB0640.1; -.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

KW AIDS; Coat protein; Glycoprotein.

FT NON_TER 1

FT NON_TER 202

SO SEQUENCE 202 AA; 22526 MW; 76AAA09215F29A39 CRC64;

Query Match

Best Local Similarity 100.0%; Score 6; DB 15; Length 202;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 18 ISGQIN 23
 |||||

Db 168 ISGQIN 173

RESULT 36

ID 090010 PRELIMINARY; PRT; 203 AA.

AC 090010;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RP SEQUENCE FROM N.A.

RC STRAIN=08-121V4;

EX MEDLINE=98248614; PubMed=9582120;
 RA Frenkel L.M., Mullins J.I., Learn G.H., Manns-Arcuino L.,
 RA Herring B.L., Kallish M.L., Steketee R.W., Thea D.M., Nichols J.E.,
 RA Liu S.-L., Harmache A., He X., Muthul D., Madan A., Hood L.,
 RA Haase A.T., Zupanic M., Steakus K., Wolinsky S.M., Krogstad P.,
 RA Zhao J.-Q., Chen I., Koup R., Ho D.D., Kober B.T., Apple R.J.,
 RA Coombs R.W., Pahwa S., Roberts N.J. Jr.;
 RT "Genetic evaluation of suspected cases of transient HIV-1 infection of
 RT infants."
 RL Science 280:1073-1077(1998).
 DR EMBL; AF065543; AAC21506.1; -.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 203

SO SEQUENCE 203 AA; 22676 MW; 6C269D4172E9B74B CRC64;

Query Match

Best Local Similarity 100.0%; Score 6; DB 15; Length 203;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 18 ISGQIN 23
 |||||

Db 168 ISGQIN 173

RESULT 37

ID 09YV91 PRELIMINARY; PRT; 203 AA.

AC 09YV91;

DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

SEQUENCE FROM N.A.

STRAIN=08-121V4;

RA Frenkel L.M., Mullins J.I., Learn G.H., Manns-Arcuino L.,

RA Herring B.L., Kallish M.L., Steketee R.W., Thea D.M., Nichols J.E.,

RA Liu S.-L., Harmache A., He X., Muthul D., Madan A., Hood L.,

RA Haase A.T., Zupanic M., Steakus K., Wolinsky S.M., Krogstad P.,

RA Zhao J.-Q., Chen I., Koup R., Ho D.D., Kober B.T., Apple R.J.,

RA Coombs R.W., Pahwa S., Roberts N.J. Jr.;

RT "Genetic evaluation of suspected cases of transient HIV-1 infection of

RT infants."

RL Science 280:1073-1077(1998).

DR EMBL; AF065544; AAC21507.1; -.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

KW AIDS; Coat protein; Glycoprotein.

FT NON_TER 1

FT NON_TER 203

SO SEQUENCE 203 AA; 22602 MW; 8C6C8495742F6E35 CRC64;

Query Match

Best Local Similarity 100.0%; Score 6; DB 15; Length 203;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 18 ISGQIN 23
 |||||

Db 168 ISGQIN 173

RESULT 38

ID 09YV90 PRELIMINARY; PRT; 203 AA.

AC 09YV90;

DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=08-121V4;
RX MEDLINE=98248614; PubMed=9582120;
RA Frenkel L.M., Mullins J.I., Leam G.H., Manns-Arcuino L.,
RA Herring B.L., Kalish M.L., Steketee R.W., Thea D.M., Nichols J.E.,
RA Liu S.-L., Harmache A., He X., Muchi D., Madan A., Hoog L.,
RA Haase A.T., Zupnick M., Staskus K., Wolinsky S.M., Krogstad P.,
RA Zhao J.-O., Chen I., Koup R., Ho D.D., Korber B.T., Apple R.J.,
RA Combs R.W., Pahwa S., Roberts N.J. Jr.,
RT "Genetic evaluation of suspected cases of transient HIV-1 infection of
infants.";
Science 280:1073-1077(1998).
DR EMBL: AF065546; AAC21509.1; -.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120, 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 203 AA; 22562 MW; 6130090845823D4 CRC64;

Query Match 20.0%; Score 6; DB 15; Length 203;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ISGOIN 23
Db 168 ISGOIN 173

RESULT 39
ID Q70724 PRELIMINARY; PRT; 203 AA.
AC Q70724;
DC 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Surface envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=91NE537;
RX MEDLINE=94365971; PubMed=8084001;
RA Delwart E.L., Sheppard H.W., Walker B.D., Goudsmit J., Mullins J.I.,
RT "Human immunodeficiency virus type 1 evolution in vivo tracked by DNA
heteroduplex mobility assays.";
J. Virol. 68:6672-6683(1994).
DR EMBL: U13245; AAA61890.1; -.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120, 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 203 AA; 22637 MW; CA202D16E061AB96 CRC64;

Query Match 20.0%; Score 6; DB 15; Length 203;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ISGOIN 23
Db 168 ISGOIN 173

RESULT 40
ID Q70725 PRELIMINARY; PRT; 203 AA.
AC Q70725;
DC 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Surface envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=91NE537;
RX MEDLINE=94365971; PubMed=8084001;
RA Delwart E.L., Sheppard H.W., Walker B.D., Goudsmit J., Mullins J.I.,
RT "Human immunodeficiency virus type 1 evolution in vivo tracked by DNA
heteroduplex mobility assays.";
J. Virol. 68:6672-6683(1994).
DR EMBL: U13246; AAA61891.1; -.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120, 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 203 AA; 22686 MW; 4C325CB1DA45BADE CRC64;

Query Match 20.0%; Score 6; DB 15; Length 203;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ISGOIN 23
Db 168 ISGOIN 173

Search completed: April 9, 2003, 14:16:49
Job time : 40.8624 secs

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: April 9, 2003, 14:11:20 ; Search time 7.29358 Seconds
(without alignments)
395.421 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 30
Sequence: 1 KYSLPELDYEFSAEPYISQINEIXYTX 30

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Database size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	33.3	233	1 DSBVN	superoxide dismuta
2	7	23.3	207	2 JC4351	superoxide dismuta
3	7	23.3	207	2 S15205	superoxide dismuta
4	7	23.3	207	2 S60669	superoxide dismuta
5	7	23.3	328	2 T03296	beta-glucosidase (
6	7	23.3	488	2 B69959	glycine dehydrogen
7	7	23.3	507	2 T10791	beta-glucosidase (
8	7	23.3	531	2 S23940	beta-glucosidase (
9	7	23.3	1034	2 S76134	hypothetical prote
10	7	23.3	2055	2 T31617	hypothetical prote
11	6	20.0	91	2 AH1065	hypothetical prote
12	6	20.0	202	2 JC4396	superoxide dismuta
13	6	20.0	207	2 B86498	superoxide dismuta
14	6	20.0	207	2 B72124	superoxide dismuta
15	6	20.0	207	2 AH1190	3-methyladenine DN
16	6	20.0	234	2 C83587	hypothetical prote
17	6	20.0	278	2 E64131	formyltetrahydrofo
18	6	20.0	293	2 T06212	glucose and ribito
19	6	20.0	334	2 H87192	probable isomerase
20	6	20.0	338	2 D86815	hypothetical prote
21	6	20.0	342	2 E71359	conserved hypotet
22	6	20.0	345	2 T25408	hypothetical prote
23	6	20.0	352	2 D84329	heme biosynthesis
24	6	20.0	355	2 G83003	A / G specific ade
25	6	20.0	379	2 T08277	carotenoid biosynt
26	6	20.0	384	2 G84650	probable beta-gluc
27	6	20.0	385	2 F70551	probable ketB prot
28	6	20.0	385	2 G87006	probable transmemb
29	6	20.0	405	2 A32812	repa protein - Agr

30	6	20.0	405	2 A13232	replication protei
31	6	20.0	412	2 D96939	sensory protein, c
32	6	20.0	428	2 C64080	hemy protein homol
33	6	20.0	429	2 T50362	cdc7-like protein
34	6	20.0	441	2 AH2930	oxidoreductase Atu
35	6	20.0	443	2 T31101	probable phosphom
36	6	20.0	446	2 F98351	probable oxidoredu
37	6	20.0	467	2 S30839	UTR2 protein - yea
38	6	20.0	482	2 E97012	probable non-proce
39	6	20.0	488	2 F84001	glycine dehydrogen
40	6	20.0	506	2 T02400	probable beta-gluc
41	6	20.0	508	2 AD0076	probable membrane
42	6	20.0	514	2 T47837	beta-glucosidase-1
43	6	20.0	517	2 T02403	probable beta-gluc
44	6	20.0	535	2 S40461	t-complex-type mol
45	6	20.0	535	2 S40462	t-complex-type mol
46	6	20.0	545	2 T47952	hypothetical prote
47	6	20.0	551	2 T09647	beta-glucosidase (
48	6	20.0	551	2 C64903	probable ABC-type
49	6	20.0	561	2 E90891	hypothetical prote
50	6	20.0	561	2 B95406	probable oxidoredu
51	6	20.0	588	2 T03510	hypothetical prote
52	6	20.0	617	2 T03510	fructose-bisphosph
53	6	20.0	640	2 A86857	hypothetical prote
54	6	20.0	647	2 G72346	probable lipoxigen
55	6	20.0	661	2 D69907	probable ABC-type
56	6	20.0	689	2 T11578	excinnuclease ABC
57	6	20.0	948	2 B81883	excinnuclease ABC
58	6	20.0	949	2 A81138	excinnuclease ABC
59	6	20.0	965	2 C82560	excinnuclease ABC
60	6	20.0	1146	2 S59376	hypothetical prote
61	6	20.0	1679	2 T50091	Yeast Ecm29 cell w
62	6	20.0	1687	2 T30244	phosphodiesterase
63	6	20.0	1706	2 T30175	exoribonuclease, v
64	6	20.0	1719	2 T30174	exoribonuclease, v
65	6	20.0	1822	2 S63985	collagen alpha 2 c
66	6	20.0	3188	2 A43426	collagen alpha 2 f
67	5	16.7	6	2	hM1 transcription
68	5	16.7	38	2	Circumsporozoit p
69	5	16.7	47	2	AF0727
70	5	16.7	49	2	S50999
71	5	16.7	54	2	AB1819
72	5	16.7	70	2	F81899
73	5	16.7	76	2	T29961
74	5	16.7	85	2	S44604
75	5	16.7	85	2	AB1868
76	5	16.7	88	2	AH2013
77	5	16.7	91	2	I54248
78	5	16.7	101	2	S39490
79	5	16.7	101	2	H72556
80	5	16.7	103	2	AD1172
81	5	16.7	107	2	H72506
82	5	16.7	109	2	C82913
83	5	16.7	115	1	S15822
84	5	16.7	115	2	T38514
85	5	16.7	119	2	G85846
86	5	16.7	119	2	AD2513
87	5	16.7	120	2	T07888
88	5	16.7	122	2	S75687
89	5	16.7	122	2	B86316
90	5	16.7	124	1	VKLJ51
91	5	16.7	124	2	F75373
92	5	16.7	125	2	E70332
93	5	16.7	125	2	C75305
94	5	16.7	127	2	T10311
95	5	16.7	127	2	B70910
96	5	16.7	129	1	QOCW4
97	5	16.7	129	1	JQ1871
98	5	16.7	129	2	T19154
99	5	16.7	132	2	TQ2302
100	5	16.7	132	2	S31877
101	5	16.7	133	2	H82366
102	5	16.7	134	2	A12102

replication protei
sensory protein, c
hemy protein homol
cdc7-like protein
oxidoreductase Atu
probable phosphom
probable oxidoredu
UTR2 protein - yea
probable non-proce
glycine dehydrogen
probable beta-gluc
probable membrane
beta-glucosidase-1
probable beta-gluc
t-complex-type mol
t-complex-type mol
hypothetical prote
beta-glucosidase (

103	5	16.7	135	2	B87516	conserved hypotet
104	5	16.7	135	2	AH1093	hypothetical prote
105	5	16.7	137	2	S74181	tumor antigen UK11
106	5	16.7	137	2	S39853	trkB protein - Str
107	5	16.7	138	2	D82400	TonB system transp
108	5	16.7	141	2	G91001	hypothetical prote
109	5	16.7	143	2	D90110	40S ribosomal prot
110	5	16.7	145	2	S41221	hypothetical prote
111	5	16.7	147	2	A75093	hypothetical prote
112	5	16.7	147	2	F71050	hypothetical prote
113	5	16.7	148	2	T33812	hypothetical prote
114	5	16.7	149	2	US0275	arginine metabolis
115	5	16.7	149	2	A83997	transcription regu
116	5	16.7	149	2	AC1608	arginine repressor
117	5	16.7	149	2	AG1245	hypothetical prote
118	5	16.7	150	2	F81280	hypothetical prote
119	5	16.7	152	2	S76383	hypothetical prote
120	5	16.7	154	2	C53373	hypothetical prote
121	5	16.7	154	2	D83768	bacterioferritin c
122	5	16.7	157	2	E84997	16 kD heat shock p
123	5	16.7	159	2	A70833	carbon-monoxide de
124	5	16.7	161	2	S49488	collagen alpha 3(I
125	5	16.7	162	2	S28301	hypothetical prote
126	5	16.7	162	2	F86637	hypothetical prote
127	5	16.7	164	2	T50870	hypothetical prote
128	5	16.7	165	2	PS0261	calcineurin regula
129	5	16.7	165	2	I40515	spal protein - Bac
130	5	16.7	165	2	S75265	hypothetical prote
131	5	16.7	165	2	A97759	16S rRNA processin
132	5	16.7	166	2	T13192	hypothetical prote
133	5	16.7	168	2	B75498	conserved hypotet
134	5	16.7	168	2	B86435	protein F17F8.17 l
135	5	16.7	169	2	C63994	hypothetical prote
136	5	16.7	170	1	A33391	calcineurin regula
137	5	16.7	170	1	S34127	calcineurin regula
138	5	16.7	170	1	UC1220	calcineurin regula
139	5	16.7	170	1	AA4307	calcineurin regula
140	5	16.7	170	2	JC5174	calcineurin regula
141	5	16.7	170	2	AC2917	invasion protein A
142	5	16.7	171	2	B69116	conserved hypotet
143	5	16.7	171	2	AH3585	hypothetical prote
144	5	16.7	175	2	T11151	NADH2 dehydrogenas
145	5	16.7	175	2	T11413	NADH2 dehydrogenas
146	5	16.7	175	2	D75467	bacterioferritin c
147	5	16.7	176	1	S02511	flavodoxin - Klebs
148	5	16.7	176	2	J01232	calcineurin regula
149	5	16.7	177	2	B55517	hypothetical prote
150	5	16.7	178	2	F90168	hypothetical prote
151	5	16.7	179	2	C97711	hypothetical prote
152	5	16.7	180	2	S38955	alpha-amylose inh1
153	5	16.7	180	2	F71639	hypothetical prote
154	5	16.7	181	2	T49476	hypothetical prote
155	5	16.7	183	2	B69388	hypothetical prote
156	5	16.7	184	2	B82307	16S rRNA processin
157	5	16.7	185	1	AA4559	relaxin 1 precursor
158	5	16.7	185	2	S48082	hypothetical prote
159	5	16.7	185	2	I39736	hypothetical prote
160	5	16.7	185	2	AE1902	hypothetical prote
161	5	16.7	188	2	T16749	hypothetical prote
162	5	16.7	189	2	T40699	hypothetical prote
163	5	16.7	190	2	A26630	hypothetical prote
164	5	16.7	191	2	T09985	nucleoleplasmn A -
165	5	16.7	191	2	F97691	protoporphyrinogen
166	5	16.7	195	2	H70171	hypothetical prote
167	5	16.7	195	2	S77152	hypothetical prote
168	5	16.7	196	2	G89950	conserved hypotet
169	5	16.7	196	2	AD2304	hypothetical prote
170	5	16.7	199	2	J01398	hypothetical prote
171	5	16.7	200	2	A26169	nucleoleplasmn - Af
172	5	16.7	200	2	T02173	probable alcohol d
173	5	16.7	202	2	S51097	superoxide dismuta
174	5	16.7	203	2	S04860	alpha-amylose/subt
175	5	16.7	203	2	AB1912	peptidyl-cRNA hydr
176	5	16.7	204	2	S22639	alpha-amylose/subt
177	5	16.7	205	2	E82601	conserved hypotet
178	5	16.7	206	2	H84165	hypothetical prote
179	5	16.7	207	2	G69835	hypothetical prote
180	5	16.7	208	2	H64139	guanylate kinase (
181	5	16.7	208	2	H69522	conserved hypotet
182	5	16.7	209	2	C96999	hypothetical prote
183	5	16.7	210	2	H82037	conserved hypotet
184	5	16.7	210	2	A99487	hypothetical prote
185	5	16.7	211	2	E90174	superoxide dismuta
186	5	16.7	211	2	S34616	superoxide dismuta
187	5	16.7	211	2	T42603	gene 60 protein -
188	5	16.7	211	2	S15167	fixt protein - Azo
189	5	16.7	211	2	H83239	pseudouridine synt
190	5	16.7	212	1	WZBER2	gene 60 protein -
191	5	16.7	212	2	F84862	probable extensin
192	5	16.7	212	2	AB2157	hypothetical prote
193	5	16.7	215	2	S39542	probable glutathio
194	5	16.7	215	2	F72641	hypothetical prote
195	5	16.7	216	1	S42716	calcineurin regula
196	5	16.7	216	2	S37349	luxM protein - Vib
197	5	16.7	218	2	H83485	conserved hypotet
198	5	16.7	218	2	AG0893	conserved hypotet
199	5	16.7	219	2	C81038	phosphoglycolate p
200	5	16.7	220	2	B49736	collagen alpha 3(I
201	5	16.7	220	2	H70568	hypothetical prote
202	5	16.7	221	2	T13935	envelope protein -
203	5	16.7	223	2	F83034	urease accessory p
204	5	16.7	224	2	A53143	testis-determining
205	5	16.7	225	2	H75088	pteromone shutdown
206	5	16.7	225	2	T20250	hypothetical prote
207	5	16.7	226	1	S19715	nitrite hydratase
208	5	16.7	226	2	A35968	tox regulon trans
209	5	16.7	226	2	AI2774	ribose 5-phosphate
210	5	16.7	226	2	AF2362	transcription regu
211	5	16.7	228	2	H97336	uncharacterized co
212	5	16.7	230	2	B86824	two-component syst
213	5	16.7	230	2	S76832	hypothetical prote
214	5	16.7	231	2	G97554	ribose 5-phosphate
215	5	16.7	231	2	H64850	flagellar hook for
216	5	16.7	231	2	E90810	flagellar biosynth
217	5	16.7	231	2	A85670	hypothetical prote
218	5	16.7	231	2	G75451	conserved hypotet
219	5	16.7	232	2	S47641	flagellar hook for
220	5	16.7	232	2	AI0639	flagellar hook for
221	5	16.7	234	1	S76823	hypothetical prote
222	5	16.7	236	2	F64964	yeep protein - Bsc
223	5	16.7	236	2	B84812	hypothetical prote
224	5	16.7	237	2	D97852	hypothetical prote
225	5	16.7	237	2	T22859	hypothetical prote
226	5	16.7	237	2	AI2062	hypothetical prote
227	5	16.7	238	2	AC2043	heme oxygenase (im
228	5	16.7	239	2	G82834	D-ribulose-5-phosp
229	5	16.7	239	2	F82386	amino acid ABC tra
230	5	16.7	239	2	C65222	probable 2-compone
231	5	16.7	239	2	B91267	two-component tran
232	5	16.7	239	2	G86107	probable 2-compone
233	5	16.7	239	2	F96908	uncharacterized co
234	5	16.7	241	2	T25506	hypothetical prote
235	5	16.7	241	2	T26676	hypothetical prote
236	5	16.7	242	2	T46543	hypothetical prote
237	5	16.7	242	1	IOECO	DNA-directed DNA p
238	5	16.7	243	1	E64452	conserved hypotet
239	5	16.7	243	2	C90655	DNA polymerase III
240	5	16.7	243	2	C85506	DNA polymerase III
241	5	16.7	244	2	H70905	DNA polymerase III
242	5	16.7	244	2	S38568	transcription init
243	5	16.7	245	1	A44914	tRNA nucleotidyltr
244	5	16.7	245	2	B70480	ribosomal protein
245	5	16.7	246	2	T48302	collagen alpha 3(I
246	5	16.7	246	2	AG2138	hypothetical prote
247	5	16.7	247	2	AG0966	conserved hypotet
248	5	16.7	248	2	A97486	prokaryotic type I

249	5	16.7	248	2	A12703	prokaryotic type I	322	5	16.7	303	2	B84744	hypothetical prote
250	5	16.7	248	2	E89820	hypothetical prote	323	5	16.7	303	2	T46405	hypothetical prote
251	5	16.7	248	2	F69198	conserved hypochet	324	5	16.7	304	2	E90521	hypothetical prote
252	5	16.7	250	2	A1268	probable tRNA (gua	325	5	16.7	305	1	IDECRK	replication initia
253	5	16.7	250	2	B87921	protein P56G4.5 [i	326	5	16.7	306	2	T06297	hypothetical prote
254	5	16.7	251	1	BVECB	biotin biosynthesi	327	5	16.7	309	2	B72342	conserved hypochet
255	5	16.7	251	2	G90735	probable enzyme B1	328	5	16.7	310	2	B86825	aspartate carboxy
256	5	16.7	251	2	H85585	hypothetical prote	329	5	16.7	310	2	S07522	capsid assembly pr
257	5	16.7	251	2	AB0597	biotin synthetase p	330	5	16.7	310	2	AC3238	hypothetical prote
258	5	16.7	252	2	AG3472	phosphoenolpyruv	331	5	16.7	311	2	D69881	yabc protein homol
259	5	16.7	253	2	S48430	probable membrane	332	5	16.7	312	2	E90929	probable flavoprot
260	5	16.7	254	2	E71203	hypothetical prote	333	5	16.7	312	2	A85778	probable flavoprot
261	5	16.7	255	2	JG0179	superoxide dismuta	334	5	16.7	312	2	B64928	electron transfer
262	5	16.7	256	2	T51150	probable transmemb	335	5	16.7	312	2	T23646	hypothetical prote
263	5	16.7	257	1	QUECTP	transfer protein t	336	5	16.7	312	2	B64072	spermidine/putresc
264	5	16.7	257	2	AB1297	ABC transporter (A	337	5	16.7	312	2	H97342	ABC-type MDR trans
265	5	16.7	257	2	AH1668	ABC transporter (A	338	5	16.7	312	2	T50705	transcription fact
266	5	16.7	257	2	T40655	hypothetical prote	339	5	16.7	313	2	E90634	probable flavoprot
267	5	16.7	258	2	T02176	probable alcohol d	340	5	16.7	313	2	E85485	probable flavoprot
268	5	16.7	258	2	A10566	hydroxypyruvate is	341	5	16.7	313	2	AF0511	FlxB protein [lipo
269	5	16.7	259	2	D64362	hypothetical prote	342	5	16.7	313	2	B64725	electron transfer
270	5	16.7	260	2	D24584	spectinomycin resi	343	5	16.7	313	2	S60713	polylactatrase-
271	5	16.7	260	2	AB2469	exodeoxyribonuclea	344	5	16.7	314	2	H83321	conserved hypochet
272	5	16.7	260	2	JQ2330	Brl protein - Indl	345	5	16.7	314	2	C75003	na+/ca+ exchanging
273	5	16.7	260	2	T50725	reaction center pr	346	5	16.7	315	1	HQDVSB	cytochrome-c3 hydr
274	5	16.7	260	2	A26538	reaction center pr	347	5	16.7	315	2	T37901	probable purine nu
275	5	16.7	261	2	A34476	collagen alpha 2(I	348	5	16.7	315	2	A91118	probable ferrichro
276	5	16.7	262	2	AB2488	hypothetical prote	349	5	16.7	315	2	H85962	probable ferrichro
277	5	16.7	263	2	AD2517	hypothetical prote	350	5	16.7	316	2	C64963	transcription regu
278	5	16.7	267	2	AB0615	SmA protein [lipo	351	5	16.7	316	2	E85823	transcription regu
279	5	16.7	268	2	D75574	hypothetical prote	352	5	16.7	316	2	G90976	transcription regu
280	5	16.7	269	2	I51539	MHC class II beta	353	5	16.7	316	2	T15896	hypothetical prote
281	5	16.7	270	1	AC1956	phosphoenolpyruv	354	5	16.7	318	2	F81205	chiamin-phosphat
282	5	16.7	270	2	F86177	protein Flp19.1 [355	5	16.7	318	2	H81781	hypothetical prote
283	5	16.7	271	2	AC0157	probable short cha	356	5	16.7	318	2	A83708	hypothetical prote
284	5	16.7	271	2	F82261	hypothetical prote	357	5	16.7	319	2	H69364	hypothetical prote
285	5	16.7	272	2	E64248	hypothetical prote	358	5	16.7	320	2	AG0934	bifunctional prote
286	5	16.7	273	2	AC0294	Conserved hypochet	359	5	16.7	320	2	G70365	glucose-6-phosphat
287	5	16.7	273	2	T12793	hypothetical prote	360	5	16.7	320	2	B72656	hypothetical prote
288	5	16.7	274	2	G83186	hypothetical prote	361	5	16.7	321	1	BVECBP	biotin-lacetyl-CoA
289	5	16.7	274	2	F81250	probable membrane	362	5	16.7	321	2	D91241	hypothetical prote
290	5	16.7	276	2	S56550	hypothetical 30.6K	363	5	16.7	321	2	A86089	hypothetical prote
291	5	16.7	276	2	D91289	hypothetical prote	364	5	16.7	322	2	D64996	putative glycosyl
292	5	16.7	276	2	G86130	hypothetical prote	365	5	16.7	322	2	F91021	probable sugar tra
293	5	16.7	276	2	D84547	NM (no apical mer	366	5	16.7	322	2	E85865	probable sugar tra
294	5	16.7	276	2	T46368	hypothetical prote	367	5	16.7	322	2	E70306	conserved hypochet
295	5	16.7	278	2	A11977	hypothetical prote	368	5	16.7	323	2	A96670	hypothetical prote
296	5	16.7	278	2	T31935	hypothetical prote	369	5	16.7	323	2	H89923	hypothetical prote
297	5	16.7	279	2	B70180	conserved hypochet	370	5	16.7	324	2	A10434	probable sodium/ca
298	5	16.7	280	2	AG0987	conserved hypochet	371	5	16.7	325	2	C91138	hypothetical prote
299	5	16.7	281	2	C69709	superoxide dismuta	372	5	16.7	325	2	H70773	probable protoporp
300	5	16.7	283	2	B98257	lysR-type transcri	373	5	16.7	325	2	F85983	hypothetical prote
301	5	16.7	283	2	AI3027	transcription regu	374	5	16.7	325	2	AI0904	probable membrane
302	5	16.7	285	2	AG1045	hypothetical prote	375	5	16.7	325	2	F65110	hypothetical 34.7
303	5	16.7	286	2	H90066	hypothetical prote	376	5	16.7	326	2	H83187	hypothetical prote
304	5	16.7	287	2	G90301	hypothetical prote	377	5	16.7	326	2	S76400	hypothetical prote
305	5	16.7	288	2	A87051	probable protoporp	378	5	16.7	326	2	D70548	probable muconate
306	5	16.7	288	2	T12462	hypothetical prote	379	5	16.7	327	2	D10793	probable lipopolys
307	5	16.7	289	2	A72030	ypoc translocation	380	5	16.7	327	2	S47965	polylactatrase
308	5	16.7	289	2	E86593	ypoc translocation	381	5	16.7	328	2	H90193	hypothetical prote
309	5	16.7	289	2	C90803	hypothetical prote	382	5	16.7	328	2	T41074	hypothetical prote
310	5	16.7	290	2	G85611	probable histone Z	383	5	16.7	332	2	T35917	probable regulator
311	5	16.7	293	2	AF0617	probable DNA methy	384	5	16.7	332	2	B89258	ribose ABC transpo
312	5	16.7	295	2	AH1773	transcription regu	385	5	16.7	332	2	AG3026	hypothetical prote
313	5	16.7	297	2	E86461	FLAM2.8 protein -	386	5	16.7	332	2	H82064	hypothetical prote
314	5	16.7	298	2	UC7323	cyclic ADP-ribose-	387	5	16.7	332	1	QQVZF9	conserved hypochet
315	5	16.7	298	2	H97072	zn-dependent hydro	388	5	16.7	333	1	F42513	poly(A) polymerase
316	5	16.7	299	2	T39602	conserved hypochet	389	5	16.7	333	2	E36845	U3R protein - vacc
317	5	16.7	300	2	A70433	hypothetical prote	390	5	16.7	333	2	T28518	hypothetical prote
318	5	16.7	300	2	AE2088	hypothetical prote	391	5	16.7	333	2	F72160	hypothetical prote
319	5	16.7	301	2	C86666	flu operon transcr	392	5	16.7	334	2	C95272	conserved hypochet
320	5	16.7	302	2	C64311	Na+/Ca2+-exchangin	393	5	16.7	337	2	AF0086	periplasmic bindin
321	5	16.7	303	2	A69749	hypothetical prote	394	5	16.7	337	2	T43372	Chromo domain prot

395	5	16.7	338	2	E95244	glycerol-3-phospha
396	5	16.7	338	2	C98109	glycerol-3-phospha
397	5	16.7	338	2	E71872	hypothetical prote
398	5	16.7	339	2	D83201	probable glycosyl
399	5	16.7	341	2	D82852	biotin synthase (E
400	5	16.7	343	2	AG2075	iron(III) dicitrat
401	5	16.7	343	2	C75260	conserved hypotet
402	5	16.7	343	2	A57253	chaperone-like pro
403	5	16.7	343	2	T32232	hypothetical prote
404	5	16.7	344	1	S11776	hydrogenase (EC 1.
405	5	16.7	344	2	E83445	hypothetical prote
406	5	16.7	346	2	H70860	alcohol dehydrogen
407	5	16.7	346	2	UC1376	alcohol dehydrogen
408	5	16.7	346	2	G83127	conserved hypotet
409	5	16.7	347	2	T39550	probable quinone o
410	5	16.7	347	2	G86675	carotenoid biosynt
411	5	16.7	347	2	VQ2359	wheat aluminum ind
412	5	16.7	348	2	AB1496	polyol (sorbitol)
413	5	16.7	348	2	AC1138	polyol (sorbitol)
414	5	16.7	348	2	S23900	nitrogen regulatio
415	5	16.7	349	1	RGE6GL	nitrogen regulatio
416	5	16.7	349	1	QOBED5	HHRF5 protein - hu
417	5	16.7	349	2	SS3023	nitrogen regulatio
418	5	16.7	349	2	A24114	nitrogen regulatio
419	5	16.7	349	2	AB0950	Two-component syst
420	5	16.7	349	2	AH0003	Two-component regu
421	5	16.7	349	2	F86074	histidine protein
422	5	16.7	349	2	S12227	hypothetical prote
423	5	16.7	350	2	S76698	Chig protein (limpo
424	5	16.7	351	2	AG0758	v-type ATP synthas
425	5	16.7	352	2	G75487	genome polyprotein
426	5	16.7	355	2	S47219	probable sugar upt
427	5	16.7	355	2	E95990	3-dehydroquinatase
428	5	16.7	356	2	C97010	SMK1 protein - Pod
429	5	16.7	356	2	S39889	hypothetical prote
430	5	16.7	357	2	H71122	hypothetical prote
431	5	16.7	357	2	C89880	zinc metalloendope
432	5	16.7	357	2	B75578	conserved hypotet
433	5	16.7	357	2	C95960	hydrogenase (EC 1.
434	5	16.7	359	1	JG0805	hypothetical prote
435	5	16.7	359	2	D59111	hydrogenase (EC 1.
436	5	16.7	360	1	S11968	P3 protein - arabi
437	5	16.7	360	1	P3VVAM	1lipopolysaccharide
438	5	16.7	360	2	B72359	conserved hypotet
439	5	16.7	360	2	B87286	alcohol dehydrogen
440	5	16.7	362	2	D87125	3-dehydroquinatase
441	5	16.7	362	2	G64054	hydrogenase (EC 1.
442	5	16.7	363	1	HQ2JUS	cbid protein - Syn
443	5	16.7	364	1	S77360	probable membrane
444	5	16.7	366	2	S53898	iron (iii) abc tra
445	5	16.7	366	2	A75077	hypothetical prote
446	5	16.7	367	2	E69998	YopM protein - Yer
447	5	16.7	367	2	A33950	N-acetylmutamoyl-L
448	5	16.7	367	2	T12790	hypothetical prote
449	5	16.7	368	2	C72260	hypothetical prote
450	5	16.7	368	2	T22587	hypothetical prote
451	5	16.7	369	2	B71557	probable adenine g
452	5	16.7	369	2	T22708	hypothetical prote
453	5	16.7	370	2	D84846	hypothetical prote
454	5	16.7	370	2	C81120	probable RND efflu
455	5	16.7	371	2	S60903	hypothetical prote
456	5	16.7	371	2	T49908	3',5'-cyclic-nucle
457	5	16.7	372	1	G69553	AMP-dependent 26S
458	5	16.7	372	2	S51137	patA2 protein - Sy
459	5	16.7	372	2	S77549	breifeldin A estera
460	5	16.7	372	2	A53050	hypothetical prote
461	5	16.7	372	2	AB2061	glycosyltransferas
462	5	16.7	374	2	B98192	hypothetical prote
463	5	16.7	374	2	C86039	hypothetical prote
464	5	16.7	374	2	AC0972	lipopolysaccharide
465	5	16.7	374	2	B42595	glycosyltransferas
466	5	16.7	374	2	S38674	recombination prot
467	5	16.7	374	2	T35139	reca protein - Str
468	5	16.7	374	2	AH1903	hypothetical prote
469	5	16.7	375	2	S75182	glutamate 5'-kinase
470	5	16.7	375	2	B40205	Na+/H+-exchanging
471	5	16.7	376	2	TS1170	homocitrate synth
472	5	16.7	377	2	P96550	hypothetical prote
473	5	16.7	378	2	E82839	sugar transferase
474	5	16.7	379	2	C90987	probable polysacch
475	5	16.7	379	2	F85832	probable polysacch
476	5	16.7	379	2	AC0770	probable polysacch
477	5	16.7	379	2	E64972	probable polysacch
478	5	16.7	379	2	H64117	spermidine/putresc
479	5	16.7	380	2	T11381	ubiquinol-cytochro
480	5	16.7	381	2	A72601	hypothetical prote
481	5	16.7	381	2	AF0320	probable N-acetyl g
482	5	16.7	383	2	T08705	hypothetical prote
483	5	16.7	385	2	T18821	hypothetical prote
484	5	16.7	385	2	H97498	permease AGR C 211
485	5	16.7	385	2	AE2717	permease [imported
486	5	16.7	385	2	AH2200	Two-component hybr
487	5	16.7	388	2	TS0078	hypothetical prote
488	5	16.7	389	2	D82223	ribonucleoside-dip
489	5	16.7	389	2	A48966	methylase - lactoc
490	5	16.7	390	2	B40362	tryptophan synthas
491	5	16.7	390	2	SS2015	catechol O-methyl
492	5	16.7	393	2	A10319	probable 2-octapre
493	5	16.7	393	2	D75418	homocitrate synth
494	5	16.7	393	2	S67763	probable membrane
495	5	16.7	394	2	A56115	dual specificity p
496	5	16.7	395	2	A86166	protein F21B7.6 [i
497	5	16.7	395	2	T01392	leucine-rich repa
498	5	16.7	396	1	JH0631	cellular tumor ant
499	5	16.7	396	1	LPNUA4	apolipoprotein A-I
500	5	16.7	396	2	B75290	hypothetical prote
501	5	16.7	397	2	T00914	leucine-rich repa
502	5	16.7	398	2	S35264	cell division prot
503	5	16.7	398	2	D86700	hypothetical prote
504	5	16.7	403	2	T26326	hypothetical prote
505	5	16.7	404	2	G83122	hypothetical prote
506	5	16.7	406	2	T36196	probable acyl carr
507	5	16.7	409	2	T43599	yop targeted effec
508	5	16.7	411	2	S41548	translation elonga
509	5	16.7	411	2	S11961	hypothetical prote
510	5	16.7	412	1	OZ2QAF	circumsporozite p
511	5	16.7	412	2	I39554	phosphoglycerate k
512	5	16.7	412	2	T23385	hypothetical prote
513	5	16.7	413	2	I39551	phosphoglycerate k
514	5	16.7	413	2	T48635	hypothetical prote
515	5	16.7	414	2	S41609	atrolysin C (EC 3.
516	5	16.7	414	2	AE1249	competence--damage
517	5	16.7	415	2	A11611	hypothetical prote
518	5	16.7	415	2	S48253	hypothetical prote
519	5	16.7	416	1	JN0006	nerve growth facto
520	5	16.7	416	2	T23097	hypothetical prote
521	5	16.7	417	2	S58193	adenosylhomocyste
522	5	16.7	419	1	DEECNB	glycerol-3-phospha
523	5	16.7	419	2	G91019	hypothetical prote
524	5	16.7	419	2	A85864	hypothetical prote
525	5	16.7	419	2	AC0792	glycerol-3-phospha
526	5	16.7	420	2	H86715	o-succinylbenzoate
527	5	16.7	421	2	C96553	hypothetical prote
528	5	16.7	421	2	T47393	hypothetical prote
529	5	16.7	421	2	S66714	probable membrane
530	5	16.7	422	2	A99285	hypothetical prote
531	5	16.7	423	2	H75058	hypothetical prote
532	5	16.7	424	2	A54533	circumsporozite p
533	5	16.7	424	2	C83902	maltoase/maltodextr
534	5	16.7	424	2	F69723	trigger factor lig
535	5	16.7	425	1	A26431	nerve growth facto
536	5	16.7	425	1	KRXL2A	keratin, 64k type
537	5	16.7	425	1	AF2284	transcription term
538	5	16.7	426	2	B36467	hypothetical prote
539	5	16.7	427	1	T49031	acid phosphatase (
540	5	16.7	427	1	GOHUN	nerve growth facto

541	5	16.7	427	2	C86693	triglycer factor lim	614	5	16.7	460	2	T11309	NADH2 dehydrogenas
542	5	16.7	428	2	A61936	glutathyl tRNA redu	615	5	16.7	460	2	T110995	NADH2 dehydrogenas
543	5	16.7	428	2	B64301	probable phosphono	616	5	16.7	461	1	QXLL4M	NADH2 dehydrogenas
544	5	16.7	428	2	S17817	bacteriochlorophyll	617	5	16.7	462	2	S54572	probable seryl-tRN
545	5	16.7	429	2	AC1629	conserved GTP bind	618	5	16.7	463	2	B72500	probable seryl-tRN
546	5	16.7	429	2	A11266	conserved GTP bind	619	5	16.7	464	2	D85943	probable proteogly
547	5	16.7	429	2	T45040	hypothetical prote	620	5	16.7	465	2	T29696	hypothetical prote
548	5	16.7	431	2	E84031	triglycer factor (pr	621	5	16.7	465	2	H95369	BglC ENDO-1,3-1,4-
549	5	16.7	432	2	T06851	glutathyl-tRNA redu	622	5	16.7	466	2	T41375	probable phosphogl
550	5	16.7	432	2	G69977	two-component sens	623	5	16.7	466	2	C86739	hypothetical prote
551	5	16.7	433	2	S46668	MTM1 protein - Yea	624	5	16.7	467	2	B96979	spore germination
552	5	16.7	433	2	S74922	hypothetical prote	625	5	16.7	468	2	A54926	UDP-glucose 6-dehyd
553	5	16.7	434	2	H97028	xre family DNA-bin	626	5	16.7	468	2	T49117	glucosylase like p
554	5	16.7	435	2	AE1269	glutathyl-tRNA redu	627	5	16.7	468	2	A82763	UDP-N-acetylmuram
555	5	16.7	435	2	G70509	hypothetical prote	628	5	16.7	469	1	P2MLB	I2 protein - bovin
556	5	16.7	436	2	S69821	NDP-sugar dehydrog	629	5	16.7	469	2	D86309	hypothetical prote
557	5	16.7	436	2	T46107	hypothetical prote	630	5	16.7	469	2	B90110	spore germination
558	5	16.7	436	2	B84845	probable AP2 domai	631	5	16.7	471	2	A39024	TATA box-binding p
559	5	16.7	438	2	A72430	hypothetical prote	632	5	16.7	471	2	S76021	collagen alpha 3(I
560	5	16.7	439	2	D70958	hypothetical prote	633	5	16.7	472	2	T48074	probable trigger f
561	5	16.7	440	2	G71939	hypothetical prote	634	5	16.7	473	2	G72205	hypothetical prote
562	5	16.7	440	2	JC7807	Wiskott-Aldrich sy	635	5	16.7	473	2	T50920	hypothetical prote
563	5	16.7	441	2	C69834	sensory transducti	636	5	16.7	475	1	CZCICA	cellulase (EC 3.2.
564	5	16.7	442	2	T07038	probable lipoxigen	637	5	16.7	477	2	AC0122	Sodium/galactoside
565	5	16.7	442	2	C90224	s-adenosyl-L-homoc	638	5	16.7	477	2	T47753	hypothetical prote
566	5	16.7	442	2	G71930	probable transport	639	5	16.7	478	2	T110030	hypothetical prote
567	5	16.7	442	2	H91097	hypothetical prote	640	5	16.7	479	1	A32290	protein-tyrosine-p
568	5	16.7	442	2	H89770	hypothetical prote	641	5	16.7	480	2	S76206	hypothetical prote
569	5	16.7	443	2	T38239	transcription fact	642	5	16.7	481	2	B84700	probable flavonol
570	5	16.7	443	2	B95229	CBS domain protein	643	5	16.7	481	2	A46602	glutamate synthase
571	5	16.7	443	2	B84449	hypothetical prote	644	5	16.7	482	1	A46696	triacylglycerol 11
572	5	16.7	443	2	H98093	hemolysin (impor	645	5	16.7	482	1	D83024	probable secretion
573	5	16.7	444	1	S75761	cytochrome P450 -	646	5	16.7	482	2	H70463	glycine dehydrogen
574	5	16.7	445	1	S03827	diaminopimelate de	647	5	16.7	482	2	H84539	probable homedoma
575	5	16.7	445	2	T30604	hypothetical prote	648	5	16.7	482	2	T15829	hypothetical prote
576	5	16.7	447	2	B81519	UDP-N-acetylmuram	649	5	16.7	483	2	D71125	glutathyl-tRNA amid
577	5	16.7	447	2	F72021	muramoyl-dap ligas	650	5	16.7	483	2	S74637	lysine decarboxyla
578	5	16.7	447	2	A86603	muramoyl-DAP ligas	651	5	16.7	484	2	JU0091	sucrose alpha-gluc
579	5	16.7	447	2	S25817	hypothetical prote	652	5	16.7	484	2	G72395	alpha-L-arabinofur
580	5	16.7	448	2	C64437	probable urase -	653	5	16.7	485	2	F82718	Tldd protein XP112
581	5	16.7	448	2	A43304	phosphomannomutase	654	5	16.7	485	2	T25199	hypothetical prote
582	5	16.7	449	2	B83086	PmdA protein PA47	655	5	16.7	486	2	AC2424	hypothetical prote
583	5	16.7	449	2	B75451	NADH oxidase - Del	656	5	16.7	487	2	B84472	probable serine ca
584	5	16.7	449	2	C69079	probable phosphoma	657	5	16.7	487	2	S54265	glycoprotein gc -
585	5	16.7	449	2	B86763	hypothetical prote	658	5	16.7	487	2	H82298	D-alanyl-D-alanine
586	5	16.7	451	1	S49016	protein-tyrosine k	659	5	16.7	487	2	A11505	hypothetical cell
587	5	16.7	452	1	AJMSDS	adenylosuccinate s	660	5	16.7	488	2	T02257	nuclear antigen 21
588	5	16.7	452	2	T11082	coproporphyrinogen	661	5	16.7	488	2	T110675	hypothetical prote
589	5	16.7	452	2	A70389	L-seryl-tRNAsec se	662	5	16.7	489	2	D72523	hypothetical prote
590	5	16.7	454	2	H85293	hypothetical prote	663	5	16.7	489	2	B87518	magnesium transpor
591	5	16.7	455	2	B90619	NADH dehydrogenase	664	5	16.7	490	2	T26983	hypothetical prote
592	5	16.7	455	2	T05804	hypothetical prote	665	5	16.7	491	2	S74473	probable starch sy
593	5	16.7	455	2	G96708	hypothetical prote	666	5	16.7	491	2	B75554	hypothetical prote
594	5	16.7	458	2	T11528	NADH2 dehydrogenas	667	5	16.7	491	2	H89786	glucose-6-phosphat
595	5	16.7	458	2	T11176	NADH2 dehydrogenase	668	5	16.7	492	2	S71245	glucose-6-phosphat
596	5	16.7	458	2	B90615	NADH dehydrogenase	669	5	16.7	492	2	F84602	hypothetical prote
597	5	16.7	458	2	B90617	NADH dehydrogenase	670	5	16.7	492	2	C83592	hypothetical prote
598	5	16.7	458	2	B90625	NADH dehydrogenase	671	5	16.7	494	2	JR0353	uridine diphosphog
599	5	16.7	458	2	B99613	NADH dehydrogenase	672	5	16.7	497	2	G86299	F309.24 protein -
600	5	16.7	458	2	F81904	UDP-N-acetylmurama	673	5	16.7	497	2	G811284	probable Ni/Fe-hyd
601	5	16.7	458	2	B81112	major facilitator	674	5	16.7	498	2	T09021	beta-glucosidase h
602	5	16.7	459	1	B75413	NADH2 dehydrogenas	675	5	16.7	499	2	E86182	hypothetical prote
603	5	16.7	459	1	OXMS4M	NADH2 dehydrogenas	676	5	16.7	505	2	B90181	Na+/H+ antiporter
604	5	16.7	459	2	T11463	NADH2 dehydrogenas	677	5	16.7	507	2	B42249	serine-type carbox
605	5	16.7	459	2	T11084	NADH2 dehydrogenas	678	5	16.7	508	2	S54264	glycoprotein gc -
606	5	16.7	459	2	T11398	NADH2 dehydrogenas	679	5	16.7	508	2	G84564	probable sugar tra
607	5	16.7	459	2	T11489	NADH2 dehydrogenas	680	5	16.7	509	2	A57512	beta-glucosidase B
608	5	16.7	459	2	T11450	NADH2 dehydrogenas	681	5	16.7	509	2	T32201	hypothetical prote
609	5	16.7	459	2	S10196	NADH2 dehydrogenas	682	5	16.7	510	2	F86392	TikT.7 protein - A
610	5	16.7	459	2	S04756	NADH2 dehydrogenas	683	5	16.7	510	2	P90367	N-methyl hydantoin
611	5	16.7	460	2	T11773	NADH2 dehydrogenas	684	5	16.7	510	2	A12012	hypothetical prote
612	5	16.7	460	2	T11296	NADH2 dehydrogenas	685	5	16.7	511	1	S54720	glucose-6-phosphat
613	5	16.7	460	2	T11543	NADH2 dehydrogenas	686	5	16.7	511	2	B82941	ATP synthase alpha

687	5	16.7	511	2	E84685	probable seed stor
688	5	16.7	513	2	S21535	nitrate reductase
689	5	16.7	513	2	JC5920	potassium channel
690	5	16.7	513	2	G68897	hypothetical prote
691	5	16.7	513	2	E72741	hypothetical prote
692	5	16.7	514	2	AG0474	threonine ammonia-
693	5	16.7	515	1	O4H04	cytochrome P450 1A
694	5	16.7	517	1	S28229	diacylglycerol kin
695	5	16.7	520	2	E93034	conserved hypotet
696	5	16.7	520	2	B97257	lyam domain contai
697	5	16.7	521	1	VC8EHB	glycoprotein gIII
698	5	16.7	521	2	DB3399	probable ATP-bind
699	5	16.7	521	2	T21440	hypothetical prote
700	5	16.7	523	2	S47053	hypothetical prote
701	5	16.7	525	2	H70982	probable fadD pro
702	5	16.7	525	2	T32481	hypothetical prote
703	5	16.7	525	2	T12685	hypothetical prote
704	5	16.7	527	2	S39549	thioglucoisidase (E
705	5	16.7	527	2	G86390	TIK7.22 protein -
706	5	16.7	528	2	B64760	propionate catabol
707	5	16.7	528	2	C85527	regulator for prp
708	5	16.7	528	2	H90676	regulator for prp
709	5	16.7	528	2	S32593	[RNA-polymerase]-s
710	5	16.7	528	2	T33464	hypothetical prote
711	5	16.7	530	2	B86326	T29M8.12 protein -
712	5	16.7	531	1	A39740	sterol 27-monooxyg
713	5	16.7	531	2	T43551	multidrug resistan
714	5	16.7	532	2	A35149	lph protein - Shi
715	5	16.7	532	2	T05281	probable homeobox
716	5	16.7	532	2	AE1964	Dnak-type molecula
717	5	16.7	533	1	T40011	hypothetical prote
718	5	16.7	535	1	A33813	sterol 26-monooxyg
719	5	16.7	535	2	F70914	probable acid-COA
720	5	16.7	535	2	C96706	probable amp-bind
721	5	16.7	535	2	C86772	conserved hypotet
722	5	16.7	535	2	AE2710	MFS permease [impo
723	5	16.7	535	2	AD2107	serine/threonine k
724	5	16.7	536	2	S56654	thioglucoisidase (E
725	5	16.7	537	2	S25181	heat shock protein
726	5	16.7	538	2	S62566	PHF finger protein
727	5	16.7	539	2	T51215	hypothetical prote
728	5	16.7	540	2	B96747	probable alanine a
729	5	16.7	540	2	B83121	probable AMP-bind
730	5	16.7	541	2	S56653	thioglucoisidase (E
731	5	16.7	541	2	AF0547	propionate catabol
732	5	16.7	541	2	H83445	probable chemotaxi
733	5	16.7	543	2	S46713	ATP-dependent RNA
734	5	16.7	544	2	S41094	triacylglycerol 1i
735	5	16.7	544	2	S41095	triacylglycerol 1i
736	5	16.7	544	2	S41096	triacylglycerol 1i
737	5	16.7	544	2	S19149	thioglucoisidase (E
738	5	16.7	545	2	T02279	hypothetical prote
739	5	16.7	545	2	A87136	hypothetical prote
740	5	16.7	546	1	S71008	propionyl-CoA carb
741	5	16.7	546	2	G86221	protein F7G19.14
742	5	16.7	546	2	C69450	anthranilate synh
743	5	16.7	547	2	S56656	thioglucoisidase (E
744	5	16.7	548	2	S26149	thioglucoisidase (E
745	5	16.7	548	2	C82698	electon transfer
746	5	16.7	550	2	S55118	probable membrane
747	5	16.7	551	2	F75045	dihydroxy-acid deh
748	5	16.7	551	2	H96682	hypothetical prote
749	5	16.7	553	2	C71257	phenylalanine-trna
750	5	16.7	553	2	S70817	invasion genes tra
751	5	16.7	553	2	AH0849	invasion protein r
752	5	16.7	555	2	B72486	probable hydanotin
753	5	16.7	558	2	A43667	serine C-palmitoyl
754	5	16.7	559	2	T22179	hypothetical prote
755	5	16.7	559	2	P96912	adenylylulafate re
756	5	16.7	561	1	S52319	unspecific monooxy
757	5	16.7	561	2	C64459	dihydroxy-acid den
758	5	16.7	562	2	S55516	glucan 1,3-beta-gl
759	5	16.7	562	2	S38149	SIS2 protein - yea
760	5	16.7	563	1	FN0493	triacylglycerol 1i
761	5	16.7	563	2	B70918	hypothetical prote
762	5	16.7	565	2	AF1325	alpha-acetolactate
763	5	16.7	565	2	H72253	DNA primase - Ther
764	5	16.7	565	2	T47230	hypothetical prote
765	5	16.7	565	2	S27495	nodu protein - Bra
766	5	16.7	570	2	E97155	DNA repair protein
767	5	16.7	570	2	S24459	hypothetical prote
768	5	16.7	572	2	T51575	2-hydroxyphenanoyl
769	5	16.7	572	2	H96685	probable AMP-bind
770	5	16.7	573	2	T01317	probable pectinest
771	5	16.7	573	2	B97331	membrane associate
772	5	16.7	575	2	AG2566	hypothetical prote
773	5	16.7	577	2	T47838	beta-glucosidase-1
774	5	16.7	577	2	T02401	probable beta-gluc
775	5	16.7	577	2	T41727	F-box domain prote
776	5	16.7	580	2	T43732	Crp synthase (EC 6
777	5	16.7	580	2	A96683	hypothetical prote
778	5	16.7	580	2	B84552	similar to Mlo pro
779	5	16.7	582	2	A55174	kinase-associated
780	5	16.7	582	2	I50224	erythroid cell tra
781	5	16.7	583	2	E70762	probable ftda prot
782	5	16.7	583	2	B85063	hypothetical prote
783	5	16.7	583	2	F97492	probable transport
784	5	16.7	586	2	H86914	conserved hypotet
785	5	16.7	588	2	I37202	B-CAM protein - hu
786	5	16.7	593	2	D97806	penicillin-binding
787	5	16.7	594	2	C71661	penicillin-binding
788	5	16.7	597	2	T45676	hypothetical prote
789	5	16.7	599	2	S18735	centromere protein
790	5	16.7	600	2	E86854	hypothetical prote
791	5	16.7	601	2	T18787	hypothetical prote
792	5	16.7	602	2	C82581	GTP binding protei
793	5	16.7	606	2	T40556	hypothetical prote
794	5	16.7	606	2	T31557	hypothetical prote
795	5	16.7	606	2	S70358	centromere protein
796	5	16.7	607	2	T20796	hypothetical prote
797	5	16.7	609	2	T40660	hypothetical C2H2-
798	5	16.7	611	2	T41563	hypothetical prote
799	5	16.7	611	2	T03890	hypothetical prote
800	5	16.7	611	2	C84863	hypothetical prote
801	5	16.7	613	2	S15468	complement C3b/C4b
802	5	16.7	613	2	S75976	hypothetical prote
803	5	16.7	614	2	T20795	hypothetical prote
804	5	16.7	614	2	T47749	hypothetical prote
805	5	16.7	616	2	B84500	probable retroelem
806	5	16.7	617	2	T02121	hypothetical prote
807	5	16.7	617	2	G82706	conserved hypotet
808	5	16.7	619	2	F82984	hypothetical prote
809	5	16.7	621	2	A75101	aldelyde-ferredoxi
810	5	16.7	624	2	T04414	probable glucan 1,
811	5	16.7	625	2	G71072	aldelyde-ferredoxi
812	5	16.7	626	2	B97358	glucose-inhibited
813	5	16.7	627	1	S40048	1,4-alpha-glucan b
814	5	16.7	627	2	T02846	dynein light chain
815	5	16.7	627	2	G84558	probable SEC1 fami
816	5	16.7	628	2	I38000	lutheran blood gro
817	5	16.7	629	2	C82598	glucose inhibited
818	5	16.7	634	2	C70133	conserved hypotet
819	5	16.7	636	2	H96666	probable phytochro
820	5	16.7	638	2	T47569	hypothetical prote
821	5	16.7	640	2	S47865	regulatory protein
822	5	16.7	642	2	C81345	hypothetical prote
823	5	16.7	645	2	S49570	penicillin-binding
824	5	16.7	645	2	C81315	membrane bound zin
825	5	16.7	645	2	T05251	probable disease x
826	5	16.7	647	2	F90595	conserved hypotet
827	5	16.7	648	2	JC4674	Slp1 protein - rat
828	5	16.7	649	2	A33589	mismatch repair pr
829	5	16.7	649	2	A95020	DNA mismatch repai
830	5	16.7	649	2	H97891	DNA mismatch repai
831	5	16.7	654	2	T21618	hypothetical prote
832	5	16.7	655	1	S50096	probable splicing

833	5	16.7	663	2	T30621	hypothetical prote
834	5	16.7	664	2	T35122	probable ATP-depen
835	5	16.7	665	2	D96621	auxin response fac
836	5	16.7	667	2	T33526	hypothetical prote
837	5	16.7	668	2	S64123	hypothetical prote
838	5	16.7	671	2	B75607	conserved hypothet
839	5	16.7	672	2	G88651	protein B0212.3 [l
840	5	16.7	678	2	T42668	hypothetical prote
841	5	16.7	679	2	S48939	hypothetical prote
842	5	16.7	684	2	G70744	hypothetical prote
843	5	16.7	685	2	S64985	hypothetical prote
844	5	16.7	688	2	S34491	hypothetical prote
845	5	16.7	688	2	S32961	protochlorophyllid
846	5	16.7	690	2	A12516	hypothetical prote
847	5	16.7	698	2	C69208	DNA helicase relat
848	5	16.7	691	2	T25519	hypothetical prote
849	5	16.7	695	2	H86900	DNA mismatch repai
850	5	16.7	697	2	T49727	related to long-ch
851	5	16.7	698	2	C84836	hypothetical prote
852	5	16.7	699	2	G86311	hypothetical prote
853	5	16.7	702	2	D86469	protein F12K21.12
854	5	16.7	705	2	S45769	probable membrane
855	5	16.7	714	2	T25744	hypothetical prote
856	5	16.7	715	2	H90977	hypothetical prote
857	5	16.7	715	2	B75135	DNA helicase relat
858	5	16.7	716	2	AG2446	single-stranded-DN
859	5	16.7	719	2	F85824	hypothetical prote
860	5	16.7	720	2	T43854	helicase (imported
861	5	16.7	721	2	C82939	virulence associat
862	5	16.7	723	2	G84507	hypothetical prote
863	5	16.7	725	2	T52158	hypothetical prote
864	5	16.7	728	2	A75582	serine proteinase,
865	5	16.7	728	2	S57142	hypothetical prote
866	5	16.7	731	2	D71332	probable DNA topoi
867	5	16.7	738	2	E86294	hypothetical prote
868	5	16.7	740	2	D97180	relA/SpoT protein,
869	5	16.7	741	2	T05250	probable disease r
870	5	16.7	743	2	T02147	hypothetical prote
871	5	16.7	746	2	AD1622	probable integral
872	5	16.7	749	2	H82691	topoisomerase IV s
873	5	16.7	754	1	PIV50	RNA-directed RNA p
874	5	16.7	755	2	T20950	hypothetical prote
875	5	16.7	756	2	T00367	hypothetical prote
876	5	16.7	761	1	B64506	DNA topoisomerase
877	5	16.7	762	2	T00410	protein kinase hom
878	5	16.7	765	2	S38039	hypothetical prote
879	5	16.7	766	2	T48389	cucumisin-like pro
880	5	16.7	767	2	S63182	hypothetical prote
881	5	16.7	768	1	A34106	protein kinase (EC
882	5	16.7	768	2	G82251	cation transport A
883	5	16.7	768	2	T17462	disease resistance
884	5	16.7	769	2	S50966	probable membrane
885	5	16.7	772	2	C69980	transcription regu
886	5	16.7	772	2	B82888	phenylalanine-ENA
887	5	16.7	774	2	D83208	probable ferredoxi
888	5	16.7	774	2	S25284	protein kinase nek
889	5	16.7	779	2	E71825	probable type III
890	5	16.7	780	2	AB1801	amino-terminal dom
891	5	16.7	780	2	AC1427	transcription regu
892	5	16.7	781	2	A56244	DNA repair/recomb
893	5	16.7	782	2	T32155	hypothetical prote
894	5	16.7	785	2	S46672	hypothetical prote
895	5	16.7	788	1	QOBER3	HLH1 protein - hu
896	5	16.7	788	2	H96545	hypothetical prote
897	5	16.7	790	2	S61587	transcription acti
898	5	16.7	790	2	D86528	omp85 analog (impo
899	5	16.7	791	2	D72094	omp85 analog - Chl
900	5	16.7	792	2	A46140	diacylglycerol kin
901	5	16.7	792	2	T22717	hypothetical prote
902	5	16.7	795	2	T48252	ecceiferum3 (CER3)
903	5	16.7	795	2	AF2444	hypothetical prote
904	5	16.7	796	2	B46140	diacylglycerol kin
905	5	16.7	796	2	JC7355	peroxisome prolife
906	5	16.7	802	2	T32448	hypothetical prote
907	5	16.7	803	2	S45582	siderophore biosyn
908	5	16.7	809	2	T16448	hypothetical prote
909	5	16.7	811	2	T17863	vitellogenin II ho
910	5	16.7	813	2	G75331	ATP-dependent prot
911	5	16.7	815	2	T76775	09 mannan biosynth
912	5	16.7	815	2	AB2444	hypothetical prote
913	5	16.7	816	2	B95093	hypothetical prote
914	5	16.7	816	2	C88196	protein ZK1127.7 [
915	5	16.7	816	2	G97960	ATP-dependent DNA
916	5	16.7	818	2	F97772	hypothetical prote
917	5	16.7	818	2	T15380	hypothetical prote
918	5	16.7	819	2	B47057	aspartate kinase (
919	5	16.7	821	2	S67087	hypothetical prote
920	5	16.7	829	2	S75776	pled protein - Syn
921	5	16.7	830	1	RNEGB2	DNA-directed RNA p
922	5	16.7	831	2	B40204	Na+/H+-exchanging
923	5	16.7	832	2	A40205	Na+/H+-exchanging
924	5	16.7	833	1	A31593	heat shock transcr
925	5	16.7	835	2	E71691	outer membrane ass
926	5	16.7	835	2	T05259	probable disease r
927	5	16.7	836	1	QOVZRA	mRNA guanylyltrans
928	5	16.7	838	2	A32262	fatty-acid synthas
929	5	16.7	839	2	H97758	outer membrane ass
930	5	16.7	840	2	H89911	oxacillin resistanc
931	5	16.7	840	2	S48975	hypothetical prote
932	5	16.7	843	2	F96537	hypothetical prote
933	5	16.7	846	1	QOBER3	HORF1 protein - hu
934	5	16.7	849	2	T14519	probable S-recepto
935	5	16.7	850	2	AB1954	hypothetical prote
936	5	16.7	851	2	S33985	env polypeptid -
937	5	16.7	854	2	S13288	env polypeptid - huma
938	5	16.7	856	1	VCLJVL	env polypeptid pr
939	5	16.7	856	1	VCLJVL	env polypeptid pr
940	5	16.7	856	2	C85023	hypothetical prote
941	5	16.7	859	2	F69159	protoporphyrin IX
942	5	16.7	860	2	C86203	hypothetical prote
943	5	16.7	861	1	VCLJLV	env polypeptid pr
944	5	16.7	861	2	H64102	leucine-ENA ligas
945	5	16.7	863	2	G96964	probable permease,
946	5	16.7	864	2	T08575	protein kinase hom
947	5	16.7	864	2	H85335	hypothetical prote
948	5	16.7	864	2	T04518	hypothetical prote
949	5	16.7	867	2	T27136	hypothetical prote
950	5	16.7	867	2	T14777	hypothetical prote
951	5	16.7	870	2	G81348	valine-cRNA ligase
952	5	16.7	870	2	E71698	hypothetical prote
953	5	16.7	871	2	T27135	hypothetical prote
954	5	16.7	873	2	F86426	95.1K hypothetical
955	5	16.7	874	2	AC2287	hypothetical prote-
956	5	16.7	877	2	T43449	hypothetical prote
957	5	16.7	878	2	B84977	alanine-cRNA ligas
958	5	16.7	879	2	S49910	chloroplast outer
959	5	16.7	882	2	E96931	hypothetical prote
960	5	16.7	889	2	H96606	hypothetical prote
961	5	16.7	892	2	J00424	probable transposa
962	5	16.7	892	2	T01899	disease resistance
963	5	16.7	895	1	EXCKP	H+-exporting ATPas
964	5	16.7	895	2	B96775	hypothetical prote
965	5	16.7	896	2	T07408	lipoxigenase (EC 1
966	5	16.7	896	2	J02391	lipoxigenase (EC 1
967	5	16.7	898	2	T21179	hypothetical prote
968	5	16.7	899	2	T07062	probable lipoxigen
969	5	16.7	900	2	C71339	probable DNA misma
970	5	16.7	904	2	C70559	probable po1a prot
971	5	16.7	905	2	T39572	probable proteinas
972	5	16.7	908	2	A83424	asacetylatory nitra
973	5	16.7	910	2	B83451	aconitate hydratase
974	5	16.7	910	2	F81974	leucine-cRNA ligas
975	5	16.7	911	2	S77659	DNA-directed DNA p
976	5	16.7	911	2	A39967	inter-alpha-trypsi
977	5	16.7	917	2	T04661	hypothetical prote
978	5	16.7	918	2	AB2445	hypothetical prote

	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000
	5	16.7	5	16.7	5	16.7	5	16.7	5	16.7	5	16.7	5	16.7	5	16.7	5	16.7	5	16.7	5	16.7
	920	924	925	925	928	928	928	930	932	932	936	942	942	943	944	947	950	951	951	951	951	956
	2	2	2	2	1	1	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
	T41050	T25007	JC2033	T16235	S38001	AC1312	AC1684	AC2412	T25008	T659045	T06190	T33032	G83038	T24707	AG9624	H85088	BE4135	STECVT	C91283	E86124	AC1061	B71468
	conserved hypothet	hypothetical prote	G protein-coupled	hypothetical prote	probable serine/tn	ATP-dependent heli	ATP-dependent heli	preprotein translo	hypothetical prote	hypothetical prote	lipoxigenase (EC 1	hypothetical prote	probable sensor/re	hypothetical prote	protein F21A10.2 (hypothetical prote	oxoglutarate dehyd	valine-tRNA ligase	valine tRNA synthe	valine tRNA synthe	valine-tRNA ligase	probable insulinas

ALIGNMENTS

RESULT 1
DSBYN
superoxide dismutase (EC 1.15.1.1) (Mn) precursor [validated] - Yeast (Saccharomyces cer
N;Alternate names: protein YHR008C
C;Species: Saccharomyces cerevisiae
C;Date: 19-Feb-1994 #sequence revision 17-Mar-1997 #text_change 23-Mar-2001
C;Accession: A00521; S46785; A90766
R;Marrez, C.A.M.; Van Loon, A.P.G.M.; Oudhoorn, P.; Van Steeg, H.; Grivell, L.A.; Slate
Eur. J. Biochem. 147, 153-161, 1985
A;Title: Nucleotide sequence analysis of the nuclear gene coding for manganese superoxid
A;Reference number: A91141; MUID:85127011; PMID:3882422
A;Accession: A00521
A;Molecule type: DNA
A;Residues: 1-233 <MMR>
A;Cross-references: EMBL:X02156; NID:G4513; PIDN:CAA26092.1; PID:G4514
R;Du, Z.
Submitted to the EMBL Data Library, June 1994
A;Description: The sequence of S. cerevisiae cosmid L2825.
A;Reference number: S46774
A;Accession: S46785
A;Molecule type: DNA
A;Residues: 1-233 <DUZ>
A;Cross-references: EMBL:U10400; NID:G500701; PIDN:AAB68939.1; PID:G500704; GSPDB:GN0000
K;Dilow, C.; Johansen, J.T.; Martin, B.M.; Svendsen, I.
Carlsberg Res. Commun. 47, 81-91, 1982
A;Title: The complete amino acid sequence of manganese-superoxide dismutase from Sacchar
A;Reference number: A90766
A;Accession: A90766
A;Molecule type: Protein
A;Residues: 27-229 <DT>
C;Genetics:
A;Gene: SCD:SOD2; MIPS:YHR008C
A;Cross-references: SGD:S0001050; MIPS:YHR008C
A;Map position: 8R
A;Genome: nuclear
A;Complex: homotrimer
C;Function:
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: homotrimer; manganese; metalloprotein; mitochondrial matrix; mitochondrion
F;1-26/Domin: trnasit peptide (mitochondrion) #status predicted <TMP>
F;27-229/Product: superoxide dismutase (Mn) #status experimental <MNT>
F;52,107,194,198/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 33.3%; Score 10; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.002;

	Matches	10;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	15	EPYISQINE	24							
Db	41	EPYISQINE	50							

RESULT 2
superoxide dismutase (EC 1.15.1.1) (Mn) - Nocardia asteroides
C;Species: Nocardia asteroides
C;Date: 22-Dec-1995 #sequence revision 08-Feb-1996 #text_change 05-May-2000
C;Accession: J04351
R;Alcendor, D.J.; Chapman, G.D.; Beaman, B.L.
Gene 164, 143-147, 1995
A;Title: Isolation, sequencing and expression of the superoxide dismutase-encoding gene
A;Reference number: J04351; MUID:96060854; PMID:7550304
A;Accession: J04351
A;Molecule type: DNA
A;Residues: 1-207 <ALC>
A;Cross-references: GB:U02341
A;Experimental source: GUN-2
A;Note: The authors translated the initiation codon GTG for residue 1 as Val
C;Genetics:
A;Gene: sod
A;Start codon: GTG
C;Function:
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase; virulence factor
F;28,76,160,164/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 23.3%; Score 7; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

	Oy	18	ISQINE	24
Db	20 <td>ISQINE</td> <td>26</td> <td></td>	ISQINE	26	

RESULT 3
superoxide dismutase (EC 1.15.1.1) (Fe) [validated] - Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 21-Nov-1993 #sequence revision 26-May-1995 #text_change 20-Jun-2000
C;Accession: S15205; C70654; S10908
R;Zhang, Y.; Lathigra, R.; Garbe, T.; Catty, D.; Young, D.
Mol. Microbiol. 5, 381-391, 1991
A;Title: Genetic analysis of superoxide dismutase, the 23 kilodalton antigen of Mycobac
A;Reference number: S15205; MUID:91251768; PMID:1904126
A;Accession: S15205
A;Molecule type: DNA
A;Residues: 1-207 <ZHA>
A;Cross-references: EMBL:X52861; NID:G794079; PIDN:CAA37042.1; PID:G581379
A;Experimental source: strain H37Rv
A;Note: the authors translated the codon GAA for residue 3 as Gin
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70654
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-207 <COL>
A;Cross-references: GB:Z83864; GB:AL123456; NID:G3261687; PIDN:CAB06220.1; PID:G1781110
A;Experimental source: strain H37Rv
R;Cooper, U.B.; McInyre, K.; Wood, S.P.; Zhang, Y.; Young, D.
submitted to the Brookhaven Protein Data Bank, September 1994
A;Reference number: A52807; PDB:1IDS

A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 2-199
 R;Cooper, J.B.; Driessen, H.P.C.; Wood, S.P.; Zhang, Y.; Young, D.
 J. Mol. Biol. 235, 1156-1158, 1994
 A;Title: Crystallisation and preliminary X-ray analysis of the iron-dependent superoxide
 A;Reference number: A59029; MUID:94118350; PMID:8289318
 A;Contents: annotation; X-ray crystallography
 C;Genetics:
 A;Gene: socA
 A;Start codon: GTG
 C;Function:
 A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C;Superfamily: superoxide dismutase (Mn)
 C;Keywords: iron; metalloprotein; oxidoreductase; tetramer
 F;28,76,160,164/Binding site: iron (His, His, Asp, His) #status experimental

Query Match 23.3%; Score 7; DB 2; Length 207;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

18 ISGQINE 24
 |||||
 20 ISGQINE 26

RESULT 4
 S60669
 superoxide dismutase (EC 1.15.1.1) (Mn) - Mycobacterium fortuitum
 C;Species: Mycobacterium fortuitum
 C;Date: 19-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
 C;Accession: S60669
 R;Kendrick, C.; Domenech, P.; Prieto, J.; Garcia, M.J.
 submitted to the EMBL Data Library, August 1995
 A;Description: Cloning and expression of the superoxide dismutase gene of Mycobacterium
 A;Reference number: S60669
 A;Accession: S60669
 A;Molecule type: DNA
 A;Residues: 1-207 <MEN>
 A;Cross-references: EMBL:X70914; NID:9550078; PIDN:CAM50266.1; PID:9550079
 A;Experimental source: ATCC 6841
 C;Genetics:
 A;Gene: sod
 A;Start codon: GTG
 C;Function:
 A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C;Superfamily: superoxide dismutase (Mn)
 C;Keywords: manganese; metalloprotein; oxidoreductase
 F;28,76,160,164/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 23.3%; Score 7; DB 2; Length 207;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 ISGQINE 24
 |||||
 DB 20 ISGQINE 26

RESULT 5
 T03296
 beta-glucosidase (EC 3.2.1.21), chloroplast - rice
 N;Alternate names: beta-D-glucoside glucosylhydrolase
 C;Species: Oryza sativa (rice)
 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
 C;Accession: T03296
 R;Ben, A.
 submitted to the EMBL Data Library, May 1995
 A;Reference number: Z14892
 A;Accession: T03296
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-328 <ESE>
 A;Cross-references: EMBL:U028047; NID:9143863; PID:9143864
 C;Genetics:

A;Genome: nuclear
 C;Function:
 A;Description: catalyzes the release of either gibberellin or cyanogenic substances from
 C;Keywords: chloroplast; glucosidase; hydrolase

Query Match 23.3%; Score 7; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SATPEYI 18
 |||||
 DB 56 SATPEYI 62

RESULT 6
 B69959
 glycine dehydrogenase homolog yghK - Bacillus subtilis
 C;Species: Bacillus subtilis
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 C;Accession: B69959
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
 C.; Bron, S.; Brouillet, S.; Brunsch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A;Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
 lech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hullo, M.F
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
 Y.; Authors: lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 A.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli
 Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
 A;Authors: Schleich, S.; Schreiber, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Serc
 akenchi, M.; Yamashiro, A.; Tanaka, T.; Terstara, P.; Tognoni, A.; Tosato, V.; Uchiyama
 T.; Wintner, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
 A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A;Reference number: A69580; MUID:98044033; PMID:9384377
 A;Accession: B69959
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-488 <KUN>
 A;Cross-references: GB:Z99116; GB:AL009126; NID:92634723; PIDN:CAM14386.1; PID:92634889
 A;Experimental source: strain 168
 C;Genetics:
 A;Gene: yghK

Query Match 23.3%; Score 7; DB 2; Length 488;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLPELD 8
 |||||
 DB 20 YSLPELD 26

RESULT 7
 T10791
 beta-glucosidase (EC 3.2.1.21) - cassava
 N;Alternate names: linamarase
 C;Species: Manihot esculenta (cassava)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C;Accession: T10791
 R;McMahon, J.M.; Sayre, R.T.
 submitted to the EMBL Data Library, March 1997
 A;Description: Genomic sequence for a linamarase gene from cassava (Manihot esculenta C
 A;Reference number: Z17147
 A;Accession: T10791
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-507 <MCM>
 A;Cross-references: EMBL:U05298; NID:92443453; PID:92443454
 A;Experimental source: strain MTail
 C;Genetics:
 A;Insertions: 27/2; 48/1; 67/3; 93/1; 119/1; 149/3; 233/3; 273/2; 344/3; 356/3; 391/1; 427

A/Note: PLIN-GEN
C/Function:
A/Description: responsible for hydrolysis of two structurally related cyanoglucosides (1
C/Superfamily: Agrobacterium beta-glucosidase
C/Keywords: glucosidase; hydrolase

Query Match 23.3%; Score 7; DB 2; Length 507;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SATEPYI 18
DB 206 SATEPYI 212

RESULT 8
S23940
beta-glucosidase (EC 3.2.1.21) - cassava
N/Alternate names: linamarase
C/Species: Manihot esculenta (cassava)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
Accession: S23940; S51196
R/Hughes, M.A.; Brown, K.; Pancoro, A.; Murray, B.S.; Oxtoby, E.; Hughes, J.
Arch. Biochem. Biophys. 295, 273-279, 1992
A/Title: A molecular and biochemical analysis of the structure of the cyanogenic beta-gl
A/Reference number: S23940; MUID:92264724; PMID:1586156
A/Accession: S23940
A/Molecule type: mRNA
A/Residues: 1-531 <HUG>
A/Cross-references: GB:S51175; NID:G249261; PID:AMB22162.1; PID:G249262
A/Experimental source: seed
R/Kereszteszy, Z.; Kiss, L.; Hughes, M.A.
Arch. Biochem. Biophys. 315, 323-330, 1994
A/Title: Investigation of the active site of the cyanogenic beta-D-glucosidase (linamar
with acid catalytic function.
A/Reference number: S51196; MUID:95077406; PMID:7986074
A/Accession: S51196
A/Molecule type: Protein
A/Residues: 128-215 <KER>
C/Function:
A/Description: responsible for hydrolysis of two structurally related cyanoglucosides (1
C/Superfamily: Agrobacterium beta-glucosidase
C/Keywords: glycoprotein; glycosidase; hydrolase
F/198/Active site: Glu #status experimental
F/366,398,421,489,506/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 23.3%; Score 7; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SATEPYI 18
DB 230 SATEPYI 236

RESULT 9
S76134
hypothetical protein - Synecocystis sp. (strain PCC 6803)
C/Species: Synecocystis sp.
A/Variety: PCC 6803
C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
Accession: S76134
R/Kaneko, T.; Saito, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Matanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-116, 1996
A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
8.
A/Reference number: S74332; MUID:97061201; PMID:8905231
A/Accession: S76134
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1034 <KAN>
A/Cross-references: EMBL:D90914; GB:AB001339; NID:G1653477; PID:BAA18393.1; PID:G165348

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C/Superfamily: phosphoenolpyruvate carboxylase

Query Match 23.3%; Score 7; DB 2; Length 1034;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYSLPEL 7
DB 754 KYSLPEL 760

RESULT 10
T31617
hypothetical protein Y50B8A.m - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
Accession: T31617
R/Steward, C.
submitted to the EMBL Data Library, September 1999
A/Accession: T31617
A/Reference number: Z21047
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2055 <MIL>
A/Cross-references: EMBL:AL117200; NID:e1549770; PID:CA855056.1; CESP:Y50B8A.m
A/Experimental source: clone Y50B8A
C/Genetics:
A/Gene: CESP:Y50B8A.m
A/Introns: 273/3; 447/1; 526/1; 735/1; 1247/1; 1418/1; 1494/1; 1753/3

Query Match 23.3%; Score 7; DB 2; Length 2055;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PELDYEF 11
DB 1780 PELDYEF 1786

RESULT 11
AH1065
hypothetical protein STY4854 [imported] - Salmonella enterica subsp. enterica serovar T
C/Species: Salmonella enterica subsp. enterica serovar Typh
A/Note: this species has also been called Salmonella typh
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
Accession: AH1065
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
Ch, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skellon, J.; Stevens, K.
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A/Reference number: AB0502; PMID:11677608
Accession: AH1065
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <PAR>
A/Cross-references: GB:AL513382; PID:CAD06573.1; PID:G1505614; GSPDB:GN00176
C/Genetics:
A/Gene: STY4854

Query Match 20.0%; Score 6; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 YISQOI 22
DB 79 YISQOI 84

RESULT 12
JC4396

superoxide dismutase (EC 1.15.1.1) (Fe/Mn) [validated] - *Propionibacterium freudenreichii*
C/Species: *Propionibacterium freudenreichii* subsp. *shermanii*
C/Date: 20-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 20-Apr-2000
A/Accession: J04396; S41106
R/Gibbs: 100%; R/Batistoni, A.; Polizio, F.; Carri, M.T.; De Martino, A.; Meier, B.;
Biochem. Biophys. Res. Commun. 216, 841-847, 1995
A/Title: Metal uptake of recombinant catalytic superoxide dismutase from *Propionibacterium*
A/Reference number: J04396; MUID:96074560; PMID:7488202
A/Accession: J04396
A/Molecule type: DNA
A/Residues: 1-202 <GB>
A/Cross-references: EMBL:X01650
A/Experimental source: PZ3
R/Meier, B.; Sehn, A.P.; Schinina, M.E.; Barra, D.
Eur. J. Biochem. 219, 463-468, 1994
A/Title: In vivo incorporation of copper into the iron-exchangeable and manganese-exchangeable sites.
A/Reference number: S41106; MUID:94139724; PMID:8307013
A/Accession: S41106
A/Molecule type: protein
A/Residues: 2-202 <MEI>
A/Experimental source: strain PZ3
C/Genetics:
A/Gene: *sod*
A/Complex: homotetramer
C/Function:
A/Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
A/Note: can use iron or manganese as cofactor
C/Superfamily: superoxide dismutase (Mn)
C/Keywords: homocitrate; iron; manganese; metalloprotein; oxidoreductase
F/2-202/Product: superoxide dismutase #status experimental <MAT>
F/28,76,162,166/Binding site: iron/manganese (His, His, Asp, His) #status predicted

Query Match 20.0%; Score 6; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EPIYISG 20
|||||
Db 17 EPIYISG 22

RESULT 13
B86498
Superoxide dismutase (Mn) [imported] - *Chlamydomonas reinhardtii* (strain J138)
C/Species: *Chlamydomonas reinhardtii*
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
A/Accession: B86498
R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishiguro, M.;
J. Biol. Chem. 276, 2311-2314, 2000
A/Title: Comparison of whole genome sequences of *Chlamydomonas reinhardtii* J138.
A/Reference number: A86491; MUID:20330349; PMID:10871362
A/Accession: B86498
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-207 <STO>
A/Cross-references: GB:BA000008; NID:9878431; PIDN:BA98268.1; GSPDB:GN00142
A/Experimental source: strain J138
C/Genetics:
A/Gene: *sodM*
C/Superfamily: superoxide dismutase (Mn)

Query Match 20.0%; Score 6; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLPEL 7
|||||
Db 6 YSLPEL 11

RESULT 14
B72124

superoxide dismutase (EC 1.15.1.1) (Mn) CP0718 [similarity] - *Chlamydomonas reinhardtii*
C/Species: *Chlamydomonas reinhardtii*
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-May-2000
A/Accession: B72124; B81547
R/Kalman, S.; Mitchell, W.; Marathe, R.; Lamm, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nature Genet. 21, 385-389, 1999
A/Title: Comparative genomics of *Chlamydomonas reinhardtii* and *C. trachomatis*.
A/Reference number: A72000; MUID:99206606; PMID:10192388
A/Accession: B72124
A/Molecule type: DNA
A/Residues: 1-207 <ARN>
A/Cross-references: GB:AE001591; GB:AE001363; NID:94376311; PIDN:AA18210.1; PID:943763
A/Experimental source: strain CWL029
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of *Chlamydomonas reinhardtii* and *Chlamydomonas trachomatis*.
A/Reference number: A81500; MUID:20150255; PMID:10684935
A/Accession: B81547
A/Molecule type: DNA
A/Residues: 1-207 <REA>
A/Cross-references: GB:AE002230; GB:AE002161; NID:97189624; PIDN:AA38524.1; PID:971896
A/Experimental source: strain AR39, HL cells
C/Genetics:
A/Gene: *sodM*; CP0718
C/Superfamily: superoxide dismutase (Mn)
C/Keywords: manganese; metalloprotein; oxidoreductase
F/30,78,166,170/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 20.0%; Score 6; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLPEL 7
|||||
Db 6 YSLPEL 11

RESULT 15
AH1190
3-methyladenine DNA glycosylase homolog lmo0928 [imported] - *Listeria monocytogenes* (str
C/Species: *Listeria monocytogenes*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
A/Accession: AH1190
R/Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baguer, F.; Berche, P.; Bloeker,
D.; Jones, L.M.; Karc, U.
Science 294, 849-852, 2001
A/Authors: Krc, U.; Kuhn, M.; Kunz, F.; Kurapkat, G.; Madueno, E.; Moutouram, A.; M
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland
A/Title: Comparative genomics of *Listeria monocytogenes*.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AH1190
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-207 <GLA>
A/Cross-references: GB:NC_003210; PIDN:CAC99006.1; PID:916410330; GSPDB:GN00177
A/Experimental source: strain EGD-e
C/Genetics:
A/Gene: *lmo0928*
C/Superfamily: *Bacillus subtilis* DNA-3-methyladenine glycosylase homolog yx1J

Query Match 20.0%; Score 6; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 PYISGQ 21
|||||
Db 191 PYISGQ 196

RESULT 16
C83587

hypothetical protein PA0462 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G63587
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,
L.; Lory, S.; Olson, M.V.
N:Date: 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
gen.
A:Reference number: AB2950; MUID:20437373; PMID:10984043
A:Accession: G63587
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-234 <STO>
A:Cross-references: GB:AE004484; GB:AE004091; NID:G9946320; PIDN:AA03851.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0462

Query Match 20.0%; Score 6; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 SLPELD 8
Db 95 SLPELD 100

RESULT 17
E64131
Formyltetrahydrofolate deformylase (EC 3.5.1.10) - Haemophilus influenzae (strain Rd KW2
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 17-Mar-2000
C:Accession: E64131; PNO606
R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Goodyne, J.D.; Scott, J.; Shiley, R.; Liu, L.T.; Glodex, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fine, L.D.; Fritschman, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: E64131
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-278 <TIGR>
A:Cross-references: GB:U52833; GB:L42023; NID:G1574432; PIDN:AA03236.1; PID:G1574433; T
R:Maekel, D.
Gene 129, 155-156, 1993
A:Title: Cloning and sequencing of the Haemophilus influenzae aroA gene.
A:Reference number: JN0758; MUID:93328119; PMID:8335255
A:Accession: PNO606
A:Molecule type: DNA
A:Residues: 64-114, 'RNR', 118-137, 'PK', 141-204, 'E', 206-278 <MAS>
A:Cross-references: GB:L04686; NID:G148863; PIDN:AA24942.1; PID:G148864
C:Genetics:
A:Gene: purN
C:Function:
A:Description: catalyzes hydrolysis of 10-formyltetrahydrofolate to tetrahydrofolate and
A:Pathway: one-carbon metabolism
A>Note: activated by methionine and inhibited by glycine
C:Superfamily: phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide fo
C:Keywords: hydrolase
F:85-277/Domain: phosphoribosylglycinamide formyltransferase homology <PRGF>
F:223/Active site: Asp #status predicted

Query Match 20.0%; Score 6; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KYSLPE 6
Db 66 KYSLPE 71

RESULT 18
T06212
glucose and ribitol dehydrogenase homolog - barley
C:Species: Hordeum vulgare (barley)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
C:Accession: T06212
R:Alexander, R.; Alamilli, J.M.; Salami, F.; Bartels, D.
Planta 192, 519-525, 1994
A:Title: A novel embryo-specific barley cDNA clone encodes a protein with homologies to
A:Reference number: Z15538; MUID:94198754; PMID:7764620
A:Accession: T06212
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-293 <ALB>
A:Cross-references: EMBL:S7926; NID:G633889; PIDN:AA060580.1; PID:G633890
A:Experimental source: cv. Aura, embryo
C:Genetics:
A:introns: 34/3
A:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F:41-228/Domain: short-chain alcohol dehydrogenase homology <SAD>

Query Match 20.0%; Score 6; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 17 YISGOI 22
Db 277 YISGOI 282

RESULT 19
H87192
probable isomerase/racemase [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: H87192
R:Coile, S.T.; Eigemeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: H87192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-334 <STO>
A:Cross-references: GB:AL450380; NID:G13093906; PIDN:CA031784.1; GSPDB:GN00147
C:Genetics:
A:Gene: ML2268

Query Match 20.0%; Score 6; DB 2; Length 334;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LPEDLY 9
Db 252 LPEDLY 257

RESULT 20
D86815
hypothetical protein purM [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: D86815
R:Boctorn, A.; Winkler, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrh
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86825; MUID:2125186; PMID:11337471
A:Accession: D86815
A:Status: preliminary

A;Molecule type: DNA
A;Residues: 1-338 <STO>
A;Cross-references: GB:AB005176; PID:G12724523; PIDN:AAK05622.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: purM
C;Superfamily: phosphoribosylformylglycinamide cyclo-ligase; phosphoribosylformylglycyl

Query Match 20.0%; Score 6; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SLPELD 8
|||||
DB 208 SLPELD 213

RESULT 21
E71339
Inferred hypothetical protein TP0307 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C;Accession: E71339
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khailak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Ueterbach, T.; Mcd
they, L.; Weisman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: E71339
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-342 <COL>
A;Cross-references: GB:AB001211; GB:AE000520; NID:G3322582; PIDN:AAC65296.1; PID:G332258
C;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0307

Query Match 20.0%; Score 6; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLPEL 7
|||||
DB 187 YSLPEL 192

RESULT 22
5408
Hypothetical protein T28C6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000
C;Accession: T25408
R;Lloyd, C.
Submitted to the EMBL Data Library, September 1995
A;Reference number: Z20030
A;Accession: T25408
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-345 <WIL>
A;Cross-references: EMBL:Z54238; PIDN:CAA90996.1; GSPDB:GN00022; CESP:T28C6.5
C;Experimental source: clone T28C6
C;Genetics:
A;Gene: CESP:T28C6.5
A;Map position: 4
A;Intons: 44/2; 156/1; 201/1; 238/3; 286/2
C;Superfamily: Caenorhabditis elegans hypothetical protein BE10.1

Query Match 20.0%; Score 6; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LDYEF5 12

|||||
DB 265 LDYEF5 270

RESULT 23
DB4329
heme biosynthesis protein [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: DB4329
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky,
J.; Lettner, B.; Keller, K.; Cruz, R.; Hanson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
Jung, K.H.; Alam, M.; Freilich, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; I
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: DB4329
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <STO>
A;Cross-references: GB:AB004437; NID:G10581232; PIDN:AAG20000.1; GSPDB:GN00138
C;Genetics:
A;Gene: ntrH

Query Match 20.0%; Score 6; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EFSATE 15
|||||
DB 43 EFSATE 48

RESULT 24
G83003
A / G specific adenine glycosylase PA5147 [imported] - Pseudomonas aeruginosa (strain F
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: G83003
R;Stover, C.K.; Pham, X.Q.; Errin, A.L.; Micozuchi, S.D.; Warriner, P.; Hickey, M.J.; E
adman, S.; Yuan, Y.; Brody, L.V.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lathig, K.; Lin
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83003
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-355 <STO>
A;Cross-references: GB:AE004927; GB:AE004091; NID:G9951437; PIDN:AAG08532.1; GSPDB:GN00
C;Experimental source: strain PA01
C;Genetics:
A;Gene: mutY; PA5147
C;Superfamily: A/G-specific adenine glycosylase

Query Match 20.0%; Score 6; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SLPELD 8
|||||
DB 261 SLPELD 266

RESULT 25
T08277
carotenoid biosynthesis protein homolog H0660 - Halobacterium sp. (strain NRC-1) plasmid
N;Alternate names: hypothetical protein H1696
C;Species: Halobacterium sp.
A;Variety: strain NRC-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Jan-2000
C;Accession: T08277; T08366

R;Ng, W.V.; Ciffo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baekin, D.; Faust, J.; Hall, B.;
Genome Res. 8, 1131-1141, 1998
A:Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or m
A:Reference number: Z16408; MUID:99063795; PMID:9847077
A:Accession: T08277
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-379 <NGM>
A:Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822338; HALOSP:H0660
A:Experimental source: strain NRC-1
A:Genetics: COP1
A:Accession: T08366
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-379 <DAS>
A:Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822427; HALOSP:H1696
A:Experimental source: strain NRC-1
A:Genetics: COP2
C:Genetics: <COP1>
A:Gene: HALOSP:H0660
A:Genetics: <COP2>
A:Genome: plasmid pNRC100
C:Superfamily: carotenoid biosynthesis protein homolog

Query Match 20.0%; Score 6; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LPELDY 9
|||||
Db 61 LPELDY 66

RESULT 26
G84650
Probable beta-glucosidase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
C:Accession: G84650
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Unayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84650
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-384 <STO>
A:Cross-references: GB:A802093; NID:g4874302; PID:AD031364.1; GSPDB:GN00139
C:Genetics: B
A:Gene: At2g25630
A:Map position: 2
C:Superfamily: Agrobacterium beta-glucosidase

Query Match 20.0%; Score 6; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 ATEPYI 18
|||||
Db 232 ATEPYI 237

RESULT 27
F70591
Probable kefB protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: F70591
R:Cole, S.T.; Broech, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajadram, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9654230
A:Accession: F70591
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-385 <COL>
A:Cross-references: GB:295121; GB:AL123456; NID:g3261742; PID:CA08337.1; PID:g2072703
A:Experimental source: strain H37Kv
C:Genetics:
A:Gene: kefB
C:Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napA1

Query Match 20.0%; Score 6; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 EFSATE 15
|||||
Db 76 EFSATE 81

RESULT 28
G87006
Probable transmembrane transport protein ML0782 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
C:Accession: G87006
R:Cole, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Fellwell, T.; Fraser, A.; Hamlin, N.; Holroyd
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: G87006
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-385 <STO>
A:Cross-references: GB:AL450380; NID:g13092891; PID:CA030291.1; GSPDB:GN00147
C:Genetics: B
A:Gene: ML0782
C:Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napA1

Query Match 20.0%; Score 6; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 EFSATE 15
|||||
Db 76 EFSATE 81

RESULT 29
A32812
repa protein - Agrobacterium tumefaciens plasmid pTiBES3
C:Species: Agrobacterium tumefaciens
C:Date: 20-Oct-1989 #sequence_revision 28-Aug-1992 #text_change 08-Oct-1999
C:Accession: A32812
R:Tabata, S.; Hooykaas, P.J.J.; Oka, A.
J. Bacteriol. 171, 1665-1672, 1989
A:Title: Sequence determination and characterization of the replicator region in the tu
A:Reference number: A32812; MUID:89155477; PMID:2537824
A:Accession: A32812
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <TAB>
A:Cross-references: GB:M24529; NID:g154803; PID:AAA27402.1; PID:g154804
C:Genetics: B
A:Genome: plasmid

C:Superfamily: sopA protein

Query Match 20.0%; Score 6; DB 2; Length 405;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GQINEI 25
Db 90 GQINEI 95

RESULT 30

AI3332
replication protein A [imported] - Agrobacterium tumefaciens (strain C58, Dupont) plasmid
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C/Accession: AI3332

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutlyavin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AI3332

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-405 <KUR>

A:Cross-references: GB:AE008690; PIDN:AAI46279.1; PID:917744061; GSPDB:GN00189

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: repA

C:Superfamily: sopA protein

Query Match 20.0%; Score 6; DB 2; Length 405;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GQINEI 25
Db 90 GQINEI 95

RESULT 31

D96939
theory protein, containing EAL-domain [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C/Accession: D96939

R;Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: D96939

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-412 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK78303.1; PID:915023166; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC2924

C:Genetics:

A:Gene: CAC0322

Query Match 20.0%; Score 6; DB 2; Length 412;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TEPIYS 19
Db 372 TEPIYS 377

RESULT 32

C64080

hemY protein homolog - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999

C/Accession: C64080

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kiehlavage,
Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.U.; McDonald, L.A.; Small, K.V.; Frazer, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: C64080

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-428 <TIGR>

A:Cross-references: GB:U32742; GB:I42023; NID:91573593; PIDN:AAK22260.1; PID:91573594;

Query Match 20.0%; Score 6; DB 2; Length 428;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 PYISGQ 21
Db 19 PYISGQ 24

RESULT 33

TS0362
cdc7-like protein kinase [imported] - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000

C/Accession: TS0362

R;Seeger, K.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, February 2000

A:Reference number: Z25064

A:Accession: TS0362

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-429 <SEB>

A:Cross-references: EMBL:AL157918; PIDN:CAB76054.1; GSPDB:GN00067; SPDB:SPBC21C3.18

A:Experimental source: strain 972h(-); cosmid c21C3

C:Genetics:

A:Gene: SPDB:SPBC21C3.18

A:Map position: 2

A:Insertions: 332/1; 388/1

Query Match 20.0%; Score 6; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYSLPE 6
Db 153 KYSLPE 158

RESULT 34

AH2930

oxido-reductase Atu3046 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002

C/Accession: AH2930

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutlyavin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AH2930

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-441 <KUR>
A:Cross-references: GB:AE008689; PIDN:AA143862.1; PID:GL77411407; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3046
A:Map position: linear chromosome

Query Match 20.0%; Score 6; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLPEL 7
|||||
DB 83 YSLPEL 88

RESULT 35

Probable phosphomannomutase - Haemophilus ducreyi (fragment)

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 02-Mar-2001
C:Accession: J11101
C:Ward, C.K.; Lumley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
J. Bacteriol. 180, 6013-6022, 1998
A:Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A:Reference number: Z20984; MUID:99030326; PMID:9811662
A:Accession: J11101
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-443 <MAR>
A:Cross-references: EMBL:AF057695; NID:g3929017; PID:g3929019; PIDN:AACT9758.1
C:Genetics:
A:Gene: pmm
C:Superfamily: Mycoplasma pitum phosphomannomutase

Query Match 20.0%; Score 6; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 YISQI 22
|||||
DB 331 YISQI 336

RESULT 36

E98351

Probable oxidoreductase PA1028 [imported] - Agrobacterium tumefaciens (strain C58, Cerec)

C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Accession: F98351.
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A:Reference number: A97359; PMID:11743194
A:Accession: F98351
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-446 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK90336.1; PID:GL5160373; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L_3517
A:Map position: linear chromosome

Query Match 20.0%; Score 6; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLPEL 7
|||||
DB 88 YSLPEL 93

RESULT 37

S30839
UTR2 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YEL040w
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 06-Feb-1998
C:Accession: S30839; S50504; S38545
R:Milligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Seh1, P.; Komp, C.; Wei, Y.; Taylor, submitted to the EMBL Data Library, February 1993
A:Reference number: S30812
A:Accession: S30839

A:Molecule type: DNA
A:Residues: 1-467 <MUL>
A:Cross-references: GB:U18779; EMBL:U10830; NID:g603625; PID:g603639
R:Dietrich, F.S. EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmid 8199, 8334, and 9871.
A:Reference number: S50491
A:Accession: S50504

A:Molecule type: DNA
A:Residues: 1-467 <DIE>
A:Cross-references: EMBL:U18779; NID:g603625; PID:g603639; MIPS:YEL040w
R:Meinick, L.; Sherman, F.
J. Mol. Biol. 233, 372-388, 1993
A:Title: The gene clusters ARC and COR on chromosomes 5 and 10, respectively, of Saccha

A:Reference number: S38543; MUID:94016558; PMID:8411151
A:Accession: S38545
A:Molecule type: DNA
A:Residues: 121-129, 'V', 131-290, 'R', 292-353, 'C', 355-467 <MEL>
A:Cross-references: EMBL:S66130; NID:g430829; PID:g430830
C:Genetics:
A:Gene: SGD:UTR2
A:Cross-references: SGD:S0000766; MIPS:YEL040w
A:Map position: 5L

Query Match 20.0%; Score 6; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ELDYEF 11
|||||
DB 166 ELDYEF 171

RESULT 38

E97012

probable non-processive endoglucanase family 5, secreted, Cella homolog secreted, docker

C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: E97012
R:No1ling, J.; Berton, G.; Ome1chenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
J. Dairy, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E97012
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-482 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK78888.1; PID:GL5023812; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0912

Query Match 20.0%; Score 6; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 YISQI 22
|||||
DB 445 YISQI 450

Job time : 37.2936 secs

RESULT 39

F84001
glycine dehydrogenase subunit 2 BH2814 [imported] - Bacillus halodurans (strain C-125)
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C/Accession: F84001
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: F84001
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-488 <STO>
A/Cross-references: GB:AP001516; GB:BA000004; NID:G10175192; PIDN:BA0653.1; GSPDB:GN00
A/Experimental source: strain C-125
C/Genetics:
Gene: BH2814

Query Match 20.0%; Score 6; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SLPELD 8
|||||
Db 21 SLPELD 26

RESULT 40

T02400
Probable beta-glucosidase [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C/Accession: T02400; F84878
R/Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, May 1998
A/Description: Arabidopsis thaliana chromosome II BAC F411 genomic sequence.
A/Reference number: Z14667
A/Accession: T02400
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-506 <ROU>

A/Cross-references: EMBL:AC004521; NID:G3128166; PIDN:AC16091.1; PID:G3128187
A/Experimental source: cultivar Columbia
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
; D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
ature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197

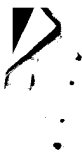
A/Accession: F84878
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-506 <STO>
A/Cross-references: GB:AE002093; NID:G3128187; PIDN:AC16091.1; GSPDB:GN00139
C/Genetics:

A/Gene: F411.26; At2g44450
A/Map position: 2
A/Intons: 50/3; 74/1; 93/3; 119/1; 145/1; 174/2; 259/3; 370/1; 380/3; 415/1; 447/2
C/Superfamily: Agrobacterium beta-glucosidase

Query Match 20.0%; Score 6; DB 2; Length 506;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ATEPYI 18
|||||
Db 233 ATEPYI 238

Search completed: April 9, 2003, 14:17:53



GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 8, 2003, 02:14:28 ; Search time 9.3578 Seconds
(without alignments)
983.170 Million cell updates/sec

Title: US-09-987-190-2
Perfect score: 145
Sequence: 1 KXSLPELDYFSATPEYISQGINEIXYTX 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+p2n.model -DEV=x1h
-G=/cgn2_1/USPTO_spool/US09987190/rnat 02042003 092633 19253/app query.fasta_1.526
-DB=Issued Patents_NA -OPMT=fastp -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCMATCH=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09987190 @CGN 1 1 47 @rnat 02042003 092633 19253 -NCPU=6 -ICPU=3
-NO_XLPEXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-MAEN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Issued Patents_NA.*
2: /cgn2_6/prodata/1/ina/5A COMB.seq.*
3: /cgn2_6/prodata/1/ina/5B COMB.seq.*
4: /cgn2_6/prodata/1/ina/6A COMB.seq.*
5: /cgn2_6/prodata/1/ina/6B COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	54.5	812	4	US-09-091-097-7
2	74	51.0	594	4	US-09-075-019-1
3	74	51.0	600	6	5240847-8
4	74	51.0	600	6	5240847-9
5	74	51.0	600	6	5240847-16
6	74	51.0	600	6	5240847-17
7	74	51.0	681	4	US-09-075-019-6
8	74	51.0	813	3	US-08-927-230A-1
9	74	51.0	813	2	US-09-151-052-1
10	74	51.0	969	2	US-08-365-486A-27
11	74	51.0	969	4	US-08-880-342-27
12	74	51.0	976	4	US-09-126-109-1

C	13	74	51.0	977	2	US-08-023-980B-2	Sequence 2, Appli
	14	74	51.0	977	2	US-08-486-953A-2	Sequence 2, Appli
	15	74	51.0	987	6	5240847-19	Sequence 2, Appli
	16	74	51.0	1032	6	5240847-25	Patent No. 5240847
	17	74	51.0	3789	4	US-09-075-019-8	Patent No. 5240847
	18	71	49.0	721	4	US-09-262-856A-8	Sequence 8, Appli
	19	67	46.2	99	6	5240847-7	Sequence 8, Appli
	20	62	42.8	728	4	US-09-091-097-5	Patent No. 5240847
	21	58	40.0	719	4	US-09-411-578-39	Sequence 59, Appli
	22	57	39.3	606	4	US-09-134-001C-747	Sequence 39, Appli
	23	53	36.6	780	1	US-08-445-909A-28	Sequence 747, Appli
	24	53	36.6	1294	1	US-08-445-909A-16	Sequence 28, Appli
	25	50.5	34.8	747	2	US-08-894-772-4	Sequence 16, Appli
	26	50.5	34.8	747	2	US-09-207-844-4	Sequence 4, Appli
	27	50	34.5	2904	4	US-09-605-785-703	Sequence 4, Appli
	28	50	34.5	3410	4	US-09-020-956-110	Sequence 703, Appli
	29	50	34.5	3410	4	US-09-030-607-110	Sequence 110, Appli
	30	50	34.5	3410	4	US-09-605-785-110	Sequence 110, Appli
	31	50	34.5	3410	4	US-09-439-313-110	Sequence 110, Appli
	32	50	34.5	3410	4	US-09-352-616A-110	Sequence 110, Appli
	33	50	34.5	3410	4	US-09-602-877A-100	Sequence 110, Appli
	34	50	34.5	3410	4	US-09-232-149A-110	Sequence 110, Appli
	35	50	34.5	4034	4	US-09-605-785-704	Sequence 110, Appli
C	36	50	34.5	4137	4	US-09-221-017B-329	Sequence 704, Appli
	37	50	34.5	4894	4	US-09-605-785-702	Sequence 329, Appli
	38	50	34.5	6976	4	US-09-605-785-705	Sequence 702, Appli
C	39	49	33.8	99500	4	US-09-798-096-10	Sequence 705, Appli
	40	48.5	33.4	5044	4	US-09-735-935-3	Sequence 10, Appli
	41	48	33.1	2943	1	US-08-042-747A-7	Sequence 3, Appli
C	42	48	33.1	3572	2	US-08-713-815A-2	Sequence 7, Appli
	43	48	33.1	4080	2	US-08-446-345-35	Sequence 2, Appli
	44	48	33.1	8931	3	US-09-028-934-28	Sequence 35, Appli
	45	47.5	32.8	1769	4	US-09-257-584-6	Sequence 28, Appli

ALIGNMENTS

RESULT 1
US-09-091-097-7
Sequence 7, Application US/09091097
Patent No. 6432407
GENERAL INFORMATION:
APPLICANT: TAKESAKO, KAZUTOH
APPLICANT: OKADO, TAKASHI
APPLICANT: YAGIHARA, TOMOKO
APPLICANT: KURODA, MASANOBU
APPLICANT: ONISHI, YOSHIMI
APPLICANT: KATO, IKUNOSHIN
APPLICANT: AKIYAMA, KAZUO
APPLICANT: YASUEDA, HIROSHI
APPLICANT: YAMAGUCHI, HIDEYO
TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091, 097
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181

REFERENCE/DOCKET NUMBER: 1422-0346P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..673
US-09-091-097-7
Alignment Scores:
Pred. No.: 1.05e-05 Length: 812
Score: 79.00 Matches: 15
Percent Similarity: 70.37% Conservative: 4
Best Local Similarity: 55.56% Mismatches: 8
Query Match: 54.48% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x US-09-091-097-7 (1-812)
Oy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 74 AAGTACAGCGCTGCCCCGCTGCGTACGACTGAGCGCGCTGAGCCGCGCATCTCGGAC 133
Oy 21 GlnIleAsnGluIle**Tyr 27
Db 134 GAGATCATGAGAGACGACTAC 154
RESULT 2
US-09-075-019-1
Sequence 1, Application US/09075019
Patent No. 6190658
GENERAL INFORMATION:
APPLICANT: UTC IR459
TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Rose P. C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,019
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2848-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 594 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 1..594
US-09-075-019-1
Alignment Scores:
Pred. No.: 6.04e-05 Length: 594
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x US-09-075-019-1 (1-594)
Oy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 1 AAGCAGCGCTGCCCGACCTGCTTACGACTGCGCGCTGGAACCTCACATCAACGCG 60
Oy 21 GlnIleAsnGluIle**TyrThr 28
Db 61 CAGATCATGACGCTGCACACAGC 84
RESULT 3
5240847-8
Patent No. 5240847
APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
ZOEHEL, ANDREAS; KRYSTEK, EDELTRAUD; MAURER-FOGY, INGRID;
WITCHE-CASPARON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
(HNN-SOD)
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/167,261
FILING DATE: 11-MAR-1988
SEQ ID NO: 8
LENGTH: 600
5240847-8
Alignment Scores:
Pred. No.: 6.12e-05 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x 5240847-8 (1-600)
Oy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4 AAGCAGCTTTGGCAGACTTGCCATACGACTGCGTCTCTAGAACACACATCAATGCT 63
Oy 21 GlnIleAsnGluIle**TyrThr 28
Db 64 CAATCATGCAATGACACACTCT 87
RESULT 4
5240847-9
Patent No. 5240847
APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
ZOEHEL, ANDREAS; KRYSTEK, EDELTRAUD; MAURER-FOGY, INGRID;
WITCHE-CASPARON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
(HNN-SOD)
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/167,261
FILING DATE: 11-MAR-1988
SEQ ID NO: 9
LENGTH: 600
5240847-9

US-09-987-190-2 (1-30) x 5240847-9 (1-600)	US-09-987-190-2 (1-30) x 5240847-16 (1-600)	US-09-987-190-2 (1-30) x 5240847-16 (1-600)
<p>Qy 1 LysTyzSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProYrYrIleSerGly 200</p> <p>Db 4 AAGACGCTTTGGCAGACTTTGCCATTCAGCATACGGTGCCTTCAAGAACACACATCAATGCT 600</p> <p>Qy 21 GlnIleAsnGluIle***TyrThr 28</p> <p>Db 64 CAATCATGCATTCAGACCACTCT 87</p>	<p>Qy 1 LysTyzSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProYrYrIleSerGly 200</p> <p>Db 4 AAGACGCTTTGGCAGACTTTGCCATTCAGCATACGGTGCCTTCAAGAACACACATCAATGCT 600</p> <p>Qy 21 GlnIleAsnGluIle***TyrThr 28</p> <p>Db 64 CAATCATGCATTCAGACCACTCT 87</p>	<p>Qy 1 LysTyzSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProYrYrIleSerGly 200</p> <p>Db 4 AAGACGCTTTGGCAGACTTTGCCATTCAGCATACGGTGCCTTCAAGAACACACATCAATGCT 600</p> <p>Qy 21 GlnIleAsnGluIle***TyrThr 28</p> <p>Db 64 CAATCATGCATTCAGACCACTCT 87</p>
<p>Alignment Scores:</p> <p>Pred. No.: 5240847</p> <p>Score: 6,12e-05</p> <p>Percent Similarity: 74.00</p> <p>Best Local Similarity: 78.57%</p> <p>Query Match: 42.86%</p> <p>DB: 51.03%</p> <p>Gaps: 6</p>	<p>Alignment Scores:</p> <p>Pred. No.: 5240847</p> <p>Score: 6,12e-05</p> <p>Percent Similarity: 74.00</p> <p>Best Local Similarity: 78.57%</p> <p>Query Match: 42.86%</p> <p>DB: 51.03%</p> <p>Gaps: 6</p>	<p>Alignment Scores:</p> <p>Pred. No.: 5240847</p> <p>Score: 6,12e-05</p> <p>Percent Similarity: 74.00</p> <p>Best Local Similarity: 78.57%</p> <p>Query Match: 42.86%</p> <p>DB: 51.03%</p> <p>Gaps: 6</p>
<p>TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE</p> <p>(HMN-SOD)</p> <p>NUMBER OF SEQUENCES: 34</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/07/167,261</p> <p>FILING DATE: 11-MAR-1988</p> <p>SEQ ID NO:17:</p> <p>LENGTH: 600</p>	<p>TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE</p> <p>(HMN-SOD)</p> <p>NUMBER OF SEQUENCES: 34</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/07/167,261</p> <p>FILING DATE: 11-MAR-1988</p> <p>SEQ ID NO:16:</p> <p>LENGTH: 600</p>	<p>TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE</p> <p>(HMN-SOD)</p> <p>NUMBER OF SEQUENCES: 34</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/07/167,261</p> <p>FILING DATE: 11-MAR-1988</p> <p>SEQ ID NO:16:</p> <p>LENGTH: 600</p>
<p>Alignment Scores:</p> <p>Pred. No.: 5240847</p> <p>Score: 6,12e-05</p> <p>Percent Similarity: 74.00</p> <p>Best Local Similarity: 78.57%</p> <p>Query Match: 42.86%</p> <p>DB: 51.03%</p> <p>Gaps: 6</p>	<p>Alignment Scores:</p> <p>Pred. No.: 5240847</p> <p>Score: 6,12e-05</p> <p>Percent Similarity: 74.00</p> <p>Best Local Similarity: 78.57%</p> <p>Query Match: 42.86%</p> <p>DB: 51.03%</p> <p>Gaps: 6</p>	<p>Alignment Scores:</p> <p>Pred. No.: 5240847</p> <p>Score: 6,12e-05</p> <p>Percent Similarity: 74.00</p> <p>Best Local Similarity: 78.57%</p> <p>Query Match: 42.86%</p> <p>DB: 51.03%</p> <p>Gaps: 6</p>
<p>TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE</p> <p>(HMN-SOD)</p> <p>NUMBER OF SEQUENCES: 34</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/07/167,261</p> <p>FILING DATE: 11-MAR-1988</p> <p>SEQ ID NO:17:</p> <p>LENGTH: 600</p>	<p>TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE</p> <p>(HMN-SOD)</p> <p>NUMBER OF SEQUENCES: 34</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/07/167,261</p> <p>FILING DATE: 11-MAR-1988</p> <p>SEQ ID NO:16:</p> <p>LENGTH: 600</p>	<p>TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE</p> <p>(HMN-SOD)</p> <p>NUMBER OF SEQUENCES: 34</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/07/167,261</p> <p>FILING DATE: 11-MAR-1988</p> <p>SEQ ID NO:16:</p> <p>LENGTH: 600</p>

```

Query Match: 51.03% Indels: 0
DB: 6 Gaps: 0

US-09-987-190-2 (1-30) x 5240847-17 (1-600)

OY 1 LysTySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 4 AAGCACTCTTTGCCAGACTTTCGCATACGACTACGCTGCTCTGAAACACACATCATGCT 63

OY 21 GlnIleAenGluIle**TyrThr 28
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 64 CAATCATGCAATTCACCACTCT 87

RESULT 7
US-09-075-019-6
; Sequence 6, Application US/09075019
; Patent No. 6190658
; GENERAL INFORMATION:
; APPLICANT: UTC IR459
; TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
; TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph B.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2848-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..681
; US-09-075-019-6

Alignment Scores:
Pred. No.: 7.23e-05 Length: 681
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-075-019-6 (1-681)

OY 1 LysTySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 7 AAGCACTCTTTGCCAGACTTTCGCATACGAGCGCCCTGGAACCTCACATCAACGCG 66

OY 21 GlnIleAenGluIle**TyrThr 28
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 67 CAGATCATGACGTGACACACAGC 90

RESULT 8

US-08-927-230A-1

Sequence 1, Application US/08927230A

Patent No. 5985633

GENERAL INFORMATION:

APPLICANT: Nick et al.

TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street, Floor 24

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/927,230A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Remillard, Jane

REGISTRATION NUMBER: 38,872

REFERENCE/DOCKET NUMBER: UFI-001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 813 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 43..708

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 115..708

US-08-927-230A-1

Alignment Scores:

Pred. No.: 9.09e-05

Score: 74.00

Percent Similarity: 78.57%

Best Local Similarity: 42.86%

Query Match: 51.03%

DB: 2

Length: 813

Matches: 12

Conservative: 10

Mismatches: 6

Indels: 0

Gaps: 0

US-09-987-190-2 (1-30) x US-08-927-230A-1 (1-813)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 115 AAGCACACGCTCCCGACCTGCGCTACGACTACGCGCGCCCTGGAACCTCATCAACGCG 174

Qy 21 GlnIleangluile**TyrThr 28

Db 175 CAGATCATGACGTGACACACAGC 198

RESULT 9

US-08-151-052-1

Sequence 1, Application US/09151052

Patent No. 6107070

GENERAL INFORMATION:

APPLICANT: Nick et al.

TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 28 State Street, Floor 24

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/151,052

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/927,230

FILING DATE: September 10, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Remillard, Jane

REGISTRATION NUMBER: 38,872

REFERENCE/DOCKET NUMBER: UFI-001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 813 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 43..708

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 115..708

US-09-151-052-1

Alignment Scores:

Pred. No.: 9.09e-05

Score: 74.00

Percent Similarity: 78.57%

Best Local Similarity: 42.86%

Query Match: 51.03%

DB: 3

Length: 813

Matches: 12

Conservative: 10

Mismatches: 6

Indels: 0

Gaps: 0

US-09-987-190-2 (1-30) x US-09-151-052-1 (1-813)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 115 AAGCACACGCTCCCGACCTGCGCTACGACTACGCGCGCCCTGGAACCTCATCAACGCG 174

Qy 21 GlnIleangluile**TyrThr 28

Db 175 CAGATCATGACGTGACACACAGC 198

RESULT 10

US-08-365-486A-27

Sequence 27, Application US/08365486A

Patent No. 5834306

GENERAL INFORMATION:

APPLICANT: Webster, Keith A.

TITLE OF INVENTION: Tissue Specific Hypoxia Regulated

NUMBER OF SEQUENCES: 31

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dehlinger & Associates
;; STREET: 350 Cambridge Avenue, Suite 250
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94306
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/365,486A
;; FILING DATE: 23-DEC-1994
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sholtz, Charles K.
;; REGISTRATION NUMBER: 38,615
;; REFERENCE/DOCKET NUMBER: 8255-0018
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 324-0880
;; TELEFAX: (415) 324-0960
;; INFORMATION FOR SEQ ID NO: 27:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 969 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: unknown
;; MOLECULE TYPE: cDNA to mRNA
;; HYPOTHEICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; INDIVIDUAL ISOLATE: human manganese superoxide dismutase
;; INDIVIDUAL ISOLATE: EMBL #X59445
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 61..729
;;
US-08-365-486A-27
;;
Alignment Scores:
Pred. No.: 0.000114 Length: 969
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
09-987-190-2 (1-30) x US-08-365-486A-27 (1-969)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 133 AAGCAGACGCTCCCGACGCTCCCTACGACTACGGCGCCCTGGAACCTCACAATCAACGCG 192
QY 21 GlnIleAsnGluIle***TyrThr 28
Db 193 CAGATCATGCGAGCTGCACCAACAGC 216
RESULT 11
US-08-880-342-27
; Sequence 27, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates

;; STREET: 350 Cambridge Avenue, Suite 250
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94306
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/880,342
;; FILING DATE: 23-JUN-1997
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/IB95/00996
;; FILING DATE: 13-NOV-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/365,486
;; FILING DATE: 23-DEC-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sholtz, Charles K.
;; REGISTRATION NUMBER: 38,615
;; REFERENCE/DOCKET NUMBER: 8255-0018.30
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 324-0880
;; TELEFAX: (415) 324-0960
;; INFORMATION FOR SEQ ID NO: 27:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 969 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: unknown
;; MOLECULE TYPE: cDNA to mRNA
;; HYPOTHEICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; INDIVIDUAL ISOLATE: human manganese superoxide dismutase
;; INDIVIDUAL ISOLATE: EMBL #X59445
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 61..729
;;
US-08-880-342-27
;;
Alignment Scores:
Pred. No.: 0.000114 Length: 969
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x US-08-880-342-27 (1-969)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 133 AAGCAGACGCTCCCGACGCTCCCTACGACTACGGCGCCCTGGAACCTCACAATCAACGCG 192
QY 21 GlnIleAsnGluIle***TyrThr 28
Db 193 CAGATCATGCGAGCTGCACCAACAGC 216
RESULT 12
US-09-126-109-1
; Sequence 1, Application US/09126109
; Patent No. 6171856
; GENERAL INFORMATION:
; APPLICANT: Thigpen, Anice
; APPLICANT: Hommeier, Hans-Ewald
; APPLICANT: Newgard, Christopher B.
; APPLICANT: Unger, Roger H.
; APPLICANT: Shimabukuro, Michio
; APPLICANT: Chen, Guaxun

APPLICANT: Rhodes, Christopher J.
APPLICANT: Hugl, Sigron R.
APPLICANT: Cousin, Sharon
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TO NO-MEDIATED CYTOTOXICITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,109
FILING DATE: 30-JUL-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,092
FILING DATE: 30-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US Unknown
FILING DATE: 03-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabehla R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSID:560
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 976 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-126-109-1

Alignment Scores:
Pred. No.: 0.000115 Length: 976
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x US-09-126-109-1 (1-976)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 167 AAGCACAGCCTCCCGACTGCGCTACGACTACGGGCGCCGGAACCTCAGATCAACGCG 226

Qy 21 GlnIleangluile**TyrThr 28
Db 227 CAGATCATGCACTGCACACACG 250

RESULT 13
US-08-023-980B-2
Sequence 2, Application US/08023980B
Patent No. 5843641
GENERAL INFORMATION:
APPLICANT: Brown, Robert
APPLICANT: Horvitz, H. Robert
APPLICANT: Rosen, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 585 Commercial Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-1024
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/023,980B
FILING DATE: 26-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/177001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/723-4123
TELEFAX: 617/723-8962
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 977 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-023-980B-2

Alignment Scores:
Pred. No.: 0.000116 Length: 977
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x US-08-023-980B-2 (1-977)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 168 AAGCACAGCCTCCCGACTGCGCTACGACTACGGGCGCCGGAACCTCAGATCAACGCG 227

Qy 21 GlnIleangluile**TyrThr 28
Db 228 CAGATCATGCACTGCACACACG 251

RESULT 14
US-08-486-953A-2
Sequence 2, Application US/08486953A
Patent No. 5849290
GENERAL INFORMATION:
APPLICANT: Brown, Robert
APPLICANT: Horvitz, H. Robert
APPLICANT: Rosen, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FastSeq
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,953A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,052
FILING DATE: 28-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/223002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/428-0200
TELEFAX: 617/428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 977 base pairs
type: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-486-953A-2

Alignment Scores:
Pred. No.: 0.000116 Length: 977
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x US-08-486-953A-2 (1-977)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 168 AAGCAGACGCTCCCGACCTGCTACGACTACGCGCCCTGGAACCTCAATCAACCG 227
QY 21 GlnIleAsnGluIle***TyrThr 28
Db 228 CAGATCATGACGCTGCACACACG 251

RESULT 15
5240847-19
PATENT NO. 5240847
APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
ZEHLE, ANDREAS; KRISTEK, EDELTRAUD; MAURER-FOGY, INGRID;
MICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
(HNN-SOD)
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/167,261
FILING DATE: 11-MAR-1988
SEQ ID NO: 19
LENGTH: 987
5240847-19

Alignment Scores:
Pred. No.: 0.000117 Length: 987
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x 5240847-19 (1-987)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 13 AAGCAGCTCTTGGCGAGCTTGCATACGACTACGGTCTTGAACACACATCAATGCT 72

QY 21 GlnIleAsnGluIle***TyrThr 28
Db 73 CAATCATGCAATTCACCACTCT 96

RESULT 16
5240847-25
PATENT NO. 5240847
APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
ZEHLE, ANDREAS; KRISTEK, EDELTRAUD; MAURER-FOGY, INGRID;
MICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
(HNN-SOD)
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/167,261
FILING DATE: 11-MAR-1988
SEQ ID NO: 25
LENGTH: 1032
5240847-25

Alignment Scores:
Pred. No.: 0.000124 Length: 1032
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x 5240847-25 (1-1032)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 73 AAGCAGACGCTCCCGACCTGCTACGACTACGCGCCCTGGAACCTCAATCAACCG 132
QY 21 GlnIleAsnGluIle***TyrThr 28
Db 133 CAGATCATGACGCTGCACACACG 156

RESULT 17
US-09-075-019-8
Sequence 8, Application US/09075019
PATENT NO. 6190658
GENERAL INFORMATION:
APPLICANT: UTC IR459
TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,019
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2848-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-0223
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3789 base pairs

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-075-019-8

Alignment Scores:
Pred. No.: 0.000677 Length: 3789
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-075-019-8 (1-3789)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 550 AAGCAGAGCTCTCCGAGCTCCGCTACGCTACGCGCCCTGGAACCTCACTCAACGCG 609
21 GlnIleAenGluIle**TyrThr 28
610 CAGATCATGCACTGCACACACAGC 633

RESULT 18
US-09-262-856A-8
; Sequence 8, Application US/09262856A
; Patent No. 6333164
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: MIZUTANI, SHIGETOSHI
; APPLICANT: ENDO, MASAHICO
; APPLICANT: KATO, IKUNOSHIN
; TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
; FILE REFERENCE: 1422-372P
; CURRENT APPLICATION NUMBER: US/09/262,856A
; CURRENT FILING DATE: 1999-03-04
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 721
; TYPE: DNA
; ORGANISM: Candida albicans
; US-09-262-856A-8

Alignment Scores:
Pred. No.: 0.000283 Length: 721
Score: 71.00 Matches: 13
Percent Similarity: 93.75% Conservative: 2
Best Local Similarity: 81.25% Mismatches: 1
Query Match: 48.97% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-262-856A-8 (1-721)

Qy 13 AlaThrGluProTyrIleSerGlyGlnIleAenGluIle**TyrThr 28
Db 1 GCCATGAACTATCATCATCAGACGAATGAGCAATTCATCACTACT 48

RESULT 19
5240847-7
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRISTEK, EDELTAUD; MAURER-FOCY, INGRID;
; WITCHE-CASTRANO, MARIA J.; STRATOMA, CHRISTIAN; HAUFMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HNN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO: 7
; LENGTH: 99
```

```

5240847-7

Alignment Scores:
Pred. No.: 0.000119 Length: 99
Score: 67.00 Matches: 12
Percent Similarity: 76.00% Conservative: 7
Best Local Similarity: 48.00% Mismatches: 6
Query Match: 46.21% Indels: 0
DB: 6 Gaps: 0

US-09-987-190-2 (1-30) x 5240847-7 (1-99)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4 AAGCAGCTCTTGGCCAGACTTCATACGACTACGCTGCTAGAACACACATCATGCT 63
21 GlnIleAenGluIle 25
Db 64 CAAATCATGCAATT 78

RESULT 20
US-09-091-097-5
; Sequence 5, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI
; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; TITLE OF INVENTION: MALASSEZIA
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,097
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..618
; US-09-091-097-5

Alignment Scores:
```


FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,772
FILING DATE: 27-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valecia A.
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 4300.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0288
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
9-207-844-4

Alignment Scores:
Pred. No.: 2 04 Length: 747
Score: 50.50 Matches: 12
Percent Similarity: 53.33% Conservatives: 4
Best Local Similarity: 40.00% Mismatches: 9
Query Match: 34.83% Indels: 5
DB: 2 Gaps: 2

US-09-987-190-2 (1-30) x US-09-207-844-4 (1-747)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluPro-----TyrIle 18
Db 202 AAATTCGAATACCC-----TATCGTTCAACGCCACGCCCGAGTCCATATT 252

Qy 19 SerGlyIleIleangIuile***TyrThr 28
Db 253 GATGCGTCTATCACTCACTGCTTTCTACACT 282

RESULT 27

US-09-605-785-703
Sequence 703, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Scolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 703
LENGTH: 2904
TYPE: DNA
ORGANISM: Homo sapiens
US-09-605-785-703

Alignment Scores:
Pred. No.: 14.9 Length: 2904
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservatives: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-605-785-703 (1-2904)

Qy 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyIle 21
Db 40 TACCTCCTGCTGCAATGACTGGACACCAAGTGCCTGAGCCCTTACTGGGACCCAG 99

RESULT 28
US-09-020-956-110
Sequence 110, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 3410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-020-956-110

Alignment Scores:
Pred. No.: 18.3 Length: 3410
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservatives: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-020-956-110 (1-3410)

Qy 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyIle 21
Db 809 TACCTCCTGCTGCAATGACTGGACACCAAGTGCCTGAGCCCTTACTGGGACCCAG 868

RESULT 29

US-09-030-607-110
; Sequence 110, Application US/09030607
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030.607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-030-607-110
; Alignment Scores:
; Pred. No.: 18.3 Length: 3410
; Score: 50.00 Matches: 9
; Percent Similarity: 65.00% Conservative: 4
; Best Local Similarity: 45.00% Mismatches: 7
; Query Match: 34.48% Indels: 0
; Gaps: 0
; 9-987-190-2 (1-30) x US-09-030-607-110 (1-3410)
Qy 2 TySertLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 809 TACCTCCGCTGCCTGACATGACAGACACCACTGCTGCGCCCTACTGCGACCCAG 868
RESULT 30
US-09-605-785-110
; Sequence 110, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605.785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-605-785-110
; Alignment Scores:
; Pred. No.: 18.3 Length: 3410
; Score: 50.00 Matches: 9
; Percent Similarity: 65.00% Conservative: 4
; Best Local Similarity: 45.00% Mismatches: 7
; Query Match: 34.48% Indels: 0
; Gaps: 0
; US-09-987-190-2 (1-30) x US-09-605-785-110 (1-3410)
Qy 2 TySertLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 809 TACCTCCGCTGCCTGACATGACAGACACCACTGCTGCGCCCTACTGCGACCCAG 868
RESULT 31
US-09-439-313-110
; Sequence 110, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solik, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439.313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-439-313-110
; Alignment Scores:
; Pred. No.: 18.3 Length: 3410
; Score: 50.00 Matches: 9
; Percent Similarity: 65.00% Conservative: 4
; Best Local Similarity: 45.00% Mismatches: 7
; Query Match: 34.48% Indels: 0
; Gaps: 0
; US-09-987-190-2 (1-30) x US-09-439-313-110 (1-3410)
Qy 2 TySertLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 809 TACCTCCGCTGCCTGACATGACAGACACCACTGCTGCGCCCTACTGCGACCCAG 868

Db 809 TACCTCCTGCTGCATTTAGTGGGACACAGTGTGCGCCCTTACTGAGGACCCAG 868

RESULT 32

US-09-352-616A-110

Sequence 110, Application US/09352616A

Patent No. 6395278

GENERAL INFORMATION:

APPLICANT: Dillon, Davin C.

APPLICANT: Harlocker, Susan Louise

APPLICANT: Jiang, Yugu

APPLICANT: Xu, Jiangchun

APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.427C8

CURRENT FILING DATE: US/09/352,616A

CURRENT APPLICATION NUMBER: 1999-07-13

NUMBER OF SEQ ID NOS: 472

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 110

LENGTH: 3410

TYPE: DNA

ORGANISM: Homo sapien

US-09-352-616A-110

Alignment Scores:

Pred. No.: 18.3 Length: 3410

Score: 50.00 Matches: 9

Percent Similarity: 65.00% Conservative: 4

Best Local Similarity: 45.00% Mismatches: 7

Query Match: 34.48% Indels: 0

Gaps: 0

DB:

US-09-987-190-2 (1-30) x US-09-352-616A-110 (1-3410)

Qy 2 TySerleupProgluLeuAspTyrglupheserAlatrhglupProTyrlleSerclygn 21

Db 809 TACCTCCTGCTGCATTTAGTGGGACACAGTGTGCGCCCTTACTGAGGACCCAG 868

RESULT 33

US-09-602-877A-100

Sequence 100, Application US/09602877A

Patent No. 6432707

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER

FILE REFERENCE: 210121.446C5

CURRENT APPLICATION NUMBER: US/09/602,877A

CURRENT FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 107

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 100

LENGTH: 3410

TYPE: DNA

ORGANISM: Homo sapien

US-09-602-877A-100

Alignment Scores:

Pred. No.: 18.3 Length: 3410

Score: 50.00 Matches: 9

Percent Similarity: 65.00% Conservative: 4

Best Local Similarity: 45.00% Mismatches: 7

Query Match: 34.48% Indels: 0

Gaps: 0

DB:

US-09-987-190-2 (1-30) x US-09-602-877A-100 (1-3410)

Qy 2 TySerleupProgluLeuAspTyrglupheserAlatrhglupProTyrlleSerclygn 21

Db 809 TACCTCCTGCTGCATTTAGTGGGACACAGTGTGCGCCCTTACTGAGGACCCAG 868

RESULT 34

US-09-232-149A-110

Sequence 110, Application US/09232149A

Patent No. 6465611

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.427C6

CURRENT APPLICATION NUMBER: US/09/232,149A

CURRENT FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 338

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 110

LENGTH: 3410

TYPE: DNA

ORGANISM: Homo sapien

US-09-232-149A-110

Alignment Scores:

Pred. No.: 18.3 Length: 3410

Score: 50.00 Matches: 9

Percent Similarity: 65.00% Conservative: 4

Best Local Similarity: 45.00% Mismatches: 7

Query Match: 34.48% Indels: 0

Gaps: 0

DB:

US-09-987-190-2 (1-30) x US-09-232-149A-110 (1-3410)

Qy 2 TySerleupProgluLeuAspTyrglupheserAlatrhglupProTyrlleSerclygn 21

Db 809 TACCTCCTGCTGCATTTAGTGGGACACAGTGTGCGCCCTTACTGAGGACCCAG 868

RESULT 35

US-09-605-785-704

Sequence 704, Application US/09605785

Patent No. 6321716

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yugu

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedrick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C16

CURRENT APPLICATION NUMBER: US/09/605,785

CURRENT FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 835

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 704

LENGTH: 4034

TYPE: DNA

ORGANISM: Homo sapiens

US-09-605-785-704

Alignment Scores:

Pred. No.: 22.8 Length: 4034

Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-605-785-704 (1-4034)

Oy 2 TyrsleupProgluLeuAspTyrGluPheserAlaThrGluProTyrIleSerGlyGln 21

Db 806 TACCTCCTGCTGCATGACGACACCAAGTCCCTGCGCCCTACTGAGGACCCAG 865

RESULT 36

US-09-221-017B-329/C
Sequence 329, Application US/09221017B

Patent No. 6444799

GENERAL INFORMATION:

APPLICANT: Ross, Bruce C.

TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF

NUMBER OF SEQUENCES: 1120

CORRESPONDENCE ADDRESS:

ADDRESSER: MORRISON & ROEBSTER

STREET: 755 PAGE MILL ROAD

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/221.017B

FILING DATE: 23-DEC-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: P1182

FILING DATE: 31-DEC-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: P11546

FILING DATE: 30-JAN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: P2311

FILING DATE: 09-APR-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU98/01023

FILING DATE: 10-DEC-1998

ATTORNEY/AGENT INFORMATION:

NAME: Monroy, Gladys H

REGISTRATION NUMBER: 32,430

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-813-5600

TELEFAX: 650-494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 329:

SEQUENCE CHARACTERISTICS:

LENGTH: 4137 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHEICAL: NO

ANTI-SENSE: UNKNOWN

ORIGINAL SOURCE:

ORGANISM: PORPHYROMONAS GINGIVALIS

FEATURE:

NAME/KEY: m1ec_feature

LOCATION: 1...4137

US-09-221-017B-329

Alignment Scores:

Pred. No.: 23.6 Length: 4137
Score: 50.00 Matches: 9
Percent Similarity: 76.47% Conservative: 4
Best Local Similarity: 52.94% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-221-017B-329 (1-4137)

Oy 5 ProgluLeuAspTyrGluPheserAlaThrGluProTyrIleSerGlyGln 21

Db 3394 CCCGAATGAAATACAAAGCTGCTCAGATCCGTACATCTGACACCA 3334

RESULT 37

US-09-605-785-702
Sequence 702, Application US/09605785

Patent No. 6321716

GENERAL INFORMATION:

APPLICANT: Xu, Jianshun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqi

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darlick

APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.427C16

CURRENT APPLICATION NUMBER: US/09/605.785

NUMBER OF SEQ ID NOS: 835

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 702

LENGTH: 4894

TYPE: DNA

ORGANISM: Homo sapiens

US-09-605-785-702

Alignment Scores:

Pred. No.: 29.3 Length: 4894
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-605-785-702 (1-4894)

Oy 2 TyrsleupProgluLeuAspTyrGluPheserAlaThrGluProTyrIleSerGlyGln 21

Db 1665 TACCTCCTGCTGCATGACGACACCAAGTCCCTGCGCCCTACTGAGGACCCAG 1724

RESULT 38

US-09-605-785-705
Sequence 705, Application US/09605785

Patent No. 6321716

GENERAL INFORMATION:

APPLICANT: Xu, Jianshun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqi

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT FILING DATE: 2000-06-27
CURRENT APPLICATION NUMBER: US/09/605,785
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 705
LENGTH: 6976
TYPE: DNA
ORGANISM: Homo sapiens
US-09-605-785-705

Alignment Scores:
Pred. No.: 46.6 Length: 6976
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 7
Best Local Similarity: 45.00% Mismatches: 4
Query Match: 34.48% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x US-09-605-785-705 (1-6976)

QY 2 TyrsenleuprogluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
DB 1556 TACCTCCCTGCTGATGACTGAGACACCAAGTCCCTGGCCCTTACTGAGCACCAG 1615

RESULT 39
US-09-798-096-10/c
Sequence 10, Application US/09798096
Patent No. 6399378
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
FILE REFERENCE: PUS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 10
LENGTH: 99500
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-798-096-10

Alignment Scores:
Pred. No.: 2.29e+03 Length: 99500
Score: 49.00 Matches: 8
Percent Similarity: 63.64% Conservative: 6
Best Local Similarity: 36.36% Mismatches: 8
Query Match: 33.79% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x US-09-798-096-10 (1-99500)

QY 4 LeuProgluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGlnLeasn 23
DB 84101 CTGCTGACCTGACCTATGAGTTTCTTCACTGACCAACCATGGGTGCTTCCACCACTTAT 84042
QY 24 GluIle 25
:::||||

DB 84041 CAAATC 84036

RESULT 40
US-09-735-935-3
Sequence 3, Application US/09735935
Patent No. 6420150
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000970
CURRENT APPLICATION NUMBER: US/09/735,935
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 5044
TYPE: DNA
ORGANISM: Human
US-09-735-935-3

Alignment Scores:
Pred. No.: 58.2 Length: 5044
Score: 48.50 Matches: 10
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 41.67% Mismatches: 7
Query Match: 33.45% Indels: 1
DB: Gaps: 1

US-09-987-190-2 (1-30) x US-09-735-935-3 (1-5044)

QY 3 SerleuprogluLeuAsp--TyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
DB 275 TCCCTCCAAATCCPAACCTGTATGATTTCAGTCTGGACCATCTCAAGATCCATG 334

QY 22 IleAsnGluIle 25
DB 335 CTTTCAGAAATG 346

Search completed: April 8, 2003, 03:51:30
Job time: 22.3578 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 9, 2003, 14:17:20 ; Search time 6.05505 Seconds
(without alignments)
302.901 Million cell updates/sec

Title: US-09-987-190-2
Perfect score: 30
Sequence: 1 KYSLPELDYFSATEPYISQINEIXYTX 30

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 248912 seqs, 61136040 residues

Word size: 0

Total number of hits satisfying chosen parameters: 248912

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	90.0	30	10	US-09-987-190-2	Sequence 2, Appl1
2	6	20.0	50	10	US-09-864-761-43011	Sequence 43011, Appl1
3	6	20.0	65	12	US-10-078-929-24	Sequence 24, Appl2
4	6	20.0	81	9	US-09-981-876-166	Sequence 166, Appl2
5	6	20.0	81	9	US-09-148-545-166	Sequence 166, Appl2
6	20.0	98	12	US-10-078-929-26	Sequence 26, Appl2	
7	6	20.0	137	10	US-09-840-787-49	Sequence 49, Appl2
8	6	20.0	146	10	US-09-925-300-975	Sequence 975, Appl2
9	6	20.0	188	10	US-09-987-190-6	Sequence 6, Appl1
10	6	20.0	200	9	US-09-738-626-62727	Sequence 62727, Appl1
11	6	20.0	200	10	US-09-818-564-2	Sequence 2, Appl1
12	6	20.0	1536	9	US-09-909-567B-47	Sequence 47, Appl1
13	5	16.7	26	9	US-09-813-153-211	Sequence 211, Appl1
14	5	16.7	33	10	US-09-864-761-48159	Sequence 48159, Appl1
15	5	16.7	39	10	US-09-810-310-2	Sequence 2, Appl1
16	5	16.7	39	10	US-09-810-310-9	Sequence 2, Appl1
17	5	16.7	39	10	US-09-864-761-34370	Sequence 34370, Appl1
18	5	16.7	52	9	US-09-764-904-63	Sequence 63, Appl1
19	5	16.7	52	9	US-10-091-548-63	Sequence 63, Appl1

20	5	16.7	52	10	US-09-764-860-581	Sequence 581, App
21	5	16.7	65	10	US-09-864-761-34543	Sequence 34543, A
22	5	16.7	76	10	US-09-867-550-424	Sequence 424, App
23	5	16.7	77	10	US-09-864-761-47808	Sequence 47808, A
24	5	16.7	88	10	US-09-764-887-257	Sequence 257, App
25	5	16.7	91	10	US-09-864-761-40079	Sequence 40079, A
26	5	16.7	97	9	US-10-101-464A-651	Sequence 651, App
27	5	16.7	105	10	US-09-764-877-1863	Sequence 1863, App
28	5	16.7	111	12	US-10-052-817-6	Sequence 6, Appli
29	5	16.7	127	10	US-09-846-590B-2	Sequence 2, Appli
30	5	16.7	132	10	US-09-164-615-13	Sequence 13, Appli
31	5	16.7	133	9	US-10-101-464A-485	Sequence 485, App
32	5	16.7	136	9	US-10-147-454-1	Sequence 1, Appli
33	5	16.7	137	9	US-10-147-454-3	Sequence 3, Appli
34	5	16.7	137	10	US-09-291-332-1	Sequence 1, Appli
35	5	16.7	139	9	US-10-147-454-2	Sequence 2, Appli
36	5	16.7	140	9	US-09-738-626-3519	Sequence 3519, Ap
37	5	16.7	152	12	US-10-094-214-4	Sequence 4, Appli
38	5	16.7	157	9	US-09-791-932-73	Sequence 73, Appli
39	5	16.7	159	9	US-10-112-793-16	Sequence 16, Appli
40	5	16.7	159	10	US-10-101-464A-650	Sequence 650, App
41	5	16.7	159	10	US-09-880-909-6	Sequence 6, Appli
42	5	16.7	159	10	US-09-884-987-6	Sequence 6, Appli
43	5	16.7	159	10	US-09-800-908-15	Sequence 15, Appli
44	5	16.7	162	10	US-09-925-297-616	Sequence 616, App
45	5	16.7	169	10	US-09-775-925-29	Sequence 29, Appli
46	5	16.7	169	10	US-09-847-519A-14	Sequence 14, Appli
47	5	16.7	170	12	US-10-109-885-3	Sequence 3, Appli
48	5	16.7	171	9	US-09-764-868-1095	Sequence 1095, Ap
49	5	16.7	191	10	US-09-878-454A-2	Sequence 2, Appli
50	5	16.7	191	12	US-10-109-885-2	Sequence 2, Appli
51	5	16.7	196	9	US-09-738-626-5550	Sequence 5550, Ap
52	5	16.7	198	9	US-09-727-855B-7	Sequence 7, Appli
53	5	16.7	211	9	US-10-270-877-46	Sequence 46, Appli
54	5	16.7	211	9	US-10-270-877-46	Sequence 46, Appli
55	5	16.7	219	9	US-10-270-837-46	Sequence 46, Appli
56	5	16.7	219	10	US-09-815-242-13061	Sequence 13061, A
57	5	16.7	239	10	US-09-905-810-1	Sequence 1, Appli
58	5	16.7	246	9	US-09-741-669-438	Sequence 438, App
59	5	16.7	249	9	US-10-037-677-2	Sequence 2, Appli
60	5	16.7	249	10	US-09-880-748-1160	Sequence 1160, Ap
61	5	16.7	249	10	US-09-905-810-2	Sequence 2, Appli
62	5	16.7	249	10	US-09-782-980-44	Sequence 44, Appli
63	5	16.7	250	12	US-10-052-817-4	Sequence 4, Appli
64	5	16.7	251	9	US-09-880-748-1688	Sequence 1688, Ap
65	5	16.7	251	10	US-09-821-831-4	Sequence 4, Appli
66	5	16.7	262	9	US-09-738-626-6778	Sequence 6778, App
67	5	16.7	273	10	US-10-101-464A-649	Sequence 649, App
68	5	16.7	273	10	US-09-742-454A-2	Sequence 2, Appli
69	5	16.7	275	10	US-09-846-808-8	Sequence 8, Appli
70	5	16.7	275	12	US-10-059-964-28	Sequence 28, Appli
71	5	16.7	279	12	US-10-059-964-58	Sequence 58, Appli
72	5	16.7	281	12	US-10-059-964-58	Sequence 58, Appli
73	5	16.7	282	9	US-10-051-643-134	Sequence 134, App
74	5	16.7	282	9	US-09-880-505-134	Sequence 134, App
75	5	16.7	284	10	US-09-894-998-41	Sequence 41, Appli
76	5	16.7	285	9	US-10-101-464A-692	Sequence 692, App
77	5	16.7	285	10	US-09-846-808-9	Sequence 9, Appli
78	5	16.7	285	12	US-10-059-964-30	Sequence 30, Appli
79	5	16.7	289	10	US-09-846-808-24	Sequence 24, Appli
80	5	16.7	291	10	US-09-846-808-18	Sequence 18, Appli
81	5	16.7	291	12	US-10-059-964-18	Sequence 18, Appli
82	5	16.7	293	10	US-09-846-808-13	Sequence 13, Appli
83	5	16.7	293	12	US-10-062-624-40	Sequence 40, Appli
84	5	16.7	293	12	US-10-059-964-44	Sequence 44, Appli
85	5	16.7	293	12	US-10-059-964-54	Sequence 54, Appli
86	5	16.7	295	10	US-09-846-808-5	Sequence 5, Appli
87	5	16.7	295	12	US-10-059-964-22	Sequence 22, Appli
88	5	16.7	296	12	US-10-059-964-56	Sequence 56, Appli
89	5	16.7	297	9	US-10-051-643-177	Sequence 177, App
90	5	16.7	297	9	US-09-880-505-177	Sequence 177, App
91	5	16.7	297	12	US-10-059-964-14	Sequence 14, Appli
92	5	16.7	298	9	US-09-813-153-212	Sequence 212, App

93	5	16.7	298	10	US-09-846-808-11	Sequence 11, Appl	166	5	16.7	471	9	US-09-880-505-172	Sequence 172, App
94	5	16.7	298	12	US-10-059-964-52	Sequence 52, Appl	167	5	16.7	479	9	US-10-108-605-57	Sequence 57, Appl
95	5	16.7	301	9	US-10-028-072-166	Sequence 166, App	168	5	16.7	484	10	US-09-846-5908-4	Sequence 4, Appl1
96	5	16.7	301	9	US-10-123-049-166	Sequence 166, App	169	5	16.7	491	9	US-10-237-684-34	Sequence 34, Appl
97	5	16.7	301	9	US-10-123-904-166	Sequence 166, App	170	5	16.7	491	9	US-10-230-163-34	Sequence 34, Appl
98	5	16.7	301	9	US-10-140-470-166	Sequence 166, App	171	5	16.7	491	9	US-10-218-631-34	Sequence 34, Appl
99	5	16.7	301	9	US-10-175-746-166	Sequence 166, App	172	5	16.7	491	9	US-10-230-338-34	Sequence 34, Appl
100	5	16.7	301	9	US-10-176-918-166	Sequence 166, App	173	5	16.7	491	9	US-10-230-414-34	Sequence 34, Appl
101	5	16.7	301	9	US-10-176-921-166	Sequence 166, App	174	5	16.7	493	10	US-09-742-684-12	Sequence 12, Appl
102	5	16.7	301	9	US-10-137-865-166	Sequence 166, App	175	5	16.7	500	10	US-09-925-300-1382	Sequence 1382, Ap
103	5	16.7	301	9	US-10-140-474-166	Sequence 166, App	176	5	16.7	504	9	US-09-905-370-1	Sequence 1, Appl1
104	5	16.7	301	9	US-10-142-431-166	Sequence 166, App	177	5	16.7	510	9	US-10-029-180-94	Sequence 94, Appl
105	5	16.7	301	9	US-10-143-114-166	Sequence 166, App	178	5	16.7	511	10	US-09-796-202-17	Sequence 17, Appl
106	5	16.7	301	9	US-10-140-002-166	Sequence 166, App	179	5	16.7	513	12	US-10-143-002-2	Sequence 2, Appl1
107	5	16.7	301	9	US-10-142-419-166	Sequence 166, App	180	5	16.7	516	9	US-10-026-741-48	Sequence 48, Appl
108	5	16.7	301	9	US-10-123-262-166	Sequence 166, App	181	5	16.7	519	10	US-09-756-551A-8	Sequence 8, Appl1
109	5	16.7	301	9	US-10-142-423-166	Sequence 166, App	182	5	16.7	521	10	US-09-815-242-11855	Sequence 11855, A
110	5	16.7	301	9	US-10-121-050-166	Sequence 166, App	183	5	16.7	530	9	US-10-028-072-130	Sequence 130, App
111	5	16.7	301	9	US-10-141-755-166	Sequence 166, App	184	5	16.7	530	9	US-10-121-049-130	Sequence 130, App
112	5	16.7	301	9	US-10-143-033-166	Sequence 166, App	185	5	16.7	530	9	US-10-123-004-130	Sequence 130, App
113	5	16.7	302	9	US-09-736-457-806	Sequence 806, App	186	5	16.7	530	9	US-10-140-470-130	Sequence 130, App
114	5	16.7	302	9	US-09-902-941-806	Sequence 806, App	187	5	16.7	530	9	US-10-175-746-130	Sequence 130, App
115	5	16.7	302	9	US-09-849-626-806	Sequence 806, App	188	5	16.7	530	9	US-10-176-918-130	Sequence 130, App
116	5	16.7	302	9	US-10-017-754-806	Sequence 806, App	189	5	16.7	530	9	US-10-176-921-130	Sequence 130, App
117	5	16.7	316	9	US-10-101-464A-941	Sequence 941, App	190	5	16.7	530	9	US-10-137-665-130	Sequence 130, App
118	5	16.7	321	9	US-10-012-507-1	Sequence 1, Appl1	191	5	16.7	530	9	US-10-140-474-130	Sequence 130, App
119	5	16.7	331	9	US-09-738-626-4960	Sequence 4960, Ap	192	5	16.7	530	9	US-10-142-431-130	Sequence 130, App
120	5	16.7	335	10	US-09-738-626-4330	Sequence 4330, Ap	193	5	16.7	530	9	US-10-143-114-130	Sequence 130, App
121	5	16.7	338	10	US-09-815-242-13457	Sequence 13457, A	194	5	16.7	530	9	US-10-140-002-130	Sequence 130, App
122	5	16.7	338	10	US-09-815-242-13645	Sequence 13645, A	195	5	16.7	530	9	US-10-142-419-130	Sequence 130, App
123	5	16.7	339	10	US-09-802-371-2	Sequence 2, Appl1	196	5	16.7	530	9	US-10-123-662-130	Sequence 130, App
124	5	16.7	341	10	US-09-916-790-18	Sequence 18, Appl	197	5	16.7	530	9	US-10-142-423-130	Sequence 130, App
125	5	16.7	369	9	US-09-738-626-5658	Sequence 5658, Ap	198	5	16.7	530	9	US-10-121-050-130	Sequence 130, App
126	5	16.7	371	9	US-09-870-759-107	Sequence 107, App	199	5	16.7	530	9	US-10-141-755-130	Sequence 130, App
127	5	16.7	386	9	US-10-101-464A-802	Sequence 802, App	200	5	16.7	530	9	US-10-143-032-130	Sequence 130, App
128	5	16.7	394	9	US-09-736-457-805	Sequence 805, App	201	5	16.7	563	10	US-09-789-561-83	Sequence 83, Appl
129	5	16.7	394	9	US-09-736-457-827	Sequence 827, App	202	5	16.7	566	10	US-09-829-482-5	Sequence 5, Appl1
130	5	16.7	394	9	US-09-902-941-805	Sequence 805, App	203	5	16.7	598	10	US-09-875-811-12	Sequence 12, Appl
131	5	16.7	394	9	US-09-902-941-827	Sequence 827, App	204	5	16.7	605	10	US-09-875-811-8	Sequence 8, Appl1
132	5	16.7	394	9	US-09-849-626-805	Sequence 805, App	205	5	16.7	615	10	US-09-771-838A-2	Sequence 2, Appl1
133	5	16.7	394	9	US-09-849-626-827	Sequence 827, App	206	5	16.7	615	10	US-09-815-242-5211	Sequence 5211, Ap
134	5	16.7	394	9	US-10-017-754-805	Sequence 805, App	207	5	16.7	621	10	US-09-875-811-4	Sequence 4, Appl1
135	5	16.7	394	9	US-10-017-754-827	Sequence 827, App	208	5	16.7	649	9	US-10-108-605-285	Sequence 285, App
136	5	16.7	396	9	US-09-987-107-33	Sequence 33, Appl	209	5	16.7	650	10	US-09-815-242-11306	Sequence 1306, A
137	5	16.7	396	9	US-09-802-640-16	Sequence 16, Appl	210	5	16.7	650	10	US-09-875-811-13667	Sequence 13667, A
138	5	16.7	396	10	US-09-800-729-207	Sequence 207, App	211	5	16.7	656	10	US-09-875-811-2	Sequence 2, Appl
139	5	16.7	401	9	US-09-902-941-1817	Sequence 1917, Ap	212	5	16.7	666	10	US-09-942-446-2	Sequence 10, Appl
140	5	16.7	401	9	US-09-849-626-1917	Sequence 1917, Ap	213	5	16.7	663	10	US-09-875-811-6	Sequence 6, Appl1
141	5	16.7	401	9	US-10-017-754-1917	Sequence 1917, Ap	214	5	16.7	665	9	US-09-533-029-76	Sequence 76, Appl
142	5	16.7	406	10	US-09-924-256A-25	Sequence 25, Appl	215	5	16.7	679	10	US-09-875-811-2	Sequence 2, Appl1
143	5	16.7	419	10	US-09-741-669-415	Sequence 415, App	216	5	16.7	682	10	US-09-771-838A-3	Sequence 3, Appl1
144	5	16.7	421	10	US-09-742-954-14	Sequence 14, Appl	217	5	16.7	682	10	US-09-079-892-1	Sequence 1, Appl1
145	5	16.7	425	10	US-09-813-398-32	Sequence 32, Appl	218	5	16.7	715	9	US-10-101-664A-924	Sequence 924, App
146	5	16.7	425	10	US-09-748-537-14	Sequence 14, Appl	219	5	16.7	742	9	US-10-108-605-203	Sequence 203, App
147	5	16.7	425	10	US-09-821-831-2	Sequence 2, Appl1	220	5	16.7	774	9	US-10-162-706-5	Sequence 5, Appl1
148	5	16.7	427	8	US-08-681-219-26	Sequence 26, Appl	221	5	16.7	790	10	US-09-801-368-184	Sequence 184, App
149	5	16.7	427	10	US-09-826-212-5	Sequence 5, Appl1	222	5	16.7	797	9	US-10-066-443-2	Sequence 2, Appl1
150	5	16.7	427	10	US-09-826-212-5	Sequence 5, Appl1	223	5	16.7	797	10	US-09-066-236-2	Sequence 2, Appl1
151	5	16.7	427	10	US-09-748-537-13	Sequence 13, Appl	224	5	16.7	798	9	US-10-066-443-5	Sequence 5, Appl1
152	5	16.7	432	9	US-09-738-626-4678	Sequence 4678, App	225	5	16.7	798	10	US-09-900-236-5	Sequence 5, Appl1
153	5	16.7	433	10	US-09-801-368-226	Sequence 226, App	226	5	16.7	807	10	US-09-847-046-2	Sequence 2, Appl1
154	5	16.7	445	9	US-09-738-626-6951	Sequence 6951, Ap	227	5	16.7	838	10	US-09-894-998-45	Sequence 45, Appl
155	5	16.7	445	9	US-10-067-974-12	Sequence 12, Appl	228	5	16.7	853	9	US-10-003-035-33	Sequence 33, Appl
156	5	16.7	445	9	US-10-226-136-20	Sequence 20, Appl	229	5	16.7	856	10	US-09-476-242-1	Sequence 1, Appl1
157	5	16.7	449	9	US-09-738-626-6150	Sequence 6150, App	230	5	16.7	861	10	US-10-026-741-103	Sequence 103, App
158	5	16.7	450	10	US-09-896-720-2	Sequence 2, Appl1	231	5	16.7	861	10	US-09-815-242-11152	Sequence 11152, A
159	5	16.7	455	9	US-09-756-854-4	Sequence 4, Appl1	232	5	16.7	869	10	US-09-815-242-10623	Sequence 21, Appl
160	5	16.7	455	9	US-10-041-574-4	Sequence 4, Appl1	233	5	16.7	871	10	US-09-886-468-21	Sequence 21, Appl
161	5	16.7	455	9	US-10-051-643-121	Sequence 121, App	234	5	16.7	893	9	US-10-014-436-4	Sequence 4, Appl1
162	5	16.7	455	9	US-09-880-505-121	Sequence 121, App	235	5	16.7	908	10	US-09-815-242-11847	Sequence 11847, A
163	5	16.7	457	9	US-10-124-601-2	Sequence 2, Appl1	236	5	16.7	911	10	US-09-828-423-4	Sequence 4, Appl1
164	5	16.7	459	9	US-09-746-660A-44	Sequence 44, Appl	237	5	16.7	950	10	US-09-815-242-11271	Sequence 11271, A
165	5	16.7	471	9	US-10-051-643-172	Sequence 172, App	238	5	16.7	951	10	US-09-815-242-10465	Sequence 10465, A

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241	5	16.7	969	10	US-09-118-276-2	Sequence 2, Appl	314	4	13.3	11	10	US-09-758-128-19	Sequence 19, Appl
242	5	16.7	980	10	US-09-118-276-11	Sequence 11, Appl	315	4	13.3	11	10	US-09-758-128-22	Sequence 22, Appl
243	5	16.7	1050	10	US-09-866-562-38	Sequence 38, Appl	316	4	13.3	11	10	US-09-758-128-25	Sequence 25, Appl
244	5	16.7	1101	9	US-10-003-035-53	Sequence 53, Appl	317	4	13.3	11	10	US-09-758-128-28	Sequence 28, Appl
245	5	16.7	1186	9	US-10-003-035-55	Sequence 55, Appl	318	4	13.3	12	10	US-09-982-172-201	Sequence 201, App
246	5	16.7	1198	9	US-09-975-119-405	Sequence 405, Appl	319	4	13.3	12	10	US-09-982-172-249	Sequence 249, App
247	5	16.7	1211	10	US-09-801-574-60	Sequence 60, Appl	320	4	13.3	13	9	US-09-764-868-1241	Sequence 1241, Ap
248	5	16.7	1285	10	US-09-925-301-1394	Sequence 1394, Ap	321	4	13.3	13	9	US-09-955-999-121	Sequence 121, App
249	5	16.7	1422	8	US-08-424-5508-86	Sequence 86, Appl	322	4	13.3	13	10	US-09-950-313-41	Sequence 41, Appl
250	5	16.7	1474	10	US-09-873-403-5	Sequence 5, Appl	323	4	13.3	14	9	US-09-229-551A-16	Sequence 16, Appl
251	5	16.7	1474	12	US-10-052-817-2	Sequence 2, Appl	324	4	13.3	14	10	US-09-879-936-7	Sequence 7, Appl
252	5	16.7	1531	10	US-09-876-889-347	Sequence 347, App	325	4	13.3	15	1	US-08-464-563-13	Sequence 19, Appl
253	5	16.7	1531	10	US-09-998-598-2593	Sequence 2593, Ap	326	4	13.3	16	10	US-09-770-940-14	Sequence 14, Appl
254	5	16.7	1713	10	US-09-737-149-27	Sequence 27, Appl	327	4	13.3	16	10	US-09-150-940B-7	Sequence 7, Appl
255	5	16.7	1938	9	US-10-014-436-2	Sequence 2, Appl	328	4	13.3	17	9	US-09-986-480-407	Sequence 407, App
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257	5	16.7	2045	9	US-09-736-968A-109	Sequence 109, App	330	4	13.3	18	10	US-09-789-561-161	Sequence 161, App
258	5	16.7	2045	10	US-09-736-969A-95	Sequence 95, Appl	331	4	13.3	19	9	US-09-963-339-10	Sequence 10, Appl
259	5	16.7	2045	9	US-09-736-960-92	Sequence 92, Appl	332	4	13.3	19	9	US-10-062-710-113	Sequence 113, App
260	5	16.7	2047	9	US-09-736-968A-2	Sequence 2, Appl	333	4	13.3	19	10	US-09-799-576A-13	Sequence 13, Appl
261	5	16.7	2227	9	US-10-104-966-12	Sequence 12, Appl	334	4	13.3	19	10	US-09-799-540-13	Sequence 13, Appl
262	5	16.7	2227	9	US-10-135-988-2	Sequence 2, Appl	335	4	13.3	19	10	US-09-799-608-13	Sequence 13, Appl
263	5	16.7	2227	9	US-10-135-988-4	Sequence 4, Appl	336	4	13.3	19	12	US-10-059-964-63	Sequence 63, Appl
264	5	16.7	2227	9	US-10-135-988-6	Sequence 6, Appl	337	4	13.3	20	9	US-10-038-612-47	Sequence 47, Appl
265	5	16.7	2227	10	US-09-929-955-12	Sequence 12, Appl	338	4	13.3	20	9	US-09-992-982-1	Sequence 1, Appl
266	5	16.7	2383	10	US-09-912-020-302	Sequence 302, App	339	4	13.3	20	10	US-09-815-626-10	Sequence 10, Appl
267	5	16.7	2437	10	US-09-815-242-5834	Sequence 5834, Ap	340	4	13.3	21	9	US-10-038-612-117	Sequence 117, App
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269	5	16.7	2923	10	US-09-788-711A-4	Sequence 4, Appl	342	4	13.3	22	9	US-10-097-065-577	Sequence 577, App
270	5	16.7	2956	10	US-09-788-711A-2	Sequence 2, Appl	343	4	13.3	22	9	US-10-099-574A-117	Sequence 117, App
271	5	16.7	3014	10	US-09-737-149-25	Sequence 25, Appl	344	4	13.3	22	10	US-09-953-510-23	Sequence 23, Appl
272	5	16.7	3034	10	US-09-737-149-25	Sequence 25, Appl	345	4	13.3	22	10	US-09-867-852-155	Sequence 155, App
273	5	16.7	3158	10	US-09-737-149-30	Sequence 30, Appl	346	4	13.3	23	9	US-10-037-296-6	Sequence 6, Appl
274	5	16.7	3158	10	US-09-815-242-12611	Sequence 12611, A	347	4	13.3	23	9	US-09-782-816A-1	Sequence 1, Appl
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276	5	16.7	3354	9	US-10-160-758-12	Sequence 12, Appl	349	4	13.3	23	10	US-09-864-761-37623	Sequence 37623, A
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279	5	16.7	6281	10	US-09-815-242-12396	Sequence 12396, A	352	4	13.3	24	9	US-09-986-480-224	Sequence 24, App
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283	4	13.3	6	9	US-09-809-391-622	Sequence 622, Appl	356	4	13.3	25	9	US-09-774-639-311	Sequence 311, App
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291	4	13.3	9	10	US-09-753-831-7	Sequence 7, Appl	364	4	13.3	26	10	US-10-091-504-747	Sequence 747, App
292	4	13.3	10	9	US-10-025-222A-31	Sequence 31, Appl	365	4	13.3	27	9	US-09-864-761-46828	Sequence 46828, A
293	4	13.3	10	10	US-09-056-160B-91	Sequence 91, Appl	366	4	13.3	27	10	US-09-864-761-47610	Sequence 47610, A
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302	4	13.3	11	9	US-09-758-198-19	Sequence 19, Appl	375	4	13.3	31	9	US-09-955-899-138	Sequence 18, App
303	4	13.3	11	9	US-09-758-198-22	Sequence 22, Appl	376	4	13.3	31	10	US-09-730-772-19	Sequence 19, Appl
304	4	13.3	11	9	US-09-758-198-25	Sequence 25, Appl	377	4	13.3	31	10	US-09-730-772-23	Sequence 23, Appl
305	4	13.3	11	9	US-09-758-198-28	Sequence 28, Appl	378	4	13.3	31	10	US-09-735-849-19	Sequence 19, Appl
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307	4	13.3	11	9	US-09-861-661-16	Sequence 16, Appl	380	4	13.3	31	10	US-09-964-130-65	Sequence 9, Appl
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388	4	13.3	34	9	US-09-776-724A-278	Sequence 278, Appl
389	4	13.3	34	10	US-09-776-801A-39	Sequence 39, Appl
390	4	13.3	35	9	US-10-223-047-24	Sequence 24, Appl
391	4	13.3	35	9	US-09-855-698-8	Sequence 8, Appl1
392	4	13.3	35	10	US-09-776-490-8	Sequence 8, Appl1
393	4	13.3	35	10	US-09-776-491-8	Sequence 8, Appl1
394	4	13.3	35	10	US-09-150-947B-8	Sequence 8, Appl1
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396	4	13.3	35	10	US-09-864-761-44100	Sequence 44100, A
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398	4	13.3	36	9	US-10-050-704-293	Sequence 293, Appl
399	4	13.3	36	10	US-09-864-761-45243	Sequence 45243, A
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403	4	13.3	37	10	US-09-764-869-665	Sequence 665, Appl
404	4	13.3	38	9	US-09-776-724A-249	Sequence 249, Appl
405	4	13.3	38	10	US-10-196-107A-65	Sequence 65, Appl1
406	4	13.3	38	10	US-09-374-671-65	Sequence 65, Appl1
407	4	13.3	38	10	US-09-864-761-43271	Sequence 43271, A
408	4	13.3	38	10	US-09-764-898-171	Sequence 171, Appl
409	4	13.3	38	10	US-09-764-877-2002	Sequence 2002, Ap
410	4	13.3	39	9	US-09-983-802-572	Sequence 572, Appl
411	4	13.3	39	12	US-10-042-417-22	Sequence 22, Appl
412	4	13.3	40	9	US-09-994-595-119	Sequence 119, Appl
413	4	13.3	40	9	US-10-000-256A-179	Sequence 179, Appl
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415	4	13.3	41	9	US-09-966-422B-16	Sequence 16, Appl1
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421	4	13.3	42	10	US-09-864-761-48554	Sequence 48554, A
422	4	13.3	42	10	US-09-764-877-1278	Sequence 1278, Ap
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430	4	13.3	43	10	US-09-864-761-43463	Sequence 43463, A
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433	4	13.3	44	9	US-09-989-919-94	Sequence 94, Appl1
434	4	13.3	44	9	US-09-983-802-359	Sequence 359, Appl
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459	4	13.3	50	9	US-09-796-692-747	Sequence 747, Appl
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468	4	13.3	51	10	US-09-764-869-1204	Sequence 1204, Ap
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487	4	13.3	54	9	US-10-016-634A-130	Sequence 130, Appl
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533	4	13.3	64	10	US-09-864-761-46304	Sequence 46304, A	606	4	13.3	80	10	US-09-764-877-1226	Sequence 1226, Ap
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547	4	13.3	69	9	US-10-053-758-17	Sequence 17, Appl	620	4	13.3	87	10	US-09-867-550-648	Sequence 648, App
548	4	13.3	69	9	US-10-012-542-198	Sequence 198, App	621	4	13.3	87	10	US-09-815-248-4	Sequence 4, Appl1
549	4	13.3	69	9	US-10-054-295-17	Sequence 17, Appl	622	4	13.3	87	10	US-09-815-248-13	Sequence 13, Appl
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551	4	13.3	69	9	US-10-092-154-689	Sequence 689, App	624	4	13.3	88	10	US-09-905-243-64	Sequence 64, Appl
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553	4	13.3	69	10	US-09-764-847-689	Sequence 689, App	626	4	13.3	89	9	US-09-738-626-4439	Sequence 4439, App
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559	4	13.3	70	10	US-09-864-761-45440	Sequence 45440, A	632	4	13.3	89	10	US-09-764-860-472	Sequence 472, App
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565	4	13.3	71	10	US-09-864-761-45726	Sequence 45726, A	638	4	13.3	91	10	US-09-867-550-418	Sequence 418, App
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572	4	13.3	72	9	US-09-974-879-164	Sequence 164, App	645	4	13.3	94	10	US-09-764-853-716	Sequence 716, App
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588	4	13.3	76	9	US-10-083-357-703	Sequence 703, App	661	4	13.3	96	10	US-09-764-847-792	Sequence 792, App
589	4	13.3	76	10	US-09-864-761-36343	Sequence 36343, A	662	4	13.3	96	10	US-09-716-724A-210	Sequence 210, App
590	4	13.3	76	10	US-09-864-761-36963	Sequence 36963, A	663	4	13.3	97	9	US-09-738-626-4164	Sequence 4164, Appl
591	4	13.3	76	10	US-09-864-761-39363	Sequence 39363, A	664	4	13.3	99	9	US-09-738-626-4651	Sequence 4651, Ap
592	4	13.3	77	9	US-10-091-504-1073	Sequence 1073, App	665	4	13.3	97	10	US-09-925-300-1380	Sequence 1380, App
593	4	13.3	77	10	US-09-864-761-38096	Sequence 38096, A	666	4	13.3	98	10	US-09-789-560-180	Sequence 180, App
594	4	13.3	77	10	US-09-764-869-1073	Sequence 1073, Ap	667	4	13.3	98	10	US-09-867-550-442	Sequence 442, App
595	4	13.3	78	9	US-10-102-806-672	Sequence 672, App	668	4	13.3	98	10	US-09-910-151-11	Sequence 11, Appl
596	4	13.3	78	10	US-09-764-887-271	Sequence 271, App	669	4	13.3	99	9	US-09-738-626-4164	Sequence 4164, Appl
597	4	13.3	78	10	US-09-867-550-1780	Sequence 1780, Ap	670	4	13.3	99	9	US-09-738-626-4651	Sequence 4651, Ap
598	4	13.3	79	10	US-09-864-761-47317	Sequence 47317, A	671	4	13.3	99	9	US-10-083-357-827	Sequence 827, App
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600	4	13.3	79	10	US-09-734-417-19	Sequence 19, Appl	673	4	13.3	99	10	US-09-764-877-1608	Sequence 1608, Ap
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678	4	13.3	101	9	US-10-097-065-576	Sequence 576, Appl	751	4	13.3	113	9	US-09-994-595-157	Sequence 157, App
679	4	13.3	101	10	US-09-840-787-37	Sequence 37, Appl	752	4	13.3	113	9	US-10-101-464A-579	Sequence 579, App
680	4	13.3	101	10	US-09-841-132-516	Sequence 516, App	753	4	13.3	113	10	US-09-294-121A-84	Sequence 84, Appl
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682	4	13.3	101	10	US-09-751-1008-89	Sequence 89, Appl	755	4	13.3	113	10	US-09-815-248-9	Sequence 9, Appl
683	4	13.3	102	9	US-10-001-857-189	Sequence 189, Appl	756	4	13.3	113	10	US-09-899-082A-84	Sequence 84, Appl
684	4	13.3	102	10	US-09-925-301-1512	Sequence 1512, App	757	4	13.3	113	10	US-09-764-871-1517	Sequence 1547, App
685	4	13.3	102	10	US-09-841-132-586	Sequence 586, App	758	4	13.3	113	10	US-09-263-959-318	Sequence 318, App
686	4	13.3	103	9	US-09-974-298-4	Sequence 4, Appl	759	4	13.3	114	9	US-10-102-102-12	Sequence 12, Appl
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689	4	13.3	104	9	US-09-746-783-206	Sequence 206, App	762	4	13.3	114	9	US-10-230-163-52	Sequence 52, Appl
690	4	13.3	104	10	US-09-893-737-64	Sequence 64, Appl	763	4	13.3	114	9	US-10-218-631-52	Sequence 52, Appl
691	4	13.3	104	10	US-09-751-1008-72	Sequence 72, Appl	764	4	13.3	114	9	US-10-230-338-52	Sequence 52, Appl
692	4	13.3	105	9	US-10-187-088-9	Sequence 9, Appl	765	4	13.3	114	9	US-10-230-414-52	Sequence 52, Appl
693	4	13.3	105	9	US-10-043-487-314	Sequence 314, App	766	4	13.3	114	10	US-09-860-351-5	Sequence 5, Appl
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695	4	13.3	105	10	US-09-764-870-357	Sequence 357, App	768	4	13.3	114	10	US-09-925-300-1551	Sequence 1551, App
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998 4 13.3 147 10 US-10-043-487-325 Sequence 325, App
999 4 13.3 147 10 US-09-811-284-172 Sequence 172, App
1000 4 13.3 148 9 US-09-736-457-338 Sequence 338, App

ALIGNMENTS

RESULT 1
US-09-987-190-2
Sequence 2, Application US/09987190
Patent No. US20020058293A1
GENERAL INFORMATION:
APPLICANT: TAKESAKO, Kazutosh
APPLICANT: MIZUTANI, Shigetoshi
APPLICANT: ENDO, Masahiro
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
FILE REFERENCE: 1422-0502P
CURRENT APPLICATION NUMBER: US/09/987,190
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/262,856
PRIOR FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 30
TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: Unsure
LOCATION: (1)..(30)
OTHER INFORMATION: any Xaa = any amino acid, unknown or other
US-09-987-190-2

Query Match 90.0%; Score 27; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 3,46-22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 KYSLPELDYFSATEPYISGOINEIXYT 28
Db 1 KISLPELDYFSATEPYISGOINEIXYT 28

RESULT 2
US-09-864-761-43011
Sequence 43011, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenhseng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43011
LENGTH: 50
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007510.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.76
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.61
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.58
OTHER INFORMATION: EST HUMAN HIT: BF667240.1, EVALUATE 1.30e+00
OTHER INFORMATION: SWISSPROT HIT: P87145, EVALUATE 6.00e+00
US-09-864-761-43011

Query Match 20.0%; Score 6; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 8,7; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Cy 12 SATPEY 17

|||||
Db 10 SATPEY 15

RESULT 3

US-10-078-929-24

Sequence 24, Application US/10078929

Patent No. US20020152497A1

GENERAL INFORMATION:

APPLICANT: Rafalski, Antoni

APPLICANT: Miao, Guo-Hua

APPLICANT: Sakai, Hajime

APPLICANT: Farnodu, Omoayo O.

APPLICANT: Odeli, Joan T.

APPLICANT: Meyers, Blake

APPLICANT: Thorpe, Catherine

APPLICANT: Meng, Zude

TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in

TITLE OF INVENTION: Stress Response

FILE REFERENCE: B1357 US NA

CURRENT FILING DATE: US/10/078,929

CURRENT FILING DATE: 2002-02-19

PRIOR APPLICATION NUMBER: 09/566,394

PRIOR FILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: 60/133038

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: 60/133042

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: 60/133427

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133437

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133428

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133438

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133436

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133667

PRIOR FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 208

SOFTWARE: Microsoft Office 97

SEQ ID NO 24

LENGTH: 65

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

NAME/KEY: UNSURE

LOCATION: (60)

NAME/KEY: UNSURE

LOCATION: (63)

US-10-078-929-24

Query Match 20.0%; Score 6; DB 12; Length 65;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PELDYE 10

Db 44 PELDYE 49

RESULT 4

US-09-981-876-166

Sequence 166, Application US/09981876

Patent No. US2002016469A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 70 Human Secreted Proteins

FILE REFERENCE: P2001P1

CURRENT APPLICATION NUMBER: US/09/981,876

CURRENT FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: 09/148,545
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/038,621
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,161
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,626
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,334
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,336
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,163
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/047,615
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,600
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,597
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,502
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,633
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,583
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,617
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,618
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,503
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,592
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,581
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,584
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,500
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,587
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,492
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,598
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,613
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,582
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,596
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,612
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,632
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,601
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/043,580
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,568
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,314
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,569
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,311
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,671

;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,674
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,669
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,312
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,313
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,672
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,315
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/048,974
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/056,886
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,877
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,889
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,893
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,630
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,878
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,662
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,872
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,882
;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,880
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,894
;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,636
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,874
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,910
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,864
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,631
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,845
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,892
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/047,595
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/057,761
;; PRIOR FILING DATE: 05-Sep-1997
;; PRIOR APPLICATION NUMBER: 60/047,599
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,588
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,585
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,586
;; PRIOR FILING DATE: 1997-05-23

;; PRIOR APPLICATION NUMBER: 60/047,590
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,594
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,589
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,593
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,614
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/043,578
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,576
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/047,501
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/043,670
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/056,632
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,664
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,876
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,881
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,909
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,875
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,862
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,887
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,908
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/048,964
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/057,650
;; PRIOR FILING DATE: 1997-09-05
;; PRIOR APPLICATION NUMBER: 60/056,884
;; PRIOR FILING DATE: 1997-08-22
;; NUMBER OF SEQ ID NOS: 280
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 166
;; LENGTH: 81

Query Match 20.0%; Score 6; DB 9; Length 81;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ATEPYI 18
DB 71 ATEPYI 76

RESULT 5
US-09-148-545-166
; Sequence 166, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001PI
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
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EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 166
LENGTH: 81

Query Match 20.0%; Score 6; DB 9; Length 81;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 ATEPYI 18
Db 71 ATEPYI 76

US-10-078-929-26
Sequence 26, Application US/10078929
Patent No. US20020152497A1
GENERAL INFORMATION:
APPLICANT: Rafalski, Antoni
APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Carl
APPLICANT: Sakai, Hajime
APPLICANT: Pamodu, Omolayo O.
APPLICANT: Odell, Joan T.
APPLICANT: Meyers, Blake
APPLICANT: Thorpe, Catherine
APPLICANT: Meng, Zude
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
TITLE OF INVENTION: Stress Response
FILE REFERENCE: B91357 US NA
CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042

PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133428
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/137667
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Microsoft Office 97
SEQ ID NO 26
LENGTH: 98
TYPE: PRT
ORGANISM: Glycine max
US-10-078-929-26

Query Match 20.0%; Score 6; DB 12; Length 98;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PELDYE 10
Db 64 PELDYE 69

US-09-840-787-49
Sequence 49, Application US/09840787
Patent No. US20020058264A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
Shah, Purvi
Au-Young, Janice
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/840,787
FILING DATE: 23-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/518,865
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 49:

ORGANISM: *Candida albicans*

LENGTH: 200

ORGANISM: *Candida albicans*

TYPE: PRT
ORGANISM: Corynebacterium melassecola
OTHER INFORMATION: ATCC 17965
US-09-818-564-2

Query Match 20.0%; Score 6; DB 10; Length 200;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LPELDY 9
|||||
Db 6 LPELDY 11

RESULT 12
US-09-909-567B-47
Sequence 47, Application US/09090567B
Publication No. US20030022257A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto A.
APPLICANT: Nair, Manoj
APPLICANT: Chen, Seiyu

TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes

FILE REFERENCE: DEX-0214
CURRENT APPLICATION NUMBER: US/09/909,567B
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/219,834
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn version 3.1
SEQ ID NO 47

LENGTH: 1596
TYPE: PRT

ORGANISM: Homo sapien
US-09-909-567B-47

Query Match 20.0%; Score 6; DB 9; Length 1596;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SLEPDL 8
|||||
Db 1356 SLEPDL 1361

RESULT 13
US-09-813-153-211

Sequence 211, Application US/09813153
Publication No. US20030045459A1
GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 67 Human secreted proteins

FILE REFERENCE: P2023

CURRENT APPLICATION NUMBER: US/09/813,153

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US/09/363,044

PRIOR FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: 60/073,160

PRIOR FILING DATE: 1998-01-30

PRIOR APPLICATION NUMBER: 60/073,159

PRIOR FILING DATE: 1998-01-30

PRIOR APPLICATION NUMBER: 60/073,165

PRIOR FILING DATE: 1998-01-30

PRIOR APPLICATION NUMBER: 60/073,164

PRIOR FILING DATE: 1998-01-30

PRIOR APPLICATION NUMBER: 60/073,167

PRIOR FILING DATE: 1998-01-30

PRIOR APPLICATION NUMBER: 60/073,162

PRIOR FILING DATE: 1998-01-30

PRIOR APPLICATION NUMBER: 60/073,161

PRIOR FILING DATE: 1998-01-30

PRIOR APPLICATION NUMBER: 60/073,170

PRIOR FILING DATE: 1998-01-30

PRIOR APPLICATION NUMBER: 60/073,170

PRIOR FILING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 298
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 211
LENGTH: 26
TYPE: PRT
ORGANISM: Homo sapiens
US-09-813-153-211

Query Match 16.7%; Score 5; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SLEPDL 7
|||||
Db 13 SLEPDL 17

RESULT 14
US-09-864-761-48159
Sequence 48159, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: Aeonica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

SEQ ID NO 48159

LENGTH: 33

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: MAP TO AC009303.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.7
OTHER INFORMATION: EST_HUMAN HIT: A1902949.1, EVALU6 6.00e-11
US-09-864-761-48159

Query Match 16.7%; Score 5; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSLPE 6
Db 29 YSLPE 33

RESULT 15
US-09-810-310-2
Sequence 2, Application US/09810310
Patent No. US2002004948A1
GENERAL INFORMATION:
APPLICANT: Khleif, Samir N.
APPLICANT: Bezofsky, Jay A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
FILE REFERENCE: 15280-415100US
CURRENT APPLICATION NUMBER: US/09/810,310
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/189,396
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: HIV PEPTIDE
OTHER INFORMATION: ANTIGEN
US-09-810-310-2

Query Match 16.7%; Score 5; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ISGOI 22
Db 19 ISGOI 23

RESULT 16
US-09-810-310-9
Sequence 9, Application US/09810310
Patent No. US20020044948A1
GENERAL INFORMATION:
APPLICANT: Khleif, Samir N.
APPLICANT: Bezofsky, Jay A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
FILE REFERENCE: 15280-415100US
CURRENT APPLICATION NUMBER: US/09/810,310
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/189,396
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: HIV PEPTIDE
OTHER INFORMATION: ANTIGEN
US-09-810-310-9

Query Match 16.7%; Score 5; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ISGOI 22
Db 19 ISGOI 23

RESULT 17
US-09-864-761-34370
Sequence 34370, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine Vers. 1.1
SEQ ID NO 34370
LENGTH: 39
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007914.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EST_HUMAN HIT: AV659020.1, EVALU6 6.006-12
US-09-864-761-34370

Query Match 16.7%; Score 5; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SLEP 7
|||
Db 16 SLEP 20

RESULT 18
US-09-764-904-63
Sequence 63, Application US/09764904
Patent No. US20020173454A1
GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA122
CURRENT APPLICATION NUMBER: US/09/764,904
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-904-63

Query Match 16.7%; Score 5; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SLEP 7
|||
Db 8 SLEP 12

RESULT 19
US-10-091-548-63

Sequence 63, Application US/10091548
Publication No. US20030049703A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA122C1
CURRENT APPLICATION NUMBER: US/10/091,548
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 137
Prior application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
US-10-091-548-63

Query Match 16.7%; Score 5; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SLEP 7
|||
Db 8 SLEP 12

RESULT 20
US-09-764-860-581
Sequence 581, Application US/09764860
Patent No. US20020094953A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1198
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 581
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-860-581

Query Match 16.7%; Score 5; DB 10; Length 52;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SLEP 7
|||
Db 8 SLEP 12

RESULT 21
US-09-864-761-34543
Sequence 34543, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687

```
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34543
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005089.2
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.73
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
; OTHER INFORMATION: SWISSPROT HIT: Q84133, EVALU = 5.20e-01
; OTHER INFORMATION: EST_HUMAN HIT: BE258324.1, EVALU = 3.00e-32
; US-09-864-761-34543
```

```
Query Match 16.7%; Score 5; DB 10; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KYSLP 5
Db 49 KYSLP 53
```

```
RESULT 22
US-09-867-550-424
; Sequence 424, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehrtan, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells and
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 424
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-867-550-424
```

```
Query Match 16.7%; Score 5; DB 10; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 SLEPL 7
Db 65 SLEPL 69
```

```
RESULT 23
US-09-864-761-47808
; Sequence 47808, Application US/09864761
```

```
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47808
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011472.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.75
; OTHER INFORMATION: EST HUMAN HIT: BF36965.1, EVALU = 1.00e-05
; OTHER INFORMATION: SWISSPROT HIT: Q06639, EVALU = 2.50e+00
; US-09-864-761-47808
```

```
Query Match 16.7%; Score 5; DB 10; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 18 ISGQI 22
Db 73 ISGQI 77
```

```
RESULT 24
US-09-764-887-257
; Sequence 257, Application US/09764887
; Patent No. US20020042096A1
```

```
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA13
CURRENT APPLICATION NUMBER: US/09/764,887
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 658
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 257
LENGTH: 88
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (87)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-887-257
```

```
Query Match      16.7%; Score 5; DB 10; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 SATPE 16
      |||||
Db      29 SATPE 33
```

```
RESULT 25
US-09-864-761-40079
Sequence 40079, Application US/09864761
Patent No. US20020048763A1
```

```
GENERAL INFORMATION:
```

```
APPLICANT: Penn, Sharon G.
APPLICANT: Hamel, David K.
APPLICANT: Chen, Wensheng
```

```
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
```

```
CURRENT APPLICATION NUMBER: US/09/864,761
```

```
CURRENT FILING DATE: 2001-05-23
```

```
PRIOR APPLICATION NUMBER: US 60/180,312
```

```
PRIOR FILING DATE: 2000-02-04
```

```
PRIOR APPLICATION NUMBER: US 60/207,456
```

```
PRIOR FILING DATE: 2000-05-26
```

```
PRIOR APPLICATION NUMBER: US 09/632,366
```

```
PRIOR FILING DATE: 2000-08-03
```

```
PRIOR APPLICATION NUMBER: GB 24263.6
```

```
PRIOR FILING DATE: 2000-10-04
```

```
PRIOR APPLICATION NUMBER: US 60/236,359
```

```
PRIOR FILING DATE: 2000-09-27
```

```
PRIOR APPLICATION NUMBER: PCT/US01/00666
```

```
PRIOR FILING DATE: 2001-01-30
```

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PRIOR APPLICATION NUMBER: PCT/US01/00667
```

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PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00664
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PRIOR FILING DATE: 2001-01-30
```

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PRIOR APPLICATION NUMBER: PCT/US01/00669
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PRIOR FILING DATE: 2001-01-30
```

```
PRIOR APPLICATION NUMBER: PCT/US01/00665
```

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PRIOR FILING DATE: 2001-01-30
```

```
PRIOR APPLICATION NUMBER: PCT/US01/00668
```

```
PRIOR FILING DATE: 2001-01-30
```

```
PRIOR APPLICATION NUMBER: PCT/US01/00663
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```
PRIOR FILING DATE: 2001-01-30
```

```
PRIOR APPLICATION NUMBER: PCT/US01/00662
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```
PRIOR FILING DATE: 2001-01-30
```

```
PRIOR APPLICATION NUMBER: PCT/US01/00661
```

```
PRIOR FILING DATE: 2001-01-30
```

```
PRIOR APPLICATION NUMBER: PCT/US01/00670
```

```
PRIOR FILING DATE: 2001-01-30
```

```
PRIOR APPLICATION NUMBER: US 60/234,687
```

```
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO: 40079
LENGTH: 91
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004615.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HUMAN HIT: AUI18557.1, EVALUE 2.00e-19
OTHER INFORMATION: SWISSPROT HIT: Q13591, EVALUE 2.00e-50
US-09-864-761-40079
```

```
Query Match      16.7%; Score 5; DB 10; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 LPELD 8
      |||||
Db      76 LPELD 80
```

```
RESULT 26
US-10-101-464A-651
Sequence 651, Application US/10101464A
Publication No. US20030046728A1
```

```
GENERAL INFORMATION:
```

```
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
```

```
TITLE OF INVENTION: Compositions Isolated from Plant Cells
FILE REFERENCE: 11000.1020C2
```

```
CURRENT APPLICATION NUMBER: US/10/101,464A
```

```
CURRENT FILING DATE: 2002-03-18
```

```
PRIOR APPLICATION NUMBER: 09/704,302
```

```
PRIOR FILING DATE: 2000-11-01
```

```
PRIOR APPLICATION NUMBER: 09/228,986
```

```
PRIOR FILING DATE: 1999-01-12
```

```
PRIOR APPLICATION NUMBER: 60/162,866
```

```
PRIOR FILING DATE: 1999-11-01
```

```
PRIOR APPLICATION NUMBER: PCT/US00/00724
```

```
PRIOR FILING DATE: 2000-01-11
```

```
NUMBER OF SEQ ID NOS: 989
```

```
SOFTWARE: FastSeq for Windows Version 4.0
```

```
SEQ ID NO: 651
```

```
LENGTH: 97
```

```
TYPE: PRT
```

```
ORGANISM: Eucalyptus grandis
```

```
US-10-101-464A-651
```

```
Query Match      16.7%; Score 5; DB 9; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 SLPPEL 7
      |||||
Db      90 SLPPEL 94
```

```
RESULT 27
US-09-764-877-1863
```

```
; Sequence 1863, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1863
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (47)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (68)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (95)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1863
```

```
Query Match          16.7%; Score 5; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 3 SLPBL 7
    ||||
Db 14 SLPBL 18
```

```
RESULT 28
US-10-052-817-6
; Sequence 6, Application US/10052817
; Patent No. US20020114792A1
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora
; APPLICANT: Saunders, Aleister J.
; TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 0609 4460005
; CURRENT APPLICATION NUMBER: US/10/052,817
; CURRENT FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: 09/241,606
; PRIOR FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: 09/148,503
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/093,297
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-052-817-6
```

```
Query Match          16.7%; Score 5; DB 12; Length 111;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 3 SLPBL 7
    ||||
Db 80 SLPBL 84
```

RESULT 29

```
US-09-846-590B-2
; Sequence 2, Application US/09846590B
; Patent No. US2002009801A1
; GENERAL INFORMATION:
; APPLICANT: Falco, S. Carl
; APPLICANT: Farnodu, Lajo O.
; APPLICANT: Orozco, Emil M. Jr.
; TITLE OF INVENTION: Amino Acid Decarboxylases
; FILE REFERENCE: BB-1237
; CURRENT APPLICATION NUMBER: US/09/846,590B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 60/099,493
; PRIOR FILING DATE: 1998-09-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Catalpa speciosa
US-09-846-590B-2
```

```
Query Match          16.7%; Score 5; DB 10; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 4 LPELD 8
    ||||
Db 48 LPELD 52
```

```
RESULT 30
US-09-164-615-13
; Sequence 13, Application US/09164615B
; Patent No. US20020073442A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Settlege, Sharon
; TITLE OF INVENTION: Geminivirus Resistant Transgenic Plants
; FILE REFERENCE: 5051-433
; CURRENT APPLICATION NUMBER: US/09/164,615B
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 13
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Pepper huasteco virus
US-09-164-615-13
```

```
Query Match          16.7%; Score 5; DB 10; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 18 ISGOI 22
    ||||
Db 77 ISGOI 81
```

```
RESULT 31
US-10-101-464A-485
; Sequence 485, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
```

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; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 485
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-485
```

```
Query Match      16.7%; Score 5; DB 9; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      4 LPELD 8
      |||||
      83 LPELD 87
```

```
RESULT 32
US-10-147-454-1
; Sequence 1, Application US/10147454
; Publication No. US20020193308A1
; GENERAL INFORMATION:
; APPLICANT: NAKTINIS, Vytautas
; APPLICANT: CONCAS BENEVELLI, Daniela
; APPLICANT: BERRA, Bruno
; APPLICANT: COLOMBO, Irma
; APPLICANT: RONCHI, Severino
; APPLICANT: BARTORELLI, Alberto
; APPLICANT: BUMELIS, Viadas Algirdus
; TITLE OF INVENTION: Recombinant Protein and Its Use in Therapy and Diagnostics
; FILE REFERENCE: 0471-0273P
; CURRENT APPLICATION NUMBER: US/10/147,454
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Capra hircus
US-10-147-454-1
```

```
Query Match      16.7%; Score 5; DB 9; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      17 YISQ 21
      |||||
      DB      31 YISQ 35
```

```
RESULT 33
US-10-147-454-3
; Sequence 3, Application US/10147454
; Publication No. US20020193308A1
; GENERAL INFORMATION:
; APPLICANT: NAKTINIS, Vytautas
; APPLICANT: CONCAS BENEVELLI, Daniela
; APPLICANT: BERRA, Bruno
; APPLICANT: COLOMBO, Irma
; APPLICANT: RONCHI, Severino
; APPLICANT: BARTORELLI, Alberto
; APPLICANT: BUMELIS, Viadas Algirdus
; TITLE OF INVENTION: Recombinant Protein and Its Use in Therapy and Diagnostics
; FILE REFERENCE: 0471-0273P
; CURRENT APPLICATION NUMBER: US/10/147,454
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 9
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```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Capra hircus
US-10-147-454-3
```

```
Query Match      16.7%; Score 5; DB 9; Length 137;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      17 YISQ 21
      |||||
      DB      32 YISQ 36
```

```
RESULT 34
US-09-291-332-1
; Sequence 1, Application US/09291332A
; Patent No. US20010014471A1
; GENERAL INFORMATION:
; APPLICANT: NAKTINIS, Vytautas
; APPLICANT: CONCAS BENEVELLI, Daniela
; APPLICANT: BERRA, Bruno
; APPLICANT: COLOMBO, Irma
; APPLICANT: RONCHI, Severino
; APPLICANT: BARTORELLI, Alberto
; APPLICANT: BUMELIS, Viadas
; TITLE OF INVENTION: Recombinant protein and its use in therapy and
; FILE REFERENCE: zetes15
; CURRENT APPLICATION NUMBER: US/09/291,332A
; CURRENT FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Capra hircus
US-09-291-332-1
```

```
Query Match      16.7%; Score 5; DB 10; Length 137;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      17 YISQ 21
      |||||
      DB      32 YISQ 36
```

```
RESULT 35
US-10-147-454-2
; Sequence 2, Application US/10147454
; Publication No. US20020193308A1
; GENERAL INFORMATION:
; APPLICANT: NAKTINIS, Vytautas
; APPLICANT: CONCAS BENEVELLI, Daniela
; APPLICANT: BERRA, Bruno
; APPLICANT: COLOMBO, Irma
; APPLICANT: RONCHI, Severino
; APPLICANT: BARTORELLI, Alberto
; APPLICANT: BUMELIS, Viadas Algirdus
; TITLE OF INVENTION: Recombinant Protein and Its Use in Therapy and Diagnostics
; FILE REFERENCE: 0471-0273P
; CURRENT APPLICATION NUMBER: US/10/147,454
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Capra hircus
US-10-147-454-2
```

Query Match 16.7%; Score 5; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 YISGO 21
DB 34 YISGO 38

RESULT 36

US-09-738-626-3519
; Sequence 3519, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3519
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3519

Query Match 16.7%; Score 5; DB 9; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

8 DYERS 12
73 DYERS 77

RESULT 37

US-10-094-214-4
; Sequence 4, Application US/10094214
; Patent No. US20020132303A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: 69318, A Human Sodium/Calcium Exchanger
; FILE REFERENCE: MP101-038P1RM
; CURRENT APPLICATION NUMBER: US/10/094,214
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/275,078
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Artificial Sequence

OTHER INFORMATION: consensus
US-10-094-214-4

Query Match 16.7%; Score 5; DB 12; Length 152;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SLPEL 7
DB 38 SLPEL 42

RESULT 38

US-09-791-932-73
; Sequence 73, Application US/09791932
; Publication No. US20030003451A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030003451A1 G Protein-Coupled Receptors Cross-Refere
; FILE REFERENCE: 00325_US1
; CURRENT APPLICATION NUMBER: US/09/791,932
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/194,344
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/218,337
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-932-73

Query Match 16.7%; Score 5; DB 9; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SLPEL 7
DB 38 SLPEL 42

Db 86 SLPEL 90

RESULT 39

US-10-112-793-16

; Sequence 16, Application US/10112793
; Publication No. US20020192729A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESS: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Winpatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/112,793

; FILING DATE: 28-Mar-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/828,683A

; FILING DATE: 31-Mar-1997

; APPLICATION NUMBER: 08/625328

; FILING DATE: 1-Apr-1996

; APPLICATION NUMBER: 08/710802

; FILING DATE: 23-Sep-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Marchang, Diane L.

; REGISTRATION NUMBER: 35,600

; REFERENCE/DOCKET NUMBER: P1007P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-5416

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 159 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; US-10-112-793-16

; SEQUENCE DESCRIPTION: SEQ ID NO: 16:

; Query Match

; Best Local Similarity 100.0%; Score 5; DB 9; Length 159;

; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SATEP 16

Db 48 SATEP 52

RESULT 40

US-10-101-464A-650

; Sequence 650, Application US/10101464A
; Publication No. US20030046728A1

GENERAL INFORMATION:

; APPLICANT: Strabala, Timothy

; APPLICANT: Nieuwenhuizen, Nicolaas

; APPLICANT: Higgins, Colleen M.

; TITLE OF INVENTION: Compositions Isolated from Plant Cells

; FILE REFERENCE: 11000.1020C2

; CURRENT APPLICATION NUMBER: US/10/101,464A

; CURRENT FILING DATE: 2002-03-18

; PRIOR APPLICATION NUMBER: 09/704,302

; PRIOR FILING DATE: 2000-11-01

; Search completed: April 9, 2003, 14:29:02

; Job time : 27.055 secs

QY 3 SLPEL 7

Db 87 SLPEL 91

; PRIOR APPLICATION NUMBER: 09/228,986

; PRIOR FILING DATE: 1999-01-12

; PRIOR APPLICATION NUMBER: 60/162,866

; PRIOR FILING DATE: 1999-11-01

; PRIOR APPLICATION NUMBER: PCT/US00/00724

; PRIOR FILING DATE: 2000-01-11

; NUMBER OF SEQ ID NOS: 989

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 650

; LENGTH: 159

; TYPE: PRT

; ORGANISM: Eucalyptus grandis

; US-10-101-464A-650

; Query Match

; Best Local Similarity 100.0%; Score 5; DB 9; Length 159;

; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SLPEL 7

Db 87 SLPEL 91

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 9, 2003, 13:59:59 ; Search time 6.33028 Seconds
(without alignments)
289.732 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 145
Sequence: 1 KYSLPELDYFSATEPYISQINEIXYTX 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA:*
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2: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB pep:*
3: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB pep:*
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14: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	141	97.2	30	10 US-09-987-190-2	Sequence 2, Appl
2	77	53.1	200	9 US-09-738-626-6727	Sequence 6727, Ap
3	77	53.1	200	10 US-09-818-564-2	Sequence 12, Appl
4	74	51.0	95	9 US-09-993-333-12	Sequence 6, Appl
5	71	49.0	188	10 US-09-987-190-6	Sequence 7, Appl
6	67	46.2	198	9 US-09-727-8558-7	Sequence 23, Appl
7	66	45.5	22	10 US-09-953-510-23	Sequence 974, App
8	66	45.5	222	9 US-09-727-8558-5	Sequence 974, App
9	50	34.5	359	9 US-09-895-793-974	Sequence 708, App
10	50	34.5	371	10 US-09-822-827-974	Sequence 708, App
11	50	34.5	371	9 US-10-012-896-708	Sequence 708, App
12	50	34.5	371	9 US-09-895-793-708	Sequence 708, App
13	50	34.5	371	9 US-09-895-814-708	Sequence 708, App
14	50	34.5	371	10 US-09-759-143-708	Sequence 708, App
15	50	34.5	371	10 US-09-780-669-708	Sequence 708, App
16	50	34.5	371	10 US-09-822-827-708	Sequence 708, App
17	50	34.5	400	9 US-10-012-896-852	Sequence 852, App
18	50	34.5	400	9 US-09-895-793-852	Sequence 852, App
19	50	34.5	400	9 US-09-895-814-852	Sequence 852, App

20	50	34.5	400	10 US-09-759-143-852	Sequence 852, App
21	50	34.5	400	10 US-09-780-669-852	Sequence 852, App
22	50	34.5	400	10 US-09-822-827-852	Sequence 113, App
23	50	34.5	553	9 US-09-232-880-113	Sequence 113, App
24	50	34.5	553	9 US-10-012-896-113	Sequence 113, App
25	50	34.5	553	9 US-09-895-793-113	Sequence 113, App
26	50	34.5	553	9 US-09-895-814-113	Sequence 113, App
27	50	34.5	553	10 US-09-745-288-101	Sequence 101, App
28	50	34.5	553	10 US-09-838-785-2	Sequence 113, App
29	50	34.5	553	10 US-09-759-143-113	Sequence 113, App
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31	50	34.5	553	10 US-09-030-606-113	Sequence 947, App
32	50	34.5	553	10 US-09-822-827-113	Sequence 947, App
33	50	34.5	553	10 US-09-822-827-113	Sequence 947, App
34	50	34.5	1079	9 US-09-895-793-947	Sequence 947, App
35	50	34.5	1079	10 US-09-822-827-947	Sequence 947, App
36	45.5	31.4	1101	10 US-09-972-484-11	Sequence 52, Appl
37	45.5	31.4	1101	10 US-09-972-484-52	Sequence 52, Appl
38	45.5	31.0	1452	10 US-09-972-484-2	Sequence 122, Appl
39	45	31.0	280	9 US-09-832-355A-122	Sequence 96, Appl
40	45	31.0	360	9 US-09-832-355A-96	Sequence 5, Appl
41	45	31.0	495	10 US-09-998-831-5	Sequence 6, Appl
42	45	31.0	496	9 US-10-179-744-6	Sequence 6, Appl
43	45	31.0	496	9 US-10-186-817-6	Sequence 6, Appl
44	45	31.0	496	9 US-10-215-224-8	Sequence 8, Appl
45	45	31.0	496	10 US-09-998-831-4	Sequence 4, Appl

ALIGNMENTS

```
RESULT 1
US-09-987-190-2
; Sequence 2, Application US/09987190
; Patent No. US20020058293A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, Kazutoh
; APPLICANT: MIZUTANI, Shigetoshi
; APPLICANT: ENDO, Masahiro
; APPLICANT: KATO, Kunoshin
; TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
; FILE REFERENCE: 1422-0502P
; CURRENT APPLICATION NUMBER: US/09/987,190
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/262,856
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (1)..(30)
; OTHER INFORMATION: any Xaa = any amino acid, unknown or other
US-09-987-190-2

Query Match      97.2%  Score 141;  DB 10;  Length 30;
Best Local Similarity 100.0%;  Pred. No. 3.9e-15;
Matches 28;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Cy      1  KYSLPELDYFSATEPYISQINEIXYT 28
Db      1  KYSLPELDYFSATEPYISQINEIXYT 28

RESULT 2
US-09-738-626-6727
; Sequence 6727, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
```

APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6727
LENGTH: 200
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-6727

Query Match 53.1%; Score 77; DB 9; Length 200;
Best Local Similarity 48.1%; Pred. No. 0.00022;
Matches 13; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYFSAATPEYISQINEIXYT 28
DB 4 YELPELDYAYDALBPPIAAEIMELHHS 30

RESULT 3
US-09-818-564-2
Sequence 2, Application US/09818564
Patent No. US20020137151A1
GENERAL INFORMATION:
APPLICANT: MERKAM, MURIEL
APPLICANT: GUYONVARCH, ARMEL
APPLICANT: MAXX, ACHIM
TITLE OF INVENTION: A PROCESS FOR THE FERMENTATIVE PREPARATION OF METABOLIC
TITLE OF INVENTION: PRODUCTS AND FOR THE NUCLEOTIDE SEQUENCES ENCODING FOR
TITLE OF INVENTION: THE BOD GENE
FILE REFERENCE: 21123/278411/MAS
CURRENT APPLICATION NUMBER: US/09/818,564
CURRENT FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 09/373,731
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 200
TYPE: PRT
ORGANISM: Corynebacterium melassaccola
OTHER INFORMATION: ATCC 17965
US-09-818-564-2

Query Match 53.1%; Score 77; DB 10; Length 200;
Best Local Similarity 48.1%; Pred. No. 0.00022;
Matches 13; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYFSAATPEYISQINEIXYT 28
DB 4 YELPELDYAYDALBPPIAAEIMELHHS 30

RESULT 4
US-09-993-333-12
Sequence 12, Application US/09993333

Patent No. US20020156040A1
GENERAL INFORMATION:
APPLICANT: Oberley, Larry Wayne
APPLICANT: Weydert, Christine J.
APPLICANT: Smith, Benjamin Barnes
TITLE OF INVENTION: Reduction of antioxidant enzyme levels in tumor cells using anti
TITLE OF INVENTION: oligonucleotides
FILE REFERENCE: 875,042US1
CURRENT APPLICATION NUMBER: US/09/993,333
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 60/248,328
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 95
TYPE: PRT
ORGANISM: Homo sapiens
US-09-993-333-12

Query Match 51.0%; Score 74; DB 9; Length 95;
Best Local Similarity 42.9%; Pred. No. 0.00027;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXSLPELDYFSAATPEYISQINEIXYT 28
DB 25 KXSLPELDYAYDALBPPIAAEIMELHHS 52

RESULT 5
US-09-987-190-6
Sequence 6, Application US/09987190
Patent No. US20020058233A1
GENERAL INFORMATION:
APPLICANT: TAKESAKO, Kazutosh
APPLICANT: MIZUTANI, Shigetoshi
APPLICANT: ENDO, Masahiro
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
FILE REFERENCE: 1422-0502P
CURRENT APPLICATION NUMBER: US/09/987,190
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/262,856
PRIOR FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 188
TYPE: PRT
ORGANISM: Candida albicans
US-09-987-190-6

Query Match 49.0%; Score 71; DB 10; Length 188;
Best Local Similarity 81.2%; Pred. No. 0.0017;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 13 ATPEYISQINEIXYT 28
DB 1 ATPEYITGQNEIMHYT 16

RESULT 6
US-09-727-855B-7
Sequence 7, Application US/09727855B
Patent No. US20020168703A1
GENERAL INFORMATION:
APPLICANT: HOSHINO, Tatsuo
APPLICANT: OJIMA, Kazuyuki
APPLICANT: SETOGUCHI, Yutaka
TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEF
FILE REFERENCE: C38435/111694
CURRENT APPLICATION NUMBER: US/09/727,855B


```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 974
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-995-793-974

Query Match          34.5%; Score 50; DB 9; Length 359;
Best Local Similarity 45.0%; Pred. No. 5.7;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPDLDFEFSATEPYISGQ 21
Db 176 YLLPAIDWDTSLAPYLCTQ 195

RESULT 10
US-09-822-827-974
; Sequence 974, Application US/09822827
; Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 974
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-822-827-974

Query Match          34.5%; Score 50; DB 10; Length 359;
Best Local Similarity 45.0%; Pred. No. 5.7;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPDLDFEFSATEPYISGQ 21
Db 176 YLLPAIDWDTSLAPYLCTQ 195

RESULT 11
US-10-012-896-708
; Sequence 708, Application US/10012896
; Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
```

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 708
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-708

Query Match          34.5%; Score 50; DB 9; Length 371;
Best Local Similarity 45.0%; Pred. No. 5.9;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPDLDFEFSATEPYISGQ 21
Db 150 YLLPAIDWDTSLAPYLCTQ 169

RESULT 12
US-09-895-793-708
; Sequence 708, Application US/09895793
; Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 708
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-793-708

Query Match          34.5%; Score 50; DB 9; Length 371;
Best Local Similarity 45.0%; Pred. No. 5.9;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPDLDFEFSATEPYISGQ 21
Db 150 YLLPAIDWDTSLAPYLCTQ 169

RESULT 13
US-09-895-814-708
```

```
; Sequence 708, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlotca
; APPLICANT: Roy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895.814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 708
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-814-708

Query Match          34.5%; Score 50; DB 9; Length 371;
Best Local Similarity 45.0%; Pred. No. 5.9;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY      2 YSLPELDYFSATEPYISQ 21
Db      150 YLPAIDWDTSALAPYIGTQ 169

SULT 14
-09-759-143-708
; Sequence 708, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759.143
```

```
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 708
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-708

Query Match          34.5%; Score 50; DB 10; Length 371;
Best Local Similarity 45.0%; Pred. No. 5.9;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY      2 YSLPELDYFSATEPYISQ 21
Db      150 YLPAIDWDTSALAPYIGTQ 169

RESULT 15
US-09-780-669-708
; Sequence 708, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780.669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 708
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-669-708

Query Match          34.5%; Score 50; DB 10; Length 371;
Best Local Similarity 45.0%; Pred. No. 5.9;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY      2 YSLPELDYFSATEPYISQ 21
Db      150 YLPAIDWDTSALAPYIGTQ 169

RESULT 16
US-09-822-827-708
; Sequence 708, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/822.827
```

```
/ FILE REFERENCE: 210121.534C1
/ CURRENT APPLICATION NUMBER: US/09/822.827
/ CURRENT FILING DATE: 2001-03-28
/ NUMBER OF SEQ ID NOS: 982
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 708
/ LENGTH: 371
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-822-827-708
```

```
Query Match          34.5%; Score 50; DB 10; Length 371;
Best Local Similarity 45.0%; Pred. No. 5.9;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
```

```
QY      2 YSLPELDYFSGATEPYISGQ 21
DB      150 YLLPAIDWTSALAPYLGTO 169
```

```
SULT 17
-10-012-896-852
/ Sequence 852, Application US/10012896
/ Publication No. US20020183251A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yugu
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel X.
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Heppler, William T.
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Hurai, John
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: Vinals de Bassols, Carlota
/ APPLICANT: Foy, Teresa
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Mantanabe, Yoshihito
/ APPLICANT: Meesher, Madeleine Joy
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.427C27
/ CURRENT APPLICATION NUMBER: US/10/012.896
/ CURRENT FILING DATE: 2001-12-10
/ NUMBER OF SEQ ID NOS: 1011
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 852
/ LENGTH: 400
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-012-896-852
```

```
Query Match          34.5%; Score 50; DB 9; Length 400;
Best Local Similarity 45.0%; Pred. No. 6.5;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
```

```
QY      2 YSLPELDYFSGATEPYISGQ 21
DB      278 YLLPAIDWTSALAPYLGTO 297
```

```
RESULT 18
US-09-895-793-852
```

```
/ Sequence 852, Application US/09895793
/ Publication No. US20020192763A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yugu
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel X.
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Heppler, William T.
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Hurai, John
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: Vinals de Bassols, Carlota
/ APPLICANT: Foy, Teresa
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Mantanabe, Yoshihito
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.534C2
/ CURRENT APPLICATION NUMBER: US/09/895.793
/ CURRENT FILING DATE: 2001-06-29
/ NUMBER OF SEQ ID NOS: 982
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 852
/ LENGTH: 400
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-895-793-852
```

```
Query Match          34.5%; Score 50; DB 9; Length 400;
Best Local Similarity 45.0%; Pred. No. 6.5;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
```

```
QY      2 YSLPELDYFSGATEPYISGQ 21
DB      278 YLLPAIDWTSALAPYLGTO 297
```

```
RESULT 19
US-09-895-814-852
/ Sequence 852, Application US/09895814
/ Publication No. US20020193296A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yugu
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel X.
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Heppler, William T.
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Hurai, John
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: Vinals de Bassols, Carlota
/ APPLICANT: Foy, Teresa
```

```

; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 852
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-814-852
```

```

Query Match          34.5%; Score 50; DB 9; Length 400;
Best Local Similarity 45.0%; Pred. No. 6.5;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
```

```

2 YSLPELDYFSATEPYISGQ 21
|||::|||::|
278 YLPAIDMTSALAPYLGTO 297
```

```

RESULT 20
US-09-759-143-852
; Sequence 852, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 852
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-852
```

```

Query Match          34.5%; Score 50; DB 10; Length 400;
Best Local Similarity 45.0%; Pred. No. 6.5;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
```

```

QY 2 YSLPELDYFSATEPYISGQ 21
|||::|||::|
Db 278 YLPAIDMTSALAPYLGTO 297
```

```

RESULT 21
US-09-780-669-852
; Sequence 852, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
```

```

; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 852
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-669-852
```

```

Query Match          34.5%; Score 50; DB 10; Length 400;
Best Local Similarity 45.0%; Pred. No. 6.5;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
```

```

QY 2 YSLPELDYFSATEPYISGQ 21
|||::|||::|
Db 278 YLPAIDMTSALAPYLGTO 297
```

```

RESULT 22
US-09-822-827-852
; Sequence 852, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 852
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-822-827-852
```

```

Query Match          34.5%; Score 50; DB 10; Length 400;
Best Local Similarity 45.0%; Pred. No. 6.5;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
```

```

QY 2 YSLPELDYFSATEPYISGQ 21
|||::|||::|
Db 278 YLPAIDMTSALAPYLGTO 297
```

```

RESULT 23
US-09-232-880-113
; Sequence 113, Application US/09232880
; Publication No. US20020182596A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232,880
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-232-880-113

Query Match      34.5%; Score 50; DB 9; Length 553;
Best Local Similarity 45.0%; Pred. No. 9.3;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

2 YSLPELDYFSATEPYISQ 21
|||::|||::|||
Db 176 YLLPAIDWTSALAPYLGTQ 195

RESULT 24
US-10-012-896-113
; Sequence 113, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Heppler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Mantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-113

Query Match      34.5%; Score 50; DB 9; Length 553;
Best Local Similarity 45.0%; Pred. No. 9.3;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

2 YSLPELDYFSATEPYISQ 21
```

```

Db 176 YLLPAIDWTSALAPYLGTQ 195

RESULT 25
US-09-895-793-113
; Sequence 113, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Heppler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-793-113

Query Match      34.5%; Score 50; DB 9; Length 553;
Best Local Similarity 45.0%; Pred. No. 9.3;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

2 YSLPELDYFSATEPYISQ 21
|||::|||::|||
Db 176 YLLPAIDWTSALAPYLGTQ 195

RESULT 26
US-09-895-814-113
; Sequence 113, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Heppler, William T.
```



```

; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-814-113

```

```

Query Match          34.5%; Score 50; DB 9; Length 553;
Best Local Similarity 45.0%; Pred. No. 9.3;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 2 YSLPELDYFSATEPYISQ 21
Db 176 YLPAIDWTSALAPYLGTO 195

```

```

RESULT 27
US-09-745-288-101
; Sequence 101, Application US/09745288
; Patent No. US20010018058A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.44661
; CURRENT APPLICATION NUMBER: US/09/745,288
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
-09-745-288-101

```

```

Query Match          34.5%; Score 50; DB 10; Length 553;
Best Local Similarity 45.0%; Pred. No. 9.3;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 2 YSLPELDYFSATEPYISQ 21
Db 176 YLPAIDWTSALAPYLGTO 195

```

```

RESULT 28
US-09-838-785-2
; Sequence 2, Application US/09838785
; Patent No. US20020009455A1
; GENERAL INFORMATION:
; APPLICANT: Lau, Ted
; APPLICANT: Lin, Rick
; APPLICANT: Parkes, Debbie
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steindricher, Renate
; APPLICANT: Van Heutic, Pam T
; APPLICANT: Wu, John
; TITLE OF INVENTION: DNA Encoding a No. US20020009455A1e1 PROST 03

```

```

; FILE REFERENCE: 51831AUSM1
; CURRENT APPLICATION NUMBER: US/09/838,785
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/200,065
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-838-785-2

```

```

Query Match          34.5%; Score 50; DB 10; Length 553;
Best Local Similarity 45.0%; Pred. No. 9.3;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 2 YSLPELDYFSATEPYISQ 21
Db 176 YLPAIDWTSALAPYLGTO 195

```

```

RESULT 29
US-09-759-143-113
; Sequence 113, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqun
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-759-143-113

```

```

Query Match          34.5%; Score 50; DB 10; Length 553;
Best Local Similarity 45.0%; Pred. No. 9.3;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 2 YSLPELDYFSATEPYISQ 21
Db 176 YLPAIDWTSALAPYLGTO 195

```

```

RESULT 30
US-09-780-669-113
; Sequence 113, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.

```

APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 113
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapien
US-09-780-669-113

Query Match 34.5%; Score 50; DB 10; Length 553;
Best Local Similarity 45.0%; Pred. No. 9.3;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATEPYISGQ 21
DB 176 YLPAIDWTSALAPYLGTQ 195

RESULT 31
US-09-030-606-113
Sequence 113, Application US/09030606
Patent No. US20020081580A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4500
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-606-113

Query Match 34.5%; Score 50; DB 10; Length 553;
Best Local Similarity 45.0%; Pred. No. 9.3;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATEPYISGQ 21
DB 176 YLPAIDWTSALAPYLGTQ 195

RESULT 32
US-09-822-827-113
Sequence 113, Application US/09822827
Patent No. US20020081580A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 113
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapien
US-09-822-827-113

Query Match 34.5%; Score 50; DB 10; Length 553;
Best Local Similarity 45.0%; Pred. No. 9.3;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATEPYISGQ 21
DB 176 YLPAIDWTSALAPYLGTQ 195

RESULT 33
US-09-115-453-113
Sequence 113, Application US/09115453B
Patent No. US20020090372A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
FILE REFERENCE: 210121.427C4
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 113
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapien
US-09-115-453-113

Query Match 34.5%; Score 50; DB 10; Length 553;
Best Local Similarity 45.0%; Pred. No. 9.3;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATEPYISGQ 21

Db 176 YLPAIDWTSALAPYLGTO 195

RESULT 34

US-09-895-793-947
; Sequence 947, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugui
APPLICANT: Kaios, Michael D.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hedler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Basols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ. ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 947
LENGTH: 1079
TYPE: PRT
ORGANISM: Homo sapiens
US-09-895-793-947

Query Match 34.5%; Score 50; DB 9; Length 1079;
Best Local Similarity 45.0%; Pred. No. 20;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

2 YSLPDLVRSATEPYISGQ 21
Db 702 YLPAIDWTSALAPYLGTO 721

RESULT 35
US-09-822-827-947
; Sequence 947, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ. ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 947
LENGTH: 1079
TYPE: PRT
ORGANISM: Homo sapiens
US-09-822-827-947

Query Match 34.5%; Score 50; DB 10; Length 1079;
Best Local Similarity 45.0%; Pred. No. 20;

Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPDLVRSATEPYISGQ 21
Db 702 YLPAIDWTSALAPYLGTO 721

RESULT 36
US-09-972-484-11
; Sequence 11, Application US/09972484
; Patent No. US20020127245A1
; GENERAL INFORMATION:

APPLICANT: Miller, Timothy J.
Klepfier, Sharon
Reed, Albert Paul
Jones, Elaine V.
TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Smtlthkline Beecham Corporation - Corporate
Patents
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,484
FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/494,151
FILING DATE: 28-Jan-2000
APPLICATION NUMBER: 08/331,625
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SBC H85010-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-972-484-11

Query Match 31.4%; Score 45.5; DB 10; Length 203;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 9; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

QY 2 YSLPDLVRSATEPYISGQINEIXY 27
Db 79 WTVPELPDLIFNATYLNUTGEINDLEF 105

RESULT 37
US-09-972-484-52
; Sequence 52, Application US/09972484

Patent No. US20020127245A1
GENERAL INFORMATION:
APPLICANT: Miller, Timothy J.
Klepfisz, Sharon
Reed, Albert Paul
Jones, Elaine V.
TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
Therefor
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SmithKline Beecham Corporation - Corporate
Patents
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,484
FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/494,151
FILING DATE: 28-Jan-2000
APPLICATION NUMBER: 08/331,625
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SBC H85010-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5015
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1101 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
-09-972-484-52
Query Match 31.4%; Score 45.5; DB 10; Length 1101;
Best Local Similarity 33.3%; Pred. No. 98;
Matches 9; Conservative 11; Mismatches 6; Indels 1; Gaps 1;
QY 2 YSLPELDYE-PSATEPYISQGINEIXY 27
Db 977 WTVPELPIDIFNATYLNUTGEINDLEF 1003
RESULT 38
US-09-972-484-2
Sequence 2, Application US/09972484
Patent No. US20020127245A1
GENERAL INFORMATION:
APPLICANT: Miller, Timothy J.
Klepfisz, Sharon
Reed, Albert Paul
Jones, Elaine V.
TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
Therefor
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSES:

ADDRESSEE: SmithKline Beecham Corporation - Corporate
Patents
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,484
FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/494,151
FILING DATE: 28-Jan-2000
APPLICATION NUMBER: 08/331,625
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SBC H85010-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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Best Local Similarity 33.3%; Pred. No. 1.3e+02;
Matches 9; Conservative 11; Mismatches 6; Indels 1; Gaps 1;
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Db 1328 WTVPELPIDIFNATYLNUTGEINDLEF 1354
RESULT 39
US-09-832-355A-122
Sequence 122, Application US/09832355A
Publication No. US20030027751A1
GENERAL INFORMATION:
APPLICANT: Kovesdi, Imre
APPLICANT: Kessler, Paul
TITLE OF INVENTION: VEGF FUSION PROTEINS
FILE REFERENCE: 205654
CURRENT APPLICATION NUMBER: US/09/832,355A
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentin version 3.0
SEQ ID NO 122
LENGTH: 280
TYPE: PRT
ORGANISM: Artificial sequence
FEATURES:
NAME/KEY: misc feature
LOCATION: ()-()
OTHER INFORMATION: Synthetic
US-09-832-355A-122

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 Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
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 Db 45 FLDPENDNCRSSSPYVSNAY 65

RESULT 40
 US-09-832-355A-96
 ; Sequence 96, Application US/09832355A
 ; Publication No. US2003027751A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovesdi, Imre
 ; APPLICANT: Kessler, Paul
 ; TITLE OF INVENTION: VEGF FUSION PROTEINS
 ; FILE REFERENCE: 205654
 ; CURRENT APPLICATION NUMBER: US/09/832,355A
 ; CURRENT FILING DATE: 2001-04-10
 ; NUMBER OF SEQ ID NOS: 126
 ; SOFTWARE: Patent version 3.0
 ; SEQ ID NO 96
 ; LENGTH: 360
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: ()..()
 ; OTHER INFORMATION: Synthetic
 ; NAME/KEY: misc feature
 ; LOCATION: (269)..(272)
 ; OTHER INFORMATION: "Xaa" may be any amino acid
 ; US-09-832-355A-96

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 Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
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 Db 45 FLDPENDNCRSSSPYVSNAY 65

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 Job time : 8.33027 secs

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: April 9, 2003, 14:17:20 ; Search time 37.945 Seconds
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Title: US-09-987-190-6

Perfect score: 188
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Scoring table: OLIGO
Gapco 60.0 , Gapext 60.0

Database: 248812 seqs, 61136040 residues

Word size : 0

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Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

Database : Published Applications AA.*

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14: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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412	6	3.2	969	9	US-10-078-531-8	Sequence 8, Appl1	485	5	2.7	33	9	US-09-852-424-115	Sequence 115, App
413	6	3.2	970	9	US-10-078-531-4	Sequence 4, Appl1	486	5	2.7	33	9	US-09-835-107-16	Sequence 16, App
414	6	3.2	971	9	US-10-078-531-6	Sequence 6, Appl1	487	5	2.7	33	9	US-09-835-107-18	Sequence 18, App
415	6	3.2	971	9	US-10-078-531-7	Sequence 7, Appl1	488	5	2.7	33	9	US-10-081-816-78	Sequence 78, Appl
416	6	3.2	1008	9	US-10-078-531-2	Sequence 2, Appl1	489	5	2.7	33	10	US-09-864-761-48221	Sequence 48221, A
417	6	3.2	1094	9	US-09-712-363-287	Sequence 287, App	490	5	2.7	34	9	US-09-852-424-75	Sequence 75, Appl
418	6	3.2	1109	10	US-09-815-242-4930	Sequence 4930, Ap	491	5	2.7	34	9	US-09-852-424-82	Sequence 82, Appl
419	6	3.2	1109	10	US-09-815-242-10648	Sequence 10648, A	492	5	2.7	34	9	US-09-852-424-83	Sequence 83, Appl
420	6	3.2	1161	8	US-09-910-386A-20	Sequence 20, Appl	493	5	2.7	34	9	US-09-852-424-84	Sequence 84, Appl
421	6	3.2	1198	10	US-09-866-582-36	Sequence 36, Appl	494	5	2.7	34	9	US-09-852-424-85	Sequence 85, Appl
422	6	3.2	1241	12	US-10-001-215-5	Sequence 5, Appl1	495	5	2.7	34	9	US-09-852-424-98	Sequence 98, Appl
423	6	3.2	1247	10	US-09-815-242-4886	Sequence 4886, Ap	496	5	2.7	34	9	US-09-852-424-99	Sequence 99, Appl
424	6	3.2	1250	10	US-09-801-368-364	Sequence 364, App	497	5	2.7	34	9	US-09-852-424-100	Sequence 100, App
425	6	3.2	1270	9	US-10-101-454A-979	Sequence 979, App	498	5	2.7	34	9	US-09-852-424-101	Sequence 101, App
426	6	3.2	1271	10	US-09-815-242-10717	Sequence 10717, A	499	5	2.7	34	9	US-09-852-424-123	Sequence 123, App
427	6	3.2	1317	10	US-09-815-242-5118	Sequence 5118, Ap	500	5	2.7	34	9	US-09-852-424-125	Sequence 125, App
428	6	3.2	2037	10	US-09-951-402-3	Sequence 3, Appl1	501	5	2.7	34	9	US-09-835-107-11	Sequence 17, Appl
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430	6	3.2	2037	10	US-09-922-101-3	Sequence 3, Appl1	503	5	2.7	34	9	US-10-013-339-3	Sequence 3, Appl1
431	6	3.2	3092	10	US-09-801-368-172	Sequence 172, App	504	5	2.7	35	9	US-10-050-704-193	Sequence 193, App
432	5	2.7	10	8	US-08-854-825-28	Sequence 28, Appl	505	5	2.7	35	9	US-10-073-118-3	Sequence 33, Appl
433	5	2.7	11	10	US-09-873-676-37	Sequence 37, Appl	506	5	2.7	35	10	US-09-864-761-40859	Sequence 40859, A
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437	5	2.7	12	9	US-10-036-729-20	Sequence 20, Appl	510	5	2.7	38	9	US-09-798-889-83	Sequence 83, Appl
438	5	2.7	13	9	US-09-776-724A-180	Sequence 180, App	511	5	2.7	38	9	US-09-866-880-418	Sequence 418, App
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442	5	2.7	14	10	US-09-791-378-328	Sequence 328, App	515	5	2.7	43	9	US-09-939-780-2	Sequence 2, Appl1
443	5	2.7	14	10	US-09-791-378-390	Sequence 390, App	516	5	2.7	43	10	US-09-147-761-2	Sequence 2, Appl1
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446	5	2.7	15	9	US-09-826-290-197	Sequence 197, App	519	5	2.7	45	10	US-09-864-761-44415	Sequence 44415, A
447	5	2.7	15	9	US-09-826-290-287	Sequence 287, App	520	5	2.7	46	9	US-09-301-936-37	Sequence 37, Appl
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449	5	2.7	15	9	US-09-291-417-82	Sequence 82, Appl	522	5	2.7	46	10	US-09-864-761-3082	Sequence 3082, A
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453	5	2.7	19	9	US-10-045-180A-4	Sequence 4, Appl1	526	5	2.7	49	9	US-09-764-872-309	Sequence 309, App
454	5	2.7	19	10	US-09-193-538-21	Sequence 21, Appl	527	5	2.7	49	10	US-09-864-761-43011	Sequence 43011, A
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539	5	2.7	56	10	US-09-867-550-178	Sequence 178, App	612	5	2.7	89	9	US-10-102-627-47	Sequence 47, App1
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544	5	2.7	59	9	US-09-796-692-745	Sequence 745, App	617	5	2.7	91	10	US-09-864-761-37756	Sequence 37756, A
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551	5	2.7	61	10	US-09-925-299-1331	Sequence 1331, App1	624	5	2.7	93	9	US-09-764-877-1507	Sequence 1507, Ap
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555	5	2.7	62	9	US-09-966-262-240	Sequence 240, App	628	5	2.7	94	9	US-10-045-180A-10	Sequence 10, App1
556	5	2.7	62	9	US-09-983-966-240	Sequence 240, App	629	5	2.7	94	9	US-10-045-180A-12	Sequence 12, App1
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558	5	2.7	62	10	US-09-764-869-1065	Sequence 1065, Ap	631	5	2.7	94	12	US-10-013-770-3	Sequence 3, App1
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560	5	2.7	63	9	US-09-966-262-320	Sequence 320, App	633	5	2.7	95	10	US-09-917-340-76	Sequence 76, App1
561	5	2.7	63	9	US-09-983-966-320	Sequence 320, App	634	5	2.7	96	10	US-09-800-729-119	Sequence 119, App
562	5	2.7	64	10	US-09-864-761-39808	Sequence 39808, A	635	5	2.7	96	10	US-09-917-340-89	Sequence 89, App1
563	5	2.7	64	10	US-09-925-297-652	Sequence 652, App	636	5	2.7	96	10	US-09-917-340-90	Sequence 90, App1
564	5	2.7	65	9	US-09-984-245-241	Sequence 241, App	637	5	2.7	97	9	US-10-045-180A-9	Sequence 9, App1
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576	5	2.7	67	10	US-09-764-847-958	Sequence 958, App	649	5	2.7	101	9	US-10-083-357-714	Sequence 714, App
577	5	2.7	69	10	US-09-864-761-36291	Sequence 36291, A	650	5	2.7	101	10	US-09-815-242-5166	Sequence 5166, Ap
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582	5	2.7	73	9	US-09-796-692-768	Sequence 768, App	655	5	2.7	104	10	US-09-939-980-255	Sequence 265, App
583	5	2.7	74	10	US-09-110-716-35	Sequence 35, App1	656	5	2.7	105	9	US-09-808-602-2	Sequence 2, App1
584	5	2.7	74	10	US-09-864-761-41690	Sequence 41690, A	657	5	2.7	106	9	US-10-138-516-4	Sequence 4, App1
585	5	2.7	74	10	US-09-867-550-1832	Sequence 1832, Ap	658	5	2.7	106	9	US-10-146-130-6	Sequence 6, App1
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587	5	2.7	76	10	US-09-864-761-41132	Sequence 41132, A	660	5	2.7	108	10	US-09-899-896-9	Sequence 9, App1
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589	5	2.7	77	9	US-09-749-637A-77	Sequence 77, App1	662	5	2.7	109	9	US-09-796-692-2460	Sequence 2460, Ap
590	5	2.7	79	10	US-09-922-261-433	Sequence 433, App	663	5	2.7	109	10	US-09-924-946-6	Sequence 6, App1
591	5	2.7	79	10	US-09-884-441-460	Sequence 460, App	664	5	2.7	111	9	US-10-101-464A-722	Sequence 722, App
592	5	2.7	80	10	US-09-864-761-46010	Sequence 46010, A	665	5	2.7	111	10	US-09-867-550-258	Sequence 258, App
593	5	2.7	80	10	US-09-864-761-47469	Sequence 47469, A	666	5	2.7	111	10	US-09-934-054-5	Sequence 5, App1
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596	5	2.7	81	8	US-10-125-540-515	Sequence 515, App	669	5	2.7	113	10	US-09-925-300-1011	Sequence 1011, Ap
597	5	2.7	81	10	US-09-764-870-515	Sequence 515, App	670	5	2.7	114	9	US-09-759-130B-198	Sequence 198, App
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599	5	2.7	82	9	US-10-091-504-678	Sequence 678, App	672	5	2.7	114	10	US-09-867-550-14	Sequence 14, App1
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601	5	2.7	83	10	US-09-764-864-1504	Sequence 1504, Ap	674	5	2.7	116	10	US-09-939-980-304	Sequence 304, App
602	5	2.7	84	9	US-10-013-379-18	Sequence 18, App1	675	5	2.7	117	10	US-09-867-550-356	Sequence 326, App
603	5	2.7	84	9	US-09-925-299-1207	Sequence 1207, Ap	676	5	2.7	118	10	US-09-734-017A-26	Sequence 26, App1

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679	5	2.7	122	10	US-09-731-872-431	Sequence 431, App	752	5	2.7	134	9	US-10-091-483-157	Sequence 157, App
680	5	2.7	123	9	US-09-984-245-169	Sequence 169, App	753	5	2.7	134	10	US-09-164-615-5	Sequence 5, App1
681	5	2.7	123	9	US-09-966-262-169	Sequence 169, App	754	5	2.7	134	10	US-09-764-846-157	Sequence 157, App
682	5	2.7	123	9	US-09-983-966-169	Sequence 169, App	755	5	2.7	135	9	US-10-116-273-26	Sequence 26, App1
683	5	2.7	124	9	US-09-992-598-146	Sequence 146, App	756	5	2.7	136	9	US-10-116-273-23	Sequence 23, App1
684	5	2.7	124	9	US-10-060-845-9	Sequence 9, App1	757	5	2.7	136	9	US-09-738-626-6099	Sequence 6099, App
685	5	2.7	124	9	US-09-989-293A-146	Sequence 146, App	758	5	2.7	136	9	US-10-101-464A-675	Sequence 675, App
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687	5	2.7	124	9	US-09-990-444-146	Sequence 146, App	760	5	2.7	137	10	US-09-955-286-2	Sequence 2, App1
688	5	2.7	124	9	US-09-989-730-146	Sequence 146, App	761	5	2.7	137	9	US-10-116-273-24	Sequence 24, App1
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690	5	2.7	124	9	US-09-991-181-146	Sequence 146, App	763	5	2.7	138	9	US-10-116-273-23	Sequence 23, App1
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694	5	2.7	124	9	US-09-993-667-146	Sequence 146, App	767	5	2.7	140	9	US-10-116-273-34	Sequence 34, App1
695	5	2.7	124	9	US-09-990-438-146	Sequence 146, App	768	5	2.7	140	10	US-09-864-764-41841	Sequence 41841, A
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ALIGNMENTS

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; Patent No. US20020058293A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, Kazutosh
; APPLICANT: MIZUTANI, Shigetoshi
; APPLICANT: ENDO, Masahito
; APPLICANT: KATO, Ikunoshi
; TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
; FILE REFERENCE: 1422-0502P
; CURRENT APPLICATION NUMBER: US/09/987,190
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/262,856
; PRIOR FILING DATE: 1999-03-04
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 6
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-987-190-6
Query Match 100.0%; Score 188; DB 10; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.8e-173;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATEPITGQNMKEIHFKHQTYYNNLNLSIRQAVAKSGEVKKLVALQKAINFGGGYL 60
DB 1 ATEPITGQNMKEIHFKHQTYYNNLNLSIRQAVAKSGEVKKLVALQKAINFGGGYL 60
QY NHCLMWMKVLAPVSHGGGPPSEDSKLGKQIVKQFSLDKLLEITNGKLAGIQSGMARIIV 120
DB 61 NHCLMWMKVLAPVSHGGGPPSEDSKLGKQIVKQFSLDKLLEITNGKLAGIQSGMARIIV 120
QY 121 KKKANGTIDIVITTAADVTDLNLVPLIADAMKRAYLYQYQNVKADYFKNLMHVIMWK 180

DB 121 KKKANGTIDIVITTAADVTDLNLVPLIADAMKRAYLYQYQNVKADYFKNLMHVIMWK 180
QY 181 EAERREF 188
DB 181 EAERREF 188

RESULT 2
US-09-727-855B-5
; Sequence 5, Application US/09727855B
; Patent No. US20020168703A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEF
; FILE REFERENCE: C38435/111694
; CURRENT APPLICATION NUMBER: US/09/727,855B
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 5
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Phaffia rhodozyma
US-09-727-855B-5

Query Match 4.8%; Score 9; DB 9; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TKXHQTYVN 24
DB 53 TKXHQTYVN 61

RESULT 3
US-10-101-464A-721
; Sequence 721, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 721
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-721

Query Match 3.7%; Score 7; DB 9; Length 121;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 GSLDKLI 101

Db 98 GSLDKL1 104

```
RESULT 4
US-09-727-855B-7
; Sequence 7, Application US/09727855B
; Patent No. US20020168703A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
; FILE REFERENCE: C38435/111694
; CURRENT APPLICATION NUMBER: US/09/727,855B
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Phaffia rhodozyma
US-09-727-855B-7
```

Query Match 3.7%; Score 7; DB 9; Length 198;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 KHHQTV 23
Db 31 KHHQTV 37

```
RESULT 5
US-10-101-464A-702
; Sequence 702, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 702
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-702
```

Query Match 3.7%; Score 7; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 GSLDKL1 101
Db 140 GSLDKL1 146

RESULT 6
US-09-712-363-271

```
; Sequence 271, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 271
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-271
```

Query Match 3.7%; Score 7; DB 9; Length 329;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 GQPPSD 83
Db 207 GQPPSD 213

```
RESULT 7
US-09-815-242-11129
; Sequence 1129, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Onlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
US-09-815-242-11129
```

```
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11129
; LENGTH: 506
; TYPE: PR1
; ORGANISM: Haemophilus influenzae
US-09-815-242-11129
```

```
Query Match      3.7%; Score 7; DB 10; Length 506;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 105 NGKLAGI 111
Db 481 NGKLAGI 487
```

```
RESULT 8
US-09-817-913-13
; Sequence 13, Application US/09817913
; Patent No. US20020061860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Beesteman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 16101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 855
; TYPE: PR1
; ORGANISM: Human
US-09-817-913-13
```

```
Query Match      3.7%; Score 7; DB 10; Length 855;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 105 NGKLAGI 111
Db 561 NGKLAGI 567
```

```
RESULT 9
US-09-817-538-13
; Sequence 13, Application US/09817538
; Patent No. US2002013762A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Beesteman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 855
; TYPE: PR1
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```
; ORGANISM: Human
US-09-817-538-13
```

```
Query Match      3.7%; Score 7; DB 10; Length 855;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 105 NGKLAGI 111
Db 561 NGKLAGI 567
```

```
RESULT 10
US-09-738-626-4048
; Sequence 4048, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIRO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4048
; LENGTH: 1333
; TYPE: PR1
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4048
```

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Query Match      3.7%; Score 7; DB 9; Length 1333;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 38 SKGEVKK 44
Db 24 SKGEVKK 30
```

```
RESULT 11
US-09-853-830-28
; Sequence 28, Application US/09853830
; Patent No. US20020107388A1
; GENERAL INFORMATION:
; APPLICANT: Vandendark, Arthur A.
; TITLE OF INVENTION: Methods of Identifying and Monitoring
; FILE REFERENCE: P-IM 4734
; CURRENT APPLICATION NUMBER: US/09/853,830
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 21
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-853-830-28
```


Query Match 3.2%; Score 6; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 GYVKL 45
16 GYVKL 21
DB

RESULT 12
US-09-987-190-2
Sequence 2, Application US/09987190
Patent No. US20020058293A1
GENERAL INFORMATION:
APPLICANT: TAKESAKO, Kazutoh
APPLICANT: MIZUTANI, Shigetoshi
APPLICANT: ENDO, Masahiro
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
FILE REFERENCE: 1422-0502P
CURRENT APPLICATION NUMBER: US/09/987,190
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/262,856
PRIOR FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 30
TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: Unsure
LOCATION: (1)..(30)
OTHER INFORMATION: any Xaa = any amino acid, unknown or other
US-09-987-190-2

Query Match 3.2%; Score 6; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATEPYI 6
13 ATEPYI 18
DB

RESULT 13
US-09-864-761-36462
Sequence 36462, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36462
LENGTH: 39
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011257.2
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.97
OTHER INFORMATION: EST HUMAN HIT: BF219182.1, EVALUATE 3.20e+00
NAME/KEY: unsure
LOCATION: 24
US-09-864-761-36462

Query Match 3.2%; Score 6; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 GKQIVK 92
16 GKQIVK 21
DB

RESULT 14
US-09-981-876-166
Sequence 166, Application US/09981876
Patent No. US20020164669A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1
CURRENT APPLICATION NUMBER: US/09/981,876
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/148,545
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/038,621
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,161

Page 12

[illegible]

;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/043,578
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,576
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/047,501
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/043,670
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/056,632
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,664
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,876
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,881
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,909
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,875
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,862
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,887
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,908
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/048,964
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/057,650
;; PRIOR FILING DATE: 1997-09-05
;; PRIOR APPLICATION NUMBER: 60/056,884
;; PRIOR FILING DATE: 1997-08-22
;; NUMBER OF SEQ ID NOS: 280
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 166
;; LENGTH: 81

Query Match 3.2%; Score 6; DB 9; Length 81;
Best Local Similarity 100.0%; Pred.No.1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATEPYI 6
Db 71 ATEPYI 76

SULT 15
-09-148-545-166
; Sequence 166, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rozen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001PI
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07

;; EARLIER APPLICATION NUMBER: 60/040,163
;; EARLIER FILING DATE: 1997-03-07
;; EARLIER APPLICATION NUMBER: 60/047,615
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,600
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,597
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,502
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,633
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,583
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,617
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,618
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,503
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,592
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,581
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,584
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,500
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,587
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,492
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,598
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,613
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,582
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,596
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,612
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,632
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,601
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/043,580
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,568
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,314
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,569
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,311
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,671
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,674
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,669
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,312
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,313
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,672
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,315
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/048,974
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/056,886

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047, 595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/057, 761
EARLIER FILING DATE: 05-Sep-1997
EARLIER APPLICATION NUMBER: 60/047, 599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043, 578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047, 501
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/043, 670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056, 632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048, 964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057, 650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056, 884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 166
LENGTH: 81

Query Match 3.2%; Score 6; DB 9; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATEPYI 6
|||||
Db 71 ATEPYI 76

RESULT 16
US-09-867-550-1282
Sequence 1282, Application US/09867550
Patent No. US20020082206A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Ruad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1282
LENGTH: 84
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (7)
OTHER INFORMATION: Wherein Xaa may be any one of Ile or Leu or Phe or Val
NAME/KEY: VARIANT
LOCATION: (80)
OTHER INFORMATION: Wherein Xaa may be any one of Ile or Leu or Val
US-09-867-550-1282

Query Match 3.2%; Score 6; DB 10; Length 84;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 81 SEDSKL 86
| | | | |
Db 68 SEDSKL 73

RESULT 17
US-09-993-333-12
; Sequence 12, Application US/09993333
; Patent No. US20020156040A1
; GENERAL INFORMATION:
; APPLICANT: Oberley, Larry Wayne
; APPLICANT: Weydert, Christine J.
; APPLICANT: Smith, Benjamin Barnes
; TITLE OF INVENTION: Reduction of antioxidant enzyme levels in tumor cells using anti-
; FILE REFERENCE: 875.042051
; CURRENT APPLICATION NUMBER: US/09/993,333
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/248,328
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-993-333-12

Query Match 3.2%; Score 6; DB 9; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 YVNNLN 27
| | | | |
Db 58 YVNNLN 63

RESULT 18
US-09-515-806-28
; Sequence 28, Application US/09515806
; Patent No. US20020132321A1
; GENERAL INFORMATION:
; APPLICANT: COOK, WILLIAM J.
; APPLICANT: KAPILLER-LIBERMAN, ROSANA
; TITLE OF INVENTION: 14790, NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR
; FILE REFERENCE: 38155-20002.00
; CURRENT APPLICATION NUMBER: US/09/515,806
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: Kinase sequence
US-09-515-806-28

Query Match 3.2%; Score 6; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 HGGGQP 79
| | | | |
Db 45 HGGGQP 50

RESULT 19
US-09-738-626-4908

; Sequence 4908, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4908
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4908

Query Match 3.2%; Score 6; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 LVALQK 50
| | | | |
Db 52 LVALQK 57

RESULT 20
US-10-116-273-16
; Sequence 16, Application US/10116273
; Publication No. US20020192183A1
; GENERAL INFORMATION:
; APPLICANT: Anne Dam Jensen
; TITLE OF INVENTION: Interferon gamma polypeptide variants
; FILE REFERENCE: 231us410 - INFG variants
; CURRENT APPLICATION NUMBER: US/10/116,273
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-terminally
; OTHER INFORMATION: truncated [S99F]NIFNG
US-10-116-273-16

Query Match 3.2%; Score 6; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
| | | | |
Db 99 TVTDLN 104

RESULT 21
US-10-116-273-15
; Sequence 15, Application US/10116273

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/ Publication No. US20020192183A1
/ GENERAL INFORMATION:
/ APPLICANT: Anne Dam Jensen
/ TITLE OF INVENTION: Interferon gamma polypeptide variants
/ FILE REFERENCE: 231us410 - INFG variants
/ CURRENT APPLICATION NUMBER: US/10/116,273
/ CURRENT FILING DATE: 2002-04-04
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 15
/ LENGTH: 129
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: C-terminally
/ OTHER INFORMATION: truncated [S99T]huIFNG
US-10-116-273-15

Query Match
Best Local Similarity 3.2%; Score 6; DB 9; Length 129;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
| | | | |
Db 99 TVTDLN 104

RESULT 22
US-10-116-273-14
/ Sequence 14, Application US/10116273
/ Publication No. US20020192183A1
/ GENERAL INFORMATION:
/ APPLICANT: Anne Dam Jensen
/ TITLE OF INVENTION: Interferon gamma polypeptide variants
/ FILE REFERENCE: 231us410 - INFG variants
/ CURRENT APPLICATION NUMBER: US/10/116,273
/ CURRENT FILING DATE: 2002-04-04
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 130
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: C-terminally
/ OTHER INFORMATION: truncated [S99T]huIFNG
US-10-116-273-14

Query Match
Best Local Similarity 3.2%; Score 6; DB 9; Length 130;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
| | | | |
Db 99 TVTDLN 104

RESULT 23
US-10-116-273-13
/ Sequence 13, Application US/10116273
/ Publication No. US20020192183A1
/ GENERAL INFORMATION:
/ APPLICANT: Anne Dam Jensen
/ TITLE OF INVENTION: Interferon gamma polypeptide variants
/ FILE REFERENCE: 231us410 - INFG variants
/ CURRENT APPLICATION NUMBER: US/10/116,273
/ CURRENT FILING DATE: 2002-04-04
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 13
/ LENGTH: 131
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
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/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: C-terminally
/ OTHER INFORMATION: truncated [S99T]huIFNG
US-10-116-273-13

Query Match
Best Local Similarity 3.2%; Score 6; DB 9; Length 131;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
| | | | |
Db 99 TVTDLN 104

RESULT 24
US-10-116-273-12
/ Sequence 12, Application US/10116273
/ Publication No. US20020192183A1
/ GENERAL INFORMATION:
/ APPLICANT: Anne Dam Jensen
/ TITLE OF INVENTION: Interferon gamma polypeptide variants
/ FILE REFERENCE: 231us410 - INFG variants
/ CURRENT APPLICATION NUMBER: US/10/116,273
/ CURRENT FILING DATE: 2002-04-04
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 132
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: C-terminally
/ OTHER INFORMATION: truncated [S99T]huIFNG
US-10-116-273-12

Query Match
Best Local Similarity 3.2%; Score 6; DB 9; Length 132;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
| | | | |
Db 99 TVTDLN 104

RESULT 25
US-10-116-273-11
/ Sequence 11, Application US/10116273
/ Publication No. US20020192183A1
/ GENERAL INFORMATION:
/ APPLICANT: Anne Dam Jensen
/ TITLE OF INVENTION: Interferon gamma polypeptide variants
/ FILE REFERENCE: 231us410 - INFG variants
/ CURRENT APPLICATION NUMBER: US/10/116,273
/ CURRENT FILING DATE: 2002-04-04
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 11
/ LENGTH: 133
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: C-terminally
/ OTHER INFORMATION: truncated [S99T]huIFNG
US-10-116-273-11

Query Match
Best Local Similarity 3.2%; Score 6; DB 9; Length 133;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
| | | | |
Db 99 TVTDLN 104
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RESULT 26
US-10-116-273-10
; Sequence 10, Application US/10116273
; Publication No. US20020192183A1
; GENERAL INFORMATION:
; APPLICANT: Anne Dam Jensen
; TITLE OF INVENTION: Interferon gamma polypeptide variants
; FILE REFERENCE: 231us410 - INFG variants
; CURRENT APPLICATION NUMBER: US/10/116,273
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 10
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-terminally
; OTHER INFORMATION: truncated [S99T]huIFNG
; -10-116-273-10

Query Match
3.2%; Score 6; DB 9; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
|||||
Db 99 TVTDLN 104

RESULT 27
US-10-116-273-9
; Sequence 9, Application US/10116273
; Publication No. US20020192183A1
; GENERAL INFORMATION:
; APPLICANT: Anne Dam Jensen
; TITLE OF INVENTION: Interferon gamma polypeptide variants
; FILE REFERENCE: 231us410 - INFG variants
; CURRENT APPLICATION NUMBER: US/10/116,273
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 9
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-terminally
; OTHER INFORMATION: truncated [S99T]huIFNG
; -10-116-273-9

Query Match
3.2%; Score 6; DB 9; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
|||||
Db 99 TVTDLN 104

RESULT 28
US-10-116-273-8
; Sequence 8, Application US/10116273
; Publication No. US20020192183A1
; GENERAL INFORMATION:
; APPLICANT: Anne Dam Jensen
; TITLE OF INVENTION: Interferon gamma polypeptide variants
; FILE REFERENCE: 231us410 - INFG variants
; CURRENT APPLICATION NUMBER: US/10/116,273
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentln Ver. 2.1
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; SEQ ID NO 8
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-terminally
; OTHER INFORMATION: truncated [S99T]huIFNG
; -10-116-273-8

Query Match
3.2%; Score 6; DB 9; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
|||||
Db 99 TVTDLN 104

RESULT 29
US-10-116-273-7
; Sequence 7, Application US/10116273
; Publication No. US20020192183A1
; GENERAL INFORMATION:
; APPLICANT: Anne Dam Jensen
; TITLE OF INVENTION: Interferon gamma polypeptide variants
; FILE REFERENCE: 231us410 - INFG variants
; CURRENT APPLICATION NUMBER: US/10/116,273
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 7
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-terminally
; OTHER INFORMATION: truncated [S99T]huIFNG
; -10-116-273-7

Query Match
3.2%; Score 6; DB 9; Length 137;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
|||||
Db 99 TVTDLN 104

RESULT 30
US-10-116-273-6
; Sequence 6, Application US/10116273
; Publication No. US20020192183A1
; GENERAL INFORMATION:
; APPLICANT: Anne Dam Jensen
; TITLE OF INVENTION: Interferon gamma polypeptide variants
; FILE REFERENCE: 231us410 - INFG variants
; CURRENT APPLICATION NUMBER: US/10/116,273
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 6
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-terminally
; OTHER INFORMATION: truncated [S99T]huIFNG
; -10-116-273-6

Query Match
3.2%; Score 6; DB 9; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 139 TVTDLN 144
| | | | |
Db 99 TVTDLN 104

RESULT 31
US-10-116-273-5
; Sequence 5, Application US/10116273
; Publication No. US20020192183A1
; GENERAL INFORMATION:
; APPLICANT: Anne Dam Jensen
; TITLE OF INVENTION: Interferon gamma polypeptide variants
; FILE REFERENCE: 231ue410 - INFG variants
; CURRENT APPLICATION NUMBER: US/10/116,273
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-terminally
US-10-116-273-5

Query Match 3.2%; Score 6; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
| | | | |
Db 99 TVTDLN 104

RESULT 32
US-10-116-273-4
; Sequence 4, Application US/10116273
; Publication No. US20020192183A1
; GENERAL INFORMATION:
; APPLICANT: Anne Dam Jensen
; TITLE OF INVENTION: Interferon gamma polypeptide variants
; FILE REFERENCE: 231ue410 - INFG variants
; CURRENT APPLICATION NUMBER: US/10/116,273
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-terminally
US-10-116-273-4

Query Match 3.2%; Score 6; DB 9; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
| | | | |
Db 99 TVTDLN 104

RESULT 33
US-10-116-273-3
; Sequence 3, Application US/10116273
; Publication No. US20020192183A1
; GENERAL INFORMATION:
; APPLICANT: Anne Dam Jensen
; TITLE OF INVENTION: Interferon gamma polypeptide variants
; FILE REFERENCE: 231ue410 - INFG variants

; CURRENT APPLICATION NUMBER: US/10/116,273
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-terminally
US-10-116-273-3

Query Match 3.2%; Score 6; DB 9; Length 141;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
| | | | |
Db 99 TVTDLN 104

RESULT 34
US-10-116-273-2
; Sequence 2, Application US/10116273
; Publication No. US20020192183A1
; GENERAL INFORMATION:
; APPLICANT: Anne Dam Jensen
; TITLE OF INVENTION: Interferon gamma polypeptide variants
; FILE REFERENCE: 231ue410 - INFG variants
; CURRENT APPLICATION NUMBER: US/10/116,273
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-terminally
US-10-116-273-2

Query Match 3.2%; Score 6; DB 9; Length 142;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
| | | | |
Db 99 TVTDLN 104

RESULT 35
US-09-308-207-60
; Sequence 60, Application US/09308207
; Publication No. US20030022323A1
; GENERAL INFORMATION:
; APPLICANT: MARIA DIAZ-TORRES ET AL.
; TITLE OF INVENTION: METHOD FOR THE RECOMBINANT
; PRODUCTION OF 1,3 PROPANEDIOL

NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 4 Cambridge Place
CITY: Rochester
STATE: NY
COUNTRY: U.S.A
ZIP: 14618
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows


```

; SOFTWARE: FastSeq for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/308,207
;   FILING DATE: 13-May-1999
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 60/030,601
;     FILING DATE: 13-NOV-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Glaister, Debra
;     REGISTRATION NUMBER: 33,888
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 650-864-7620
;     TELEFAX: 650-845-6504
;     TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 60:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 142 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;   MOLECULE TYPE: No. US2003002233A1e
;   SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-308-207-60

Query Match          3.2%; Score 6; DB 9; Length 142;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QAVEAK 37
Db 20 QAVEAK 25

RESULT 36
US-10-116-273-1
; Sequence 1, Application US/10116273
; Publication No. US20020192183A1
; GENERAL INFORMATION:
;   APPLICANT: Anne Dam Jensen
;   TITLE OF INVENTION: Interferon gamma polypeptide variants
;   FILE REFERENCE: 231us410 - INFg variants
;   CURRENT APPLICATION NUMBER: US/10/116,273
;   CURRENT FILING DATE: 2002-04-04
;   NUMBER OF SEQ ID NOS: 49
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 1
;     LENGTH: 143
;     TYPE: PRT
;     ORGANISM: Artificial Sequence
;     FEATURE:
;     OTHER INFORMATION: Description of Artificial Sequence: [S99T]huIFNG
US-10-116-273-1

Query Match          3.2%; Score 6; DB 9; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TVTDLN 144
Db 99 TVTDLN 104

RESULT 37
US-10-147-874-6
; Sequence 6, Application US/10147874
; Publication No. US20030027237A1
; GENERAL INFORMATION:
;   APPLICANT: TARDIEUX, ISABELLE
;   APPLICANT: DELORME, VIOLENE
;   TITLE OF INVENTION: SERINE-THREONINE PHOSPHATASE PROTEIN OF A PARASITIC ORGANISM OF T
;   TITLE OF INVENTION: APICOMPLEXA PHYLLUM; APPLICATIONS IN THERAPEUTICS
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```

; FILE REFERENCE: 223316US0
;
; CURRENT APPLICATION NUMBER: US/10/147,874
;   CURRENT FILING DATE: 2002-05-20
;   PRIOR APPLICATION NUMBER: US 60/291,609
;   PRIOR FILING DATE: 2001-05-18
;   NUMBER OF SEQ ID NOS: 19
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 6
;   LENGTH: 151
;   TYPE: PRT
;   ORGANISM: Plasmodium falciparum
US-10-147-874-6

Query Match          3.2%; Score 6; DB 9; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GEVAKL 45
Db 68 GEVAKL 73

RESULT 38
US-09-765-272-224
; Sequence 224, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
;   APPLICANT: Choi et. al.
;   TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
;   NUMBER OF SEQUENCES: 452
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Human Genome Sciences, Inc.
;     STREET: 9410 Key West Avenue
;     CITY: Rockville
;     STATE: Maryland
;     COUNTRY: USA
;     ZIP: 20850
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;     COMPUTER: HP Vectra 486/33
;     OPERATING SYSTEM: MSDOS version 6.2
;   SOFTWARE: ASCII Text
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/765,272
;     FILING DATE: 22-Jan-2001
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/961,083
;     FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Brookes, A. Anders
;     REGISTRATION NUMBER: 36,373
;     REFERENCE/DOCKET NUMBER: PB340P2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (301) 309-8504
;       TELEFAX: (301) 309-8512
;   INFORMATION FOR SEQ ID NO: 224:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 153 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-765-272-224

Query Match          3.2%; Score 6; DB 10; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 LDKLIE 102
Db 145 LDKLIE 150
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RESULT 39
US-09-864-761-48707
; Sequence 48707, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48707
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007480.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.94
; OTHER INFORMATION: EST HUMAN HIT: AA132806.1, EVALUE 2.00e-10
; OTHER INFORMATION: SWISSPROT HIT: Q03112, EVALUE 2.00e-69
US-09-864-761-48707
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Query Match          3.2%; Score 6; DB 10; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 40 GEVKKL 45
Db 88 GEVKKL 93
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```
RESULT 40
US-10-101-464A-548
; Sequence 548, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 548
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-548
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Query Match          3.2%; Score 6; DB 9; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 144 NLVPLI 149
Db 137 NLVPLI 142
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Search completed: April 9, 2003, 14:29:18
Job time : 53.945 secs
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OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Eagan / Serotype B;
 RA MEDLINE=95020555; PubMed=7934846;
 RX Kroll J.S., Langford P.R., Saah J.R., Loynds B.M.;
 RT "Molecular and genetic characterization of superoxide dismutase in
 RL Haemophilus influenzae type b";
 RU Mol. Microbiol. 10:839-848 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KM20 / ATCC 51907;
 RA MEDLINE=9530630; PubMed=7542800;
 RX Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Frichman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.U., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RL Rd."; Science 269:496-512 (1995).
 RN [3]
 RP SEQUENCE OF 1-5.
 RX MEDLINE=20137488; PubMed=10675023;
 RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
 RA Gray C., Fountoulakis M.;
 RT "Two-dimensional map of the proteome of Haemophilus influenzae";
 RL Electrophoresis 21:411-429 (2000).
 CC - FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC - CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC - COFACTOR: Manganese (By similarity).
 CC - SUBUNIT: HOMODIMER (By similarity).
 CC - SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL: X73832; CAAS2054.1; -;
 DR EMBL: U32789; AAC22745.1; -;
 DR HSSP: P00448; IVEW.
 DR TIGR: H11088; -;
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sode; 1.
 DR ProDom: PD000475; SODismutase; 1.
 DR PROSITE: PS00088; SOD_MN; 1.
 KW Oxidoreductase; Manganese; Complete proteome.
 FT INIT MET 0
 FT METAL 26
 FT METAL 82
 FT METAL 169
 FT METAL 173
 FT METAL 177
 FT METAL 214
 FT CONFLICT 207
 FT SEQUENCE 214 AA; 23979 MW; B9BADDC70F17EA3 CRC64;
 QY 1 KYSLELDYFSAATEPYISGOINEIXYT 28
 Query Match 46.2%; Score 67; DB 1; Length 214;
 Best Local Similarity 44.4%; Pred. No. 0.0064;
 Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Db 2 YTLPELGAVNALPFPDQMEIHS 28
 RESULT 40
 SODM_CHAFE
 ID SODM_CHAFE STANDARD; PRT; 224 AA.
 AC 096347;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Charybdis feriatius (Crab).
 OS Charybdis feriatius (Crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Charybdis.
 OX NCBI_TaxID=65693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ian C.T., Lai Y.S., Kuo T.J., Chang T.C.;
 RT "Molecular cloning, expression, and characterization of a cDNA
 RL encoding Mn-superoxide dismutase from crab Charybdis feriatius";
 Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 CC - FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC - CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC - COFACTOR: Manganese (By similarity).
 CC - SUBUNIT: HOMOTETRAMER (By similarity).
 CC - SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC - SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF019411; AAD01640.1; -;
 DR HSSP: P04179; IABW.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sode; 1.
 DR ProDom: PD000475; SODismutase; 1.
 DR PROSITE: PS00088; SOD_MN; 1.
 KW Oxidoreductase; Manganese; Mitochondrion; Transit peptide.
 FT TRANSIT 1
 FT CHAIN 20
 FT METAL 21
 FT METAL 46
 FT METAL 94
 FT METAL 177
 FT METAL 181
 FT SEQUENCE 224 AA; 24527 MW; 107CF193829138A CRC64;
 QY 21 KHTLPDLPYVGALPRTISAEMQGLHS 48
 Search completed: April 9, 2003, 13:57:53
 Job time : 4.85321 secs

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RESULT 37
SODM_RANCA STANDARD; PRT; 23 AA.
ID SODM_RANCA
AC P36215;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment).
OS Rana catesbeiana (Bull. frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=9400;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=87126854; PubMed=3492965;
RA Abe Y., Okazaki T.;
" Purification and properties of the manganese superoxide dismutase
from the liver of bullfrog, Rana catesbeiana.";
Arch. Biochem. Biophys. 253:241-248(1987).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Manganese.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; Sodfe, 1.
DR Prodom: PD000475; SODismutase; 1.
DR PROSITE: PS00088; SOD MN; PARTIAL.
KM Oxidoreductase; Manganese; Mitochondrion.
FT NON TER 23
FT SEQUENCE 23 AA; 2594 MW; 5D80ED9B0E04FE25 CRC64;
SQ
Query Match 46.2%; Score 67; DB 1; Length 23;
Best Local Similarity 50.0%; Pred. No. 0.00054;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 1 KYSLPELDYFSATEPYISGOI 22
DB 1 KHTLPDLPYDFGALQPHISAEI 22
RESULT 38
SODM_XANCP STANDARD; PRT; 203 AA.
ID SODM_XANCP
AC P53654;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1).
OS SODA OR SOD OR SODM OR XCC2278.
GN Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8004;
RX MEDLINE=96405948; PubMed=8810073;
RA Smith S.G., Wilson T.J., Dow J.M., Daniels M.J.;
" A gene for superoxide dismutase from Xanthomonas campestris pv.
campestris and its expression during bacterial-plant interactions.";
Mol. Plant Microbe Interact. 9:584-593(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furian L.R.,

```

```

RA Ouaguo R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Canavari F., Cardozo J., Chamberg F., Clapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidants J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
host specificities.";
RL Nature 417:459-463(2002).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Manganese.
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.
CC -----
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CC -----
DR EMBL: U42464; AAB47971.1; -.
DR EMBL: AE012335; AAM41557.1; -.
DR HSSP: P00448; IVEW.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; Sodfe, 1.
DR Prodom: PD000475; SODismutase; 1.
DR PROSITE: PS00088; SOD MN; 1.
KM Oxidoreductase; Manganese.
FT METAL 27
FT METAL 81
FT METAL 164
FT METAL 168
FT CONFLICT 53
FT CONFLICT 53
FT CONFLICT 88
FT CONFLICT 123
FT CONFLICT 141
FT CONFLICT 141
FT CONFLICT 180
FT CONFLICT 188
FT CONFLICT 192
FT SEQUENCE 203 AA; 22721 MW; C2C41F9FB150C860 CRC64;
SQ
Query Match 46.2%; Score 67; DB 1; Length 203;
Best Local Similarity 48.1%; Pred. No. 0.0061;
Matches 13; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATEPYISQINIXYT 28
DB 3 YTLPLQPAYDALEPNIDAQMEIHHT 29
RESULT 39
SODM_HAEIN STANDARD; PRT; 214 AA.
ID SODM_HAEIN
AC P43725;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1).
OS SODA OR H11088.
GN Haemophilus influenzae.

```



```
RESULT 33
SODM_CAVPO STANDARD; PRT; 211 AA.
ID SODM_CAVPO
AC P49114;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1)
DE (Fragment).
GN SOD2.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Lung;
RX MEDLINE=96180320; PubMed=8597602;
RA Yuan H.T., Bingle C.D., Kelly F.J.;
RA "Differential patterns of antioxidant enzyme mRNA expression in
RA guinea pig lung and liver during development.";
RA Biochim. Biophys. Acta 1305:163-171(1996).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Manganese (By similarity).
CC -1- SUBUNIT: HOMOTETRAMER (By similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
CC -----
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CC -----
CC EMBL; U39843; AAC52719.1; -.
CC HSSP; P04179; IABM.
CC InterPro; IPR001189; SODismutase.
CC Pfam; PF00061; Sodfe; 1.
CC DR Pfam; PF02777; Sodfe; C1.
CC DR ProDom; PD000475; SODismutase; 1.
CC DR PROSITE; PS00088; SOD_MN; 1.
CC KM Oxidoreductase; Manganese; Mitochondrion; Transit peptide.
CC TRANSIT 1 24 MITOCHONDRION (By similarity).
CC CHAIN 25 >211 SUPEROXIDE DISMUTASE [Mn].
CC METAL 50 50 MANGANESE (By similarity).
CC FT METAL 98 98 MANGANESE (By similarity).
CC FT METAL 183 183 MANGANESE (By similarity).
CC FT METAL 187 187 MANGANESE (By similarity).
CC FT NON_TER 211 211 MANGANESE (By similarity).
CC SQ SEQUENCE 211 AA; 23235 MW; 2032559161993E2D CRC64;
Query Match 46.9%; Score 68; DB 1; Length 211;
Best Local Similarity 35.7%; Pred. No. 0.0045;
Matches 10; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
QY 1 KYSLPELDYEPASATPYISQGINEIXYT 28
Db 25 KHSLLDLPDYDALQPHINAEIMQLHHS 52
RESULT 34
SODF_STRCO STANDARD; PRT; 212 AA.
ID SODF_STRCO
AC O51917;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Fe-Zn] 1 (EC 1.15.1.1) (FesOD 1) (SOD2).
DE Oxidoreductase; Iron; Zinc; Complete proteome.
```

```
GN SODF1 OR SODF OR SODB OR SCO2633 OR SC984A.03.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10147;
RX MEDLINE=98215165; PubMed=9555880;
RA Kim E.-J., Chung H.-J., Suh B., Hah Y.C., Roe J.-H.;
RT "Expression and regulation of the sodF gene encoding iron- and zinc-
RT containing superoxide dismutase in Streptomyces coelicolor Muller.";
RL J. Bacteriol. 180:2014-2020(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=9250253; PubMed=10231572;
RA Chung H.J., Kim E.J., Suh B., Choi J.H., Roe J.H.;
RT "Duplicate genes for Fe-containing superoxide dismutase in
RT Streptomyces coelicolor A3(2).";
RL Gene 231:87-93(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieker H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieker T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabbittowitsch E., Rajendram M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorek A., Woodward J., Barrett B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
RN [4]
RP SEQUENCE OF 1-15.
RC STRAIN=ATCC 10147;
RX MEDLINE=97054607; PubMed=8898904;
RA Kim F.-J., Kim H.-P., Hah Y.V., Roe J.-H.;
RT "Differential expression of superoxide dismutases containing Ni and
RT Fe/Zn in Streptomyces coelicolor.";
RL Eur. J. Biochem. 241:178-185(1996).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Iron and zinc.
CC -1- SUBUNIT: TETRAMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- INDUCTION: INHIBITED BY NICKEL.
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF012087; AAC46274.1; -.
CC DR EMBL; AF099014; AAD33128.1; -.
CC DR EMBL; AL138662; CAB71808.1; -.
CC DR HSSP; P80293; IAVM.
CC DR InterPro; IPR001189; SODismutase.
CC DR Pfam; PF00061; Sodfe; 1.
CC DR Pfam; PF02777; Sodfe; C1.
CC DR ProDom; PD000475; SODismutase; 1.
CC DR PROSITE; PS00088; SOD_MN; 1.
CC KM Oxidoreductase; Iron; Zinc; Complete proteome.
```

FT METAL 189 189 MANGANESE (BY SIMILARITY)
 FT METAL 193 193 MANGANESE (BY SIMILARITY)
 SQ SEQUENCE 228 AA; 25504 MW; 9F4D7582ADAD7F6 CRC64;

Query Match 47.6%; Score 69; DB 1; Length 228;
 Best Local Similarity 46.2%; Pred. No. 0.0034;
 Matches 12; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 XSLPELDYFSATEPYISQINEIXY 27
 DB 28 FSLPDLPYDGALEPAISGIMOLHH 53

RESULT 31

SODM_AGABI STANDARD; PRT; 200 AA.

AC Q9P4T6; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

RT 15-JUN-2002 (Rel. 41, Last annotation update)

RL Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).

SOD.

OS Agaricus bisporus (Common mushroom).

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

OX Agaricales; Agaricaceae; Agaricus.

NCBI_TaxID=5341;

RP SEQUENCE FROM N.A.

RC STRAIN=Horet U3;

RA Eastwood D.C., Bains N.K., Henderson J., Burton K.S.;

RT "Oxidative stress in the harvested mushroom, Agaricus bisporus."

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Destroys radicals which are normally produced within the

CC cells and which are toxic to biological systems.

CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).

CC -1- COFACTOR: Manganese (by similarity).

CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.

CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE

CC FAMILY.

CC -----

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CC -----

CC EMBL; AJ04469; CAB94731.1; -

CC HSSP; P04179; 1VAR.

CC InterPro; IPR001189; SODismutase.

CC Pfam; PF00081; sode, 1.

CC Pfam; PF02777; sode, C; 1.

CC ProDom; PD000475; SODismutase; 2.

CC PROSITE; PS00088; SOD_MN; 1.

CC Oxidoreductase; Manganese; Mitochondrion; Transit peptide.

CC TRANSIT 1 ? MITOCHONDRION (POTENTIAL).

CC CHAIN 1 ? SUPEROXIDE DISMUTASE [MN].

CC METAL 27 27 MANGANESE (BY SIMILARITY).

CC METAL 72 72 MANGANESE (BY SIMILARITY).

CC METAL 157 157 MANGANESE (BY SIMILARITY).

CC METAL 161 161 MANGANESE (BY SIMILARITY).

CC SEQUENCE 200 AA; 22194 MW; 9758B1DD1F64F19 CRC64;

Query Match 46.9%; Score 68; DB 1; Length 200;

Best Local Similarity 54.2%; Pred. No. 0.0042;

Matches 13; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 4 LPELDYFSATEPYISQINEIXY 27
 DB 5 LPELDYFSATEPYISQINEIXY 28

RESULT 32
 SODF_SULAC STANDARD; PRT; 210 AA.

AC Q08713; 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

RT 15-JUN-2002 (Rel. 41, Last annotation update)

RL Superoxide dismutase [Fe] (EC 1.15.1.1).

SOD.

OS Sulfolobus acidocaldarius.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

OX Sulfolobus.

NCBI_TaxID=2285;

RP SEQUENCE FROM N.A.

RC MEDLINE=93326644; PubMed=8334170;

RA Klenk H.-P., Schleper C., Schwass V., Brudler R.;

RT "Nucleotide sequence, transcription and phylogeny of the gene

RL encoding the superoxide dismutase of Sulfolobus acidocaldarius."

RL Biochim. Biophys. Acta 1174:95-98 (1993).

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

RC STRAIN=ATCC 33909 / NCIB 11770 / DSM 639;

RA Knapp S., Kardinahl S., Hellgren N., Tibbelin G., Schaefer G.,

RT Ladenstein R.;

RT "Refined crystal structure of a superoxide dismutase from the

RT hyperthermophilic archaeon Sulfolobus acidocaldarius at 2.2-A

RT resolution."

CC -1- FUNCTION: Destroys radicals which are normally produced within the

CC cells and which are toxic to biological systems.

CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).

CC -1- COFACTOR: IRON.

CC -1- SUBUNIT: HOMOTETRAMER AT HIGH TEMPERATURE; HOMODIMER AT ROOM

CC TEMPERATURE.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE

CC FAMILY.

CC -----

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CC -----

CC EMBL; X63386; CAA44993.1; -

CC PIR; S34616; S34616.

CC PDB; 1B06; 1B-NOV-99.

CC InterPro; IPR001189; SODismutase.

CC Pfam; PF00081; sode, 1.

CC Pfam; PF02777; sode, C; 1.

CC ProDom; PD000475; SODismutase; 1.

CC PROSITE; PS00088; SOD_MN; FALSE NEG.

CC Oxidoreductase; Iron; 3D-structure.

CC INIT_MET 0 0 IRON.

CC METAL 33 33 IRON.

CC METAL 84 84 IRON.

CC METAL 170 170 IRON.

CC METAL 174 174 IRON.

CC SEQUENCE 210 AA; 24135 MW; 086CAB277D99FBB CRC64;

Query Match 46.9%; Score 68; DB 1; Length 210;

Best Local Similarity 44.4%; Pred. No. 0.0044;

Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSATEPYISQINEIXY 27
 DB 8 KYSLPELDYFSATEPYISQINEIXY 34

GN SODF.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RA SEQUENCE FROM N.A.
 RP Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.:
 RT "Sequence analysis of the Bacillus subtilis chromosome region between
 the t_{er}C and o_{da}B loci cloned in a yeast artificial chromosome.";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=9804403; PubMed=9384377;
 RA Kunze F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 Azevedo V., Bertoletti L., Bessieres P., Bolotin A., Borchert S.,
 Borries R., Boursier L., Brans A., Braun M., Bridgell S.C., Bron S.,
 Brouillet S., Brunsch C.V., Caldwell B., Capuano V., Carter N.M.,
 Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 Denicourt F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 Ertan C.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 Fritz S.Y., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,
 Ghim S.Y., Glaeser P., Goffeau A., Goldlighty E.J., Grandi G.,
 Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones U.,
 Joris B., Karamata D., Kasaahara Y., Klier-Blanchard M., Klein C.,
 Kobayashi Y., Koelter P., Koningsstein G., Krogh S., Kumano M.,
 Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 Lee S.M., Levine A., Liu H., Maasda S., Mauch C., Medigue C.,
 Medina D., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudga B., Park S.H.,
 Paro V., Phil T.M., Portetle D., Portwille S., Prescott A.M.,
 Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadie Y.,
 Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
 Sekiuchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Solito B.,
 Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 Takenishi M., Tamakoshi A., Tanaka T., Terpestra P., Tognoni A.,
 Tosa V., Uchiyama S., Vandenbol M., Vanlier F., Vassarotti A.,
 Varsi A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 Winters P., Wipet A., Yamamoto H., Yamane K., Yano K., Yata K.,
 Yoshida K., Yoshikawa H.F., Zumberg E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis.";
 RL Nature 390:249-256(1997).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 cells and which are toxic to biological systems
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Iron (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF027868; AAB84442.1; -;
 DR EMBL: Z99114; CAB13825.1; -;
 DR HSSP: P80293; IAVM.
 DR Subtilist; BG12676; sodF.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sodfe; 1.
 DR Pfam: PF02777; sodfe; C; 1.
 DR ProDom: PD000475; SODismutase; 1.
 DR PROSITE: PS00088; SOD MN; 1.
 KW Oxidoreductase; Iron; Complete proteome.
 FT METAL 104 104 IRON (BY SIMILARITY).
 FT METAL 152 152 IRON (BY SIMILARITY).
 FT METAL 236 236 IRON (BY SIMILARITY).

FT METAL 240 240 IRON (BY SIMILARITY).
 SQ SEQUENCE 281 AA; 33477 MW; 7F36AC0A60E74DB0 CRC64;
 Query Match 48.3%; Score 70; DB 1; Length 281;
 Best Local Similarity 50.0%; Pred. No. 0.0031;
 Matches 14; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 Oy 1 KYSLEPDLDFEFSATPEYISGQINEIXYT 28
 Db 79 KHVLPKLPKYSALPEYISRDIMLHHT 106
 RESULT 30
 SODM_NICPL STANDARD; PRT; 228 AA.
 ID SODM_NICPL
 AC P11796;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 GN SODA.
 OS Nicotiana glauca (leadwort-leaved tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4092;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P2;
 RX MEDLINE=89231633; PubMed=2540959;
 RA Bowler C., Alliotte T., de Loose M., van Montagu M., Inze D.,
 RT "The induction of manganese superoxide dismutase in response to
 stress in Nicotiana glauca.";
 RL EMBO J. 8:31-38(1989).
 RN [2]
 RP SEQUENCE OF 25-47.
 RA Bauw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.,
 RT "Alterations in the phenotype of plant cells studied by NH₂-terminal
 amino acid-sequence analysis of proteins electrophoretically separated from two-
 dimensional gel-separated total extracts.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 FAMILY.
 CC -----
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 CC -----
 DR EMBL: X14482; CAA32643.1; -;
 DR EMBL: A05355; CAA00450.1; -;
 DR PIR: S03639; S03639.
 DR PIR: I28027; I28027.
 DR HSSP: P04179; IAP6.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sodfe; 1.
 DR Pfam: PF02777; sodfe; C; 1.
 DR ProDom: PD000475; SODismutase; 1.
 DR PROSITE: PS00088; SOD MN; 1.
 KW Oxidoreductase; Manganese; Mitochondrion; Transic peptide.
 FT TRANSIT 1 24
 FT CHAIN 25 228 SUPEROXIDE DISMUTASE [MN].
 FT METAL 52 52 MANGANESE (BY SIMILARITY).
 FT METAL 100 100 MANGANESE (BY SIMILARITY).

RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
 RA Pai G., Miltischer J., Sellers P., Gill J.E., Feldlyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneke T., Nakamura Y., Sato S., Kato T., Asanizu E.,
 RA Sasamoto S., Kimura T., Ideawake K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Matanabe A., Yamada M., Yasuda M., Tabata S.,
 RA "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RT thaliana";
 RL Nature 408:820-822(2000).
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "R1XN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RL SGP consortium (Salik/Stanford/PGSC).";
 CC Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese (By similarity).
 CC -1- SUBUNIT: HOMOTETRAMER (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC -----
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CC -----
 CC EMBL: AF061518; AAC24832.1; -;
 CC DR EMBL: AC009991; AAF01529.1; -;
 CC DR EMBL: AY072495; AAL66910.1; -;
 CC DR EMBL: AY059807; AAL24289.1; -;
 CC DR HSSP: P04179; IABM.
 CC DR InterPro: IPR001189; SODismutase.
 CC DR Pfam: PF00081; sodfe, 1.
 CC DR Pfam: PF02777; sodfe_C, 1.
 CC DR Prodom: PD000475; SODismutase; 1.
 CC DR PROSITE: PS00088; SOD_MN; 1.
 CC KM Oxidoreductase; Manganese; Mitochondrion; Transit peptide.
 CC FT TRANSIT 1 29
 CC FT CHAIN 1 29
 CC FT METAL 30 231
 CC FT METAL 59 59
 CC FT METAL 103 103
 CC FT METAL 192 192
 CC FT METAL 196 196
 CC FT METAL 169 169
 CC FT CONFLICT 169 169
 CC FT SEQUENCE 231 AA; 25444 MW; 2DBD5560A9EBAD7D CRC64;
 CC -----

Query Match 48.3%; Score 70; DB 1; Length 231;
 Best Local Similarity 46.2%; Pred. No. 0.0025; Mismatches 6; Indels 0; Gaps 0;
 Matches 12; Conservative 8;

QY 2 YSLPELDYFSGATEPYISGOINEIXY 27
 Db 31 FTLPDLVYDYGALBPALISGEIMQIH 56

RESULT 28
 SODM_PEA STANDARD; PRT; 233 AA.
 ID SODM_PEA
 AC P27084; Q43069;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 GN SODA.

OS Pisum sativum (Garden pea).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC Euroside I; Fabales; Fabaceae; Papilionoideae; Viciales; Pisum.
 CC NCBI_TaxId=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RX MEDLINE=92032795; PubMed=1932701;
 RA Wong-Vega L., Burke J.J., Allen R.D.;
 RT "Isolation and sequence analysis of a cDNA that encodes pea manganese
 RT superoxide dismutase.";
 RL Plant Mol. Biol. 17:1271-1274(1991).
 RN [2]
 RP REVISIONS.
 RC STRAIN=cv. Alaska; TISSUE=Isolated bud;
 RA Jaradat T., Wong-Vega L., Allen R.D.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese (By similarity).
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC -----

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CC -----
 CC EMBL: X60170; CAA42737.1; -;
 CC DR EMBL: U30841; AAA74442.1; -;
 CC DR PIR: S18343; DSPMN.
 CC DR HSSP: P04179; IABM.
 CC DR InterPro: IPR001189; SODismutase.
 CC DR Pfam: PF00081; sodfe, 1.
 CC DR Pfam: PF02777; sodfe_C, 1.
 CC DR Prodom: PD000475; SODismutase; 1.
 CC DR PROSITE: PS00088; SOD_MN; 1.
 CC KM Oxidoreductase; Manganese; Mitochondrion; Transit peptide.
 CC FT TRANSIT 1 36
 CC FT CHAIN 1 36
 CC FT METAL 37 233
 CC FT METAL 64 64
 CC FT METAL 112 112
 CC FT METAL 194 194
 CC FT METAL 198 198
 CC FT METAL 160 160
 CC FT CONFLICT 160 160
 CC FT CONFLICT 176 176
 CC FT CONFLICT 192 192
 CC FT SEQUENCE 233 AA; 25822 MW; DB246D1FF0AF99 CRC64;
 CC -----

Query Match 48.3%; Score 70; DB 1; Length 233;
 Best Local Similarity 46.2%; Pred. No. 0.0025; Mismatches 6; Indels 0; Gaps 0;
 Matches 12; Conservative 8;

QY 2 YSLPELDYFSGATEPYISGOINEIXY 27
 Db 40 FTLPDLVYDYGALBPALISGEIMQIH 65

RESULT 29
 SODF_BACSU STANDARD; PRT; 281 AA.
 ID SODF_BACSU
 AC Q35023;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable superoxide dismutase [Fe] (EC 1.15.1.1).

DR PRODOM: PD000475; SODismutase; 1.
 KW Oxidoreductase; Iron; Complete proteome.
 FT METAL 26 IRON (BY SIMILARITY).
 FT METAL 81 IRON (BY SIMILARITY).
 FT METAL 164 164 IRON (BY SIMILARITY).
 FT METAL 168 168 IRON (BY SIMILARITY).
 SQ SEQUENCE 203 AA; 23523 MW; ABA3A24EAC591716 CRC64;
 Query Match 48.3%; Score 70; DB 1; Length 203;
 Best Local Similarity 44.4%; Pred. No. 0.0021;
 Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 QY 2 YSPLELDYFSAATEPYISGQINEIXYT 28
 DB 2 FKLPELDGYDAVEPYIDAKTMEIHS 28
 RESULT 26
 SODM_CHLBN STANDARD; PRT; 207 AA.
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase (Mn) (EC 1.15.1.1).
 GN SODA OR SODM OR CPN0057 OR CP0718.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 NCBI_TaxId=83556;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10192388;
 RA Kellman S., Mitchell W., Marache R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Mitchell J., Davis R.W., Stephens R.S.,
 RA "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
 RA Nat. Genet. 21:385-389(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Uterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Knouri H., Craven B., Bowman C., Dodson R.,
 RA Gilm M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RA "Genome sequences of Chlamydia trachomatis Morn and Chlamydia
 pneumoniae AR39";
 RA Nucleic Acids Res. 28:1397-1406(2000).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shiba T., Ishii K., Hattori M., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 from Japan and CML029 from USA";
 RA Nucleic Acids Res. 28:2311-2314(2000).
 RL
 CC -1- FUNCTION: Destroy radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese (By similarity).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL: AEO01591; AAD18210.1; -.
 DR EMBL: AEO02230; AAF38524.1; -.
 DR EMBL: AP002545; BAA98268.1; -.
 DR HSSP: P04179; IAP6.
 DR PHCI_2DPAGE; Q929C4; -.
 DR TIGR; CP0718; -.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sode; 1.
 DR Pfam; PF02777; sode_C; 1.
 DR PRODOM: PD000475; SODismutase; 1.
 KW Oxidoreductase; Manganese; Complete proteome.
 FT METAL 31 31 MANGANESE (BY SIMILARITY).
 FT METAL 78 78 MANGANESE (BY SIMILARITY).
 FT METAL 166 166 MANGANESE (BY SIMILARITY).
 FT METAL 170 170 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 207 AA; 23541 MW; 45A4A6FF096F8934 CRC64;
 Query Match 48.3%; Score 70; DB 1; Length 207;
 Best Local Similarity 61.9%; Pred. No. 0.0022;
 Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 2 YSPLELDYFSAATEPYISGQI 22
 DB 6 YSPLELDYDALEPVISSEI 26
 RESULT 27
 SODM_ARATH STANDARD; PRT; 231 AA.
 ID SODM_ARATH
 AC 081235; Q9SRK3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Superoxide dismutase (Mn), mitochondrial precursor (EC 1.15.1.1).
 GN SODA OR MSD1 OR AT3G10920 OR P9P8.26.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxId=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. Columbia;
 RX MEDLINE=98440686; PubMed=9765550;
 RA Kliebenstein D.J., Monde R.A., Last R.L.;
 RA "Superoxide dismutase in Arabidopsis: an eclectic enzyme family with
 RA disparate regulation and protein localization";
 RA Plant Physiol. 118:637-650(1998).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. Columbia;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salasoulat M., Lemcke K., Rieger M., Ansege W., Unseid M.,
 RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Delaguy M., Boutry M., Griwell L.A., Mache R., Puigdomenech P.,
 RA De Simone V., Choise N., Artiguenave F., Robert C., Brotier P.,
 RA Wincker P., Cattivello L., Weissenbach J., Saurin W., Quetier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benev V.,
 RA Wurmbech E., Drzonek H., Erle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brangert P.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.H., Nordstiek G.,
 RA Reichelt J., Schafte M., Schoen O., Bargues M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Oltenswalder B., Duchemin D.,
 RA Cooke R., Laude M., Berger-Llauró C., Purnelle B., Masny D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet R., Casasuberta E.,
 RA Montfort A., Argitrou A., Flores M., Lignori R., Vitale D.,
 RA Mannheim G., Haase D., Schoof H., Rüd S., Zaccaria P., Wewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,

DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 KW Oxidoreductase; Manganese; Mitochondrion; Transit peptide; Allergen.
 FT TRANSIT 1 2
 FT CHAIN 1 210
 FT METAL 29 29
 FT METAL 77 77
 FT METAL 163 163
 FT METAL 167 167
 SQ SEQUENCE 210 AA; 23377 MW; CE64A134780B5546 CRC64;

Query Match 49.0%; Score 71; DB 1; Length 210;
 Best Local Similarity 48.1%; Pred. No. 0.0016;
 Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 KXSLPELDYFSATEPYISQINEIXY 27
 Db 4 QYTLPLPYDALQPYISQIMELH 30

RESULT 24
 SODM_HEVER STANDARD; PRT; 233 AA.
 ID SODM_HEVER
 AC P35017;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 GN SODA.
 OS Hevea brasiliensis (Para rubber tree).
 OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosida I; Malpighiales; Euphorbiaceae; Hevea.
 NC NCBI_TaxID=3981;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RX MEDLINE=9403306; PubMed=8219064;
 RA Miao Z., Gaynor J.J.;
 RT "Molecular cloning, characterization and expression of Mn-superoxide
 RT dismutase from the rubber tree (Hevea brasiliensis).";
 RL Plant Mol. Biol. 23:267-277(1993).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- TISSUE SPECIFICITY: PRESENT IN ALL TISSUES EXAMINED (LEAF,
 CC PETIOLE, ROOT, LATEX, CALLUS) WITH YOUNG LEAVES SHOWING THE
 CC HIGHEST LEVELS IN INTACT PLANTS.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; L11707; AAA16792.1; -.
 CC PIR; S39492; S39492.
 CC HSSP; P04179; IABM.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe_1.
 DR Pfam; PF02777; sodfe_C_1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 KW Oxidoreductase; Manganese; Mitochondrion; Transit peptide.
 FT TRANSIT 1 27
 FT CHAIN 28 233
 SQ SEQUENCE 233 AA; 23377 MW; CE64A134780B5546 CRC64.

FT METAL 59 59
 FT METAL 103 103
 FT METAL 192 192
 FT METAL 196 196
 SQ SEQUENCE 233 AA; 25839 MW; D6C48D7A7E9A8B59 CRC64;

Query Match 49.0%; Score 71; DB 1; Length 233;
 Best Local Similarity 46.2%; Pred. No. 0.0018;
 Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISQINEIXY 27
 Db 31 FSLPELDYDGALEPAISGIMQLH 56

RESULT 25
 SODM_BORBU STANDARD; PRT; 203 AA.
 ID SODM_BORBU
 AC O30563;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Fe] (EC 1.15.1.1).
 GN SOD OR BB0153.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 NC NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SH-2-82;
 RX MEDLINE=9803126; PubMed=9353077;
 RA Whitehouse C.A., Williams L.R., Austin F.E.;
 RT "Identification of superoxide dismutase activity in Borrelia
 RT burgdorferi.";
 RL Infect. Immun. 65:4865-4868(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Karpavich A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman C.,
 RA Ueberlack T., Matthey L., McDonald L., Artach P., Bowman C.,
 RA Gerland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochete, Borrelia
 RT burgdorferi.";
 RL Nature 390:580-586(1997).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: IRON.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
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 CC -----
 CC EMBL; AF011226; AAB65252.1; -.
 CC EMBL; AB001126; AAC6537.1; ALT_INIT.
 DR HSSP; P09214; IMNG.
 DR TIGR; BB0153; -.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe_1.
 DR Pfam; PF02777; sodfe_C_1.

KW Oxidoreductase; Manganese; Mitochondrion; Transil peptide.
 FT TRANSIT 1 24 MITOCHONDRION.
 FT CHAIN 25 222 SUPEROXIDE DISMUTASE [MN].
 FT METAL 50 50 MANGANESE (BY SIMILARITY).
 FT METAL 98 98 MANGANESE (BY SIMILARITY).
 FT METAL 183 183 MANGANESE (BY SIMILARITY).
 FT METAL 187 187 MANGANESE (BY SIMILARITY).
 FT CONFLICT 167 167 Q -> H (IN REF. 1).
 SQ SEQUENCE 222 AA; 24674 MW; 80CCCE0E857B3138 CRC64;

Query Match 51.0%; Score 74; DB 1; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.00058;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

1 KYSLPELDYEFSAEPYISQINEIXYT 28
 25 KHSLEPLDYDGALEPHINQIMQIHHHS 52

RESULT 20
 SODF_SULSO STANDARD; PRT; 210 AA.
 AC P80857;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Fe] (EC 1.15.1.1).
 GN SOD OR SSO0316.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 CX NCBI_TaxID=2287;
 RN [1]
 RS SEQUENCE
 RC STRAIN=ATCC 49255 / DSM 5833 / MT-4;
 RX MEDLINE=98088931; PubMed=9428655;
 RA DeLio Russo A., Nitti G., Masullo M., Bocchini V.;
 RT "Iron superoxide dismutase from the archaeon Sulfolobus solfataricus:
 average hydrophobicity and amino acid weight are involved in the
 adaptation of proteins to extreme environments.";
 RL Biochim. Biophys. Acta 1343:23-30(1997).
 RN [2]
 RS SEQUENCE FROM N.A.
 RP MEDLINE=99098843; PubMed=980816;
 RA Yamano S., Maruyama T.;
 RT "An azide-insensitive superoxide dismutase from a hyperthermophilic
 archaeon, Sulfolobus solfataricus.";
 RL J. Biochem. 125:186-193(1999).
 RN [3]
 RS SEQUENCE FROM N.A.
 RP STRAIN=ATCC 49255 / DSM 5833 / MT-4;
 RX MEDLINE=21145482; PubMed=11248699;
 RA De Vendictis E., Ursby T., Rullo R., Gogliettino M.A., Masullo M.,
 Bocchini V.;
 RT "Phenylmethanesulfonyl fluoride inactivates an archaeal superoxide
 dismutase by chemical modification of a specific tyrosine residue:
 cloning, sequencing and expression of the gene coding for Sulfolobus
 solfataricus superoxide dismutase.";
 RL Eur. J. Biochem. 268:1794-1801(2001).
 RN [4]
 RS SEQUENCE FROM N.A.
 RP STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=21332296; PubMed=11427726;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 Aweyer M.J., Chan-Weiner C.C.-Y., Clausen I.G., Curtis B.A.,
 De Moers A., Eranuso G., Fletcher C., Gordon P.M.K.,
 Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 Rai-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 Garrett R.A., Regan M.A., Sensen C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 RN [5]

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=99134398; PubMed=9931259;
 RA Ursby T., Adinolfi B.S., Al-Karadaghi S., de Vendictis E.,
 Bocchini V.;
 RT "Iron superoxide dismutase from the archaeon Sulfolobus solfataricus:
 analysis of structure and thermostability.";
 RL J. Mol. Biol. 286:189-205(1999).
 RT FUNCTION: Destroys radicals which are normally produced within the
 cells and which are toxic to biological systems;
 CC CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: IRON.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 FAMILY.
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 CC EMBL; AB012620; BAA75509.1; -.
 CC EMBL; Y15326; CAAT5583.1; -.
 CC EMBL; AE006666; AAK40652.1; -.
 CC PDB; 1SS8; 09-APR-99.
 CC InterPro: IPR001189; SODismutase.
 CC Pfam; PF00081; sodfe, 1.
 CC DR Pfam; PF02777; sode_C, 1.
 CC DR ProDom; PD000475; SODismutase; 1.
 CC PROSITE; PS00088; SOD MN; FALSE NEG.
 KW Oxidoreductase; Iron; 3D-structure; Complete proteome.
 FT INIT MET 0
 FT METAL 37 37 IRON.
 FT METAL 84 84 IRON.
 FT METAL 170 170 IRON.
 FT METAL 174 174 IRON.
 SQ SEQUENCE 210 AA; 24112 MW; 7918CF1292BF98B6 CRC64;

Query Match 50.3%; Score 73; DB 1; Length 210;
 Best Local Similarity 51.9%; Pred. No. 0.00078;
 Matches 14; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

1 KYSLPELDYEFSAEPYISQINEIXYT 27
 8 KYELPPLPYKIDALEPYISKIDIDVHY 34

RESULT 21
 SODF_PYRAE STANDARD; PRT; 211 AA.
 ID SODF_PYRAE
 AC G93724;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Fe] (EC 1.15.1.1).
 GN SOD OR PAE0274.
 OS Pyrobaculum aerophilum.
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
 OC Thermoproteaceae; Pyrobaculum.
 CX NCBI_TaxID=13773;
 RN [1]
 RS SEQUENCE FROM N.A.
 RP STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX MEDLINE=11792869;
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,

DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 GN SOD2 OR SOD-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=7091590; PubMed=3797253;
 RA Halliwell R.A., Mullenbach G.T., Stempien M.M., Bell G.I.;
 RT "Sequence of a cDNA coding for mouse manganese superoxide dismutase.";
 RL Nucleic Acids Res. 14:9539-9539(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c, and C3H;
 RX MEDLINE=94010326; PubMed=8406027;
 RA Sun Y., Hegamyer G., Colburn N.M.;
 RT "Sequence of manganese superoxide dismutase-encoding cDNAs from multiple mouse organs."; Gene 131:301-302(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95180711; PubMed=7875582;
 RA Jones P.L., Kucera G., Gordon H.M., Boss J.M.;
 RT "Cloning and characterization of the murine manganese superoxide dismutase-encoding gene."; Gene 153:155-161(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9537589; PubMed=7613035;
 RA Distlvestre D., Kleiberger S.R., Johns J., Levitt R.C.;
 RT "Structure and DNA sequence of the mouse MnSOD gene."; Mamm. Genome 6:281-284(1995).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: X04972; CAA28645.1; -;
 CC EMBL: Z18857; CAA79308.1; -;
 CC EMBL: L35528; AAB60902.1; JOINED.
 CC EMBL: L35525; AAB60902.1; JOINED.
 CC EMBL: L35527; AAB60902.1; JOINED.
 CC EMBL: S78846; AAB34899.1; -;
 CC EMBL: S78843; AAB34899.1; JOINED.
 CC EMBL: S78842; AAB34899.1; JOINED.
 CC EMBL: S78844; AAB34899.1; JOINED.
 CC PIR: A25581; A25581.1; JOINED.
 CC HSSP: P04179; 1ABM.
 CC DR SWISS-2DPAGE: P06671; MOUSE.
 CC MGD: MGI:98352; SOD2.
 CC InterPro: IPR001189; SODismutase.
 CC Pfam: PF02777; sodfe_C; 1.
 CC ProDom: PD000475; SODismutase; 1.
 CC DR PROSITE: PS00088; SOD_MN; 1.
 CC Oxidoreductase; Manganese; Mitochondrion; Transf. peptide.
 FT TRANSIT 1
 FT 24 MITOCHONDRION.

FT CHAIN 25 222 SUPEROXIDE DISMUTASE [MN].
 FT METAL 50 50 MANGANESE (BY SIMILARITY).
 FT METAL 98 98 MANGANESE (BY SIMILARITY).
 FT METAL 183 183 MANGANESE (BY SIMILARITY).
 FT METAL 187 187 MANGANESE (BY SIMILARITY).
 FT CONFLICT 18 18 G -> V (IN REF. 1).
 FT CONFLICT 138 138 V -> M (IN REF. 1 AND 3).
 SQ SEQUENCE 222 AA; 24603 MW; 9AB804C55AB357D9 CRC64;
 Query Match 51.0%; Score 74; DB 1; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.00058;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KYSLPELDYFSPATPYISQINBIYXT 28
 DB 25 KHSLEPLDYDYGALPEPHINQIMQLHRS 52
 ID SODM_RAT STANDARD; PRT; 222 AA.
 AC P07895;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 GN SOD2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=88096516; PubMed=3697077;
 RA Ho Y.-S., Crapo J.D.;
 RT "Nucleotide sequences of cDNAs coding for rat manganese-containing superoxide dismutase."; Nucleic Acids Res. 15:10070-10070(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=91159005; PubMed=2001291;
 RA Ho Y.-S., Howard A.J., Crapo J.D.;
 RT "Molecular structure of a functional rat gene for manganese-containing superoxide dismutase."; Am. J. Respir. Cell Mol. Biol. 4:278-286(1991).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: Y00497; CAA68549.1; -;
 CC EMBL: X56600; CAA59537.1; -;
 CC PIR: S21661; DSRTN.
 CC HSSP: P04179; 1ABM.
 CC InterPro: IPR001189; SODismutase.
 CC Pfam: PF02777; sodfe_C; 1.
 CC ProDom: PD000475; SODismutase; 1.
 CC DR PROSITE: PS00088; SOD_MN; 1.

RP SEQUENCE OF 25-39.
 RC TISSUE=Heart;
 RX MEDLINE=95203287; Pubmed=7895732;
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
 RT "The human myocardial two-dimensional gel protein database: update
 1994.";
 RL Electrophoresis 15:1459-1465(1994).
 RN [10]
 RP SEQUENCE OF 25-39.
 RC TISSUE=Heart;
 RX MEDLINE=96007936; Pubmed=7498159;
 RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
 RA Keshova E.S., Egorov T.A., Musalimov A.K.;
 RT "The major protein expression profile and two-dimensional protein
 RT database of human heart.";
 RL Electrophoresis 16:1160-1169(1995).
 RN [11]
 RP SEQUENCE OF 25-39.
 RC TISSUE=Breast carcinoma;
 RX MEDLINE=97295304; Pubmed=9150946;
 RA Rasmussen R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E.,
 RA Simpson R.J., Dorow D.S.;
 RT "Two-dimensional electrophoretic analysis of human breast carcinoma
 RT proteins: mapping of proteins that bind to the SH3 domain of mixed
 RT lineage kinase MLK2.";
 RL Electrophoresis 18:588-598(1997).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=93008233; Pubmed=1394426;
 RA Borgstahl G.E.O., Parge H.E., Hickey M.J., Beyer W.F. Jr.,
 RA Hallett R.A., Tainer J.A.;
 RT "The structure of human mitochondrial manganese superoxide dismutase
 RT reveals a novel tetrameric interface of two 4-helix bundles.";
 RL Cell 71:107-116(1992).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF VARIANT THR-82.
 RX MEDLINE=96183289; Pubmed=8605177;
 RA Borgstahl G.E.O., Parge H.E., Hickey M.J., Johnson M.J.,
 RA Borgstahl M., Hallett R.A., Lepock J.R., Cabelli D.E.,
 RA Tainer J.A.;
 RT "Human mitochondrial manganese superoxide dismutase polymorphic
 RT variant I158Tn reduces activity by destabilizing the tetrameric
 RT interface.";
 RL Biochemistry 35:4287-4297(1996).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF VARIANT ASN-167.
 RX MEDLINE=98206886; Pubmed=9537988;
 RA Hsieh Y., Guan Y., Tu C., Bratt P.J., Angerhofer A., Lepock J.R.,
 RA Hickey M.J., Tainer J.A., Nick H.S., Silverman D.N.;
 RT "Probing the active site of human manganese superoxide dismutase: the
 RT role of glutamine 143.";
 RL Biochemistry 37:4731-4739(1998).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF VARIANT TYR-58.
 RX MEDLINE=98206887; Pubmed=9537987;
 RA Guan Y., Hickey M.J., Borgstahl G.E.O., Hallett R.A., Lepock J.R.,
 RA O'Connor D., Hsieh Y., Nick H.S., Silverman D.N., Tainer J.A.;
 RT "Crystal structure of Y34F mutant human mitochondrial manganese
 RT superoxide dismutase and the functional role of tyrosine 34.";
 RL Biochemistry 37:4722-4730(1998).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL: X59445; CAA42066.1; -;
 CC EMBL: Y00472; CAA68533.1; -;
 CC EMBL: Y00985; CAA68791.1; -;
 CC EMBL: X07834; CAA30687.1; -;
 CC EMBL: M36693; AAA36622.1; -;
 CC EMBL: X15132; CAA33228.1; -;
 CC EMBL: X14322; CAA32502.1; -;
 CC EMBL: S77127; AAD14248.1; ALT_SEQ.
 CC PIR: A27297; DSHUN.
 CC PIR: S00356; S00356.
 CC PIR: S02230; S02230.
 CC PIR: S11756; S11756.
 CC PIR: S13162; S13162.
 CC PDB: 1MSD; 15-JUL-93.
 CC PDB: 1AMW; 31-OCT-93.
 CC PDB: 1ONW; 07-JAN-98.
 CC PDB: 1VAR; 10-JUN-98.
 CC PDB: 1AP5; 28-JAN-98.
 CC PDB: 1AP6; 28-JAN-98.
 CC SWISS-2DPAGE: P04179; HUMAN.
 CC PMMA-2DPAGE: P04179; HUMAN.
 CC HSC-2DPAGE: P04179; HUMAN.
 CC Siema-2DPAGE: P04179; -;
 CC Genew; HGNC:11180; SOD2.
 CC MIM; 147460; -;
 CC InterPro: IPR001189; SODismutase.
 CC Pfam: PF00081; Sodfe; 1.
 CC Pfam: PF02777; Sodfe; 1.
 CC Prodom: PD000475; SODismutase; 1.
 CC PROSITE: PS00088; SOD_MN; 1.
 CC KW Oxidoreductase; Manganese; Mitochondrion; Transic peptide;
 CC 3D-structure; Polymorphism.
 CC TRANSIT 1 24
 CC CHAIN 25 222
 CC METAL 50 50
 CC METAL 98 98
 CC METAL 183 183
 CC METAL 187 187
 CC METAL 82 82
 CC VARIANT
 CC FT CONFLICT 14 14 /Frid=VAR 007165.
 CC FT CONFLICT 16 16 A -> V (IN REF. 3).
 CC FT CONFLICT 65 65 T -> N (IN REF. 5).
 CC FT CONFLICT 66 66 E -> Q (IN REF. 6).
 CC FT CONFLICT 112 112 E -> Q (IN REF. 6).
 CC FT CONFLICT 123 123 R -> L (IN REF. 3).
 CC FT CONFLICT 133 133 E -> Q (IN REF. 6).
 CC FT CONFLICT 148 149 MISSING (IN REF. 6).
 CC FT CONFLICT 155 155 E -> Q (IN REF. 2 AND 6).
 CC FT CONFLICT 155 155
 CC FT HELIX 35 38
 CC FT TURN 39 41
 CC FT HELIX 44 52
 CC FT TURN 53 53
 CC TURN 53 53
 CC Query Match 51.0%; Score 74; DB 1; Length 222;
 CC Best Local Similarity 42.9%; Pred. No. 0.00058;
 CC Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 CC
 CC Db 25 KXSLPDLVYGALEPHINQWQLHHS 52
 CC 1 KYSLPELVESFSAPEYISQINIEIXT 28
 CC
 CC RESULT 18
 CC SODM_MOUSE STANDARD; PRT; 222 AA.
 CC ID SODM_MOUSE
 CC AC P09671; O64670;
 CC DT 01-MAR-1989 (Rel. 10, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)

QY 1 KYSLPELDYERSATEPYISQINEXY 27
DB 9 KYSLPELDYERSATEPYISQINEXY 35

RESULT 16

SODM_BOVIN STANDARD; PRT; 222 AA.
AC P41976;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
GN Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
TISSUE=Lung;
MEDLINE=94121934; PubMed=8292376;
RA Meyrick B., Magnuson M.A.;
RT "Identification and functional characterization of the bovine
manganese superoxide dismutase promoter.";
RL Am. J. Respir. Cell Mol. Biol. 10:113-121(1994).
CC - FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC - CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC - COFACTOR: Manganese.
CC - SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC - SUBCELLULAR LOCATION: Mitochondrial matrix.
CC - SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.

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CC or send an email to license@ebi.ac.uk).

CC -----
CC EMBL; L22092; AAA30655.1; ALT_INIT.
CC EMBL; L22093; AAA30656.1; -;
CC EMBL; S67818; AAC60522.2; -;
CC EMBL; S67819; AAD14001.1; -;
CC HSSP; P04179; 1ABW.
CC InterPro: IPR001189; SOD1smutase.
CC Pfam: PF00081; sode1.1.
CC DR Pfam: PF02777; sode1.1.
CC DR Pfam: PF000475; SOD1smutase; 1.
CC DR PROSITE; PS00088; SOD_MN; 1.
CC DR Oxidoreductase; Manganese; Mitochondrion; Transit peptide.
CC KM TRANSIT 1 24
CC FT CHAIN 25 222 MITOCHONDRION (BY SIMILARITY).
CC FT METAL 50 50 MANGANESE (BY SIMILARITY).
CC FT METAL 98 98 MANGANESE (BY SIMILARITY).
CC FT METAL 183 183 MANGANESE (BY SIMILARITY).
CC FT METAL 187 187 MANGANESE (BY SIMILARITY).
CC FT METAL 187 187 MANGANESE (BY SIMILARITY).
CC FT CONFLICT 8 8 S -> R (IN REF. 1; AAD14001).
CC FT CONFLICT 90 90 F -> V (IN REF. 1; AAC60522).
CC SQ SEQUENCE 222 AA; 24638 MW; 806CC3FCB1A74413 CRC64;

Query Match 51.0%; Score 74; DB 1; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00058;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYERSATEPYISQINEXY 28
DB 25 KYSLPELDYERSATEPYISQINEXY 52

RESULT 17
SODM_HUMAN STANDARD; PRT; 222 AA.

ID AC P04179; P78434; Q16792; O9P223;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=89076921; PubMed=2462451;
RA Wiese J.R., Clark J.C., Burnans M.S., Kropp K.E., Korfhaugen T.R.,
RT Whiteett J.A.;
RT "Synthesis and processing of the precursor for human
manganese-superoxide dismutase.";
RL Biochim. Biophys. Acta 994:30-36 (1989).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=88067716; PubMed=3684581;
RA Beck Y., Oren R., Amit B., Levanon A., Gorecki M., Hartman J.R.;
RT "Human Mn superoxide dismutase cDNA sequence.";
RL Nucleic Acids Res. 15:9076-9076(1987).
[3]
SEQUENCE FROM N.A.
RX MEDLINE=88289364; PubMed=3399391;
RA Heckl K.;
RT "Isolation of cDNAs encoding human manganese superoxide dismutase.";
RL Nucleic Acids Res. 16:6224-6224(1988).
[4]
SEQUENCE FROM N.A.
RX TISSUE=Liver;
MEDLINE=88152250; PubMed=2831093;
RA Ho Y.-S., Crapo J.D.;
RT "Isolation and characterization of complementary DNAs encoding human
manganese-containing superoxide dismutase.";
RL FEBS Lett. 229:256-260(1988).
[5]
SEQUENCE FROM N.A.
RX TISSUE=Colon;
MEDLINE=91105727; PubMed=1988135;
RA St. Clair D.K., Holland J.C.;
RT "Complementary DNA encoding human colon cancer manganese superoxide
dismutase and the expression of its gene in human cells.";
RL Cancer Res. 51:939-943(1991).
[6]
SEQUENCE FROM N.A.
RX MEDLINE=91027939; PubMed=1699607;
RA Church S.L.;
RT "Manganese superoxide dismutase: nucleotide and deduced amino acid
sequence of a cDNA encoding a new human transcript.";
RL Biochim. Biophys. Acta 1087:250-252(1990).
[7]
SEQUENCE FROM N.A.
RX MEDLINE=95217333; PubMed=7702755;
RA Wan X.S., Devalaraja M.N., St. Clair D.K.;
RT "Molecular structure and organization of the human manganese
superoxide dismutase gene.";
RL DNA Cell Biol. 13:1127-1136(1994).
[8]
SEQUENCE OF 25-222.
RX MEDLINE=85030346; PubMed=6386798;
RA Barria D., Schinina M.E., Sismaco M., Bannister J.V., Bannister W.H.,
RT "The primary structure of human liver manganese superoxide
dismutase.";
RL J. Biol. Chem. 259:12595-12601(1984).
[9]

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CC EMBL; L28808; AAA31401.1; -.
 DR HSSP; P04179; IAP6.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR Pfam; PF02777; sodfe.C; 1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 KM Oxidoreductase; Manganese; Mitochondrion; Transist peptide.
 FT TRANSIT 1 1
 FT CHAIN <1 5 MITOCHONDRION (BY SIMILARITY).
 FT METAL 6 >202 SUPEROXIDE DISMUTASE [MN].
 FT METAL 31 31 MANGANESE (BY SIMILARITY).
 FT METAL 79 79 MANGANESE (BY SIMILARITY).
 FT METAL 164 164 MANGANESE (BY SIMILARITY).
 FT METAL 168 168 MANGANESE (BY SIMILARITY).
 FT NON TER 202
 SEQUENCE 202 AA; 22656 MW; 6F1BB8DA15C33AA7 CRC64;

Query Match 53.1%; Score 77; DB 1; Length 202;
 Best Local Similarity 46.4%; Pred. No. 0.00018;
 Matches 13; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

OY 1 KYSLPELYERSATEPYISQINEIXYT 28
 6 KHSLPDLPYDYGALPHEPHINQIMELHHS 33

RESULT 14
 SODF_METU STANDARD; PRT; 202 AA.
 AC P23744;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Superoxide dismutase [Mn/Fe] (EC 1.15.1.1).
 GN SODB.
 OS Methylobionas J.
 OC Bacteria; Proteobacteria; gamma subdivision; Methylococcaceae;
 OC Methylobionas.
 OX NCBI_TaxID=32038;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=9182736; PubMed=1848999;
 RA Matsuno T., Terauchi K., Isobe T., Matsuo K., Yamakura F.;
 "Iron- and manganese-containing superoxide dismutases from
 Methylobionas J: identity of the protein moiety and amino acid
 sequence";
 RT Biochemistry 30:3210-3216(1991).
 RL [2]

CHARACTERIZATION, AND SEQUENCE OF 1-32.
 RX MEDLINE=91301511; PubMed=1906419;
 RA Yamakura F., Matsuno T., Terauchi K.;
 RT "Isolation of Mn-SOD and low active Fe-SOD from Methylobionas J;
 consisting of identical proteins";
 RL Free Radic. Res. Commun. 12:329-334(1991).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: ACTIVE WITH EITHER MANGANESE OR IRON AS A COFACTOR.
 CC BOTH TYPES OF SODS ARE COMPOSED OF A SINGLE APOPROTEIN SYNTHESIZED
 CC IN CELLS GROWN IN EITHER THE FE-RICH OR THE MN-RICH MEDIUM. THE
 CC FE-SOD HAS A LOWER ACTIVITY THAN THE MN-SOD.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC PIR; A38461; A38461.
 DR HSSP; P00448; IYEW.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.

DR Pfam; PF02777; sodfe.C; 1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 KM Oxidoreductase; Manganese; Iron.
 FT METAL 26 26 MANGANESE OR IRON (BY SIMILARITY).
 FT METAL 80 80 MANGANESE OR IRON (BY SIMILARITY).
 FT METAL 163 163 MANGANESE OR IRON (BY SIMILARITY).
 FT METAL 167 167 MANGANESE OR IRON (BY SIMILARITY).
 SEQUENCE 202 AA; 22363 MW; 321A8B4697A5B58 CRC64;

Query Match 52.4%; Score 76; DB 1; Length 202;
 Best Local Similarity 51.9%; Pred. No. 0.00026;
 Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 2 YSLPELYERSATEPYISQINEIXYT 28
 2 YTLPELDYATLAPHIDQTMELHHT 28

RESULT 15
 SODF_ACIAM STANDARD; PRT; 211 AA.
 AC Q9P9J3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Fe] (EC 1.15.1.1).
 GN SOD.
 OS Acidithiobacillus ambivalens (Desulfurolobus ambivalens).
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Acidithiobacillus.
 OX NCBI_TaxID=2283;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21026956; PubMed=11154067;
 RA Kardinah S., Anemuller S., Schaefer G.;
 RT "The hyper-thermostable Fe-superoxide dismutase from the Archaeon
 Acidithiobacillus ambivalens: characterization, recombinant expression,
 RT crystallization and effects of metal exchange";
 RL Biol. Chem. 381:1089-1101(2000).

CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems (By similarity).
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Iron (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
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CC EMBL; AF236110; AAF36989.1; -.
 DR HSSP; P80857; 1SSS.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR Pfam; PF02777; sodfe.C; 1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; FALSE_NEG.
 KM Oxidoreductase; Iron.
 FT METAL 34 34 IRON (BY SIMILARITY).
 FT METAL 82 82 IRON (BY SIMILARITY).
 FT METAL 171 171 IRON (BY SIMILARITY).
 FT METAL 175 175 IRON (BY SIMILARITY).
 SEQUENCE 211 AA; 24342 MW; 5A88FF8400F77065 CRC64;

Query Match 51.0%; Score 74; DB 1; Length 211;
 Best Local Similarity 51.9%; Pred. No. 0.00055;
 Matches 14; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

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RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RP
RC SEQUENCE FROM N.A.
RA STRAIN=74-OR23-1A.
RA Schulte U., Algn V., Hohelael J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.-W., Mannhaupt G.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Manganese (By similarity).
CC -1- SUBUNIT: HOMOTETRAMER (By similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
CC
CC -----
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CC
CC -----
CC EMBL: AF118809; AAD28503.1; -.
CC EMBL: AF670011; CAD21408.1; -.
CC HSSP: P04179; IABM.
CC InterPro: IPR001189; $ODismutase.
CC DR Pfam: PF00081; $odfe; 1.
CC DR Pfam: PF02777; $odfe.C; 1.
CC DR Prodom: PD000475; $ODismutase; 1.
CC DR PROSITE: PS00089; SOD_MN; 1.
CC Oxidoreductase; Manganese; Mitochondrion; Transit peptide.
KW TRANSIT
FT FT 1 32 MITOCHONDRION (POTENTIAL).
FT CHAIN 33 245 SUPEROXIDE DISMUTASE [MN].
FT METAL 58 58 MANGANESE (BY SIMILARITY).
FT METAL 106 106 MANGANESE (BY SIMILARITY).
FT METAL 196 196 MANGANESE (BY SIMILARITY).
FT METAL 200 200 MANGANESE (BY SIMILARITY).
FT SEQUENCE 245 AA; 27019 MW; FPF88947FB7676AD CRC64;
SO
Query Match 57.2%; Score 83; DB 1; Length 245;
Best Local Similarity 55.6%; Pred. No. 2.8e-05;
Matches 15; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATPEYISQGINEIYXT 28
|||:::|||||:::
34 YSLPOLPYAYNALPEYISQIWEIHLHS 60
RESULT 12
SODM_HORSE STANDARD; PRT; 222 AA.
ID SODM_HORSE
AC O9XK41.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (BC 1.15.1.1)
DE (Mn-SOD).
DE SOD2.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OC NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC
RC TISSUE=Testis;
RX MEDLINE=99261591; PubMed=10331206;
RA Ishida N., Katayama Y., Sato F., Hasegawa T., Mukoyama H.;
RT "The cDNA sequences of equine antioxidant enzyme genes Cu/Zn-SOD and
RT Mn-SOD, and their expressions in equine tissues.",
RT J. Vet. Med. Sci. 61:291-294(1999).
RT
RT -1- FUNCTION: Destroys radicals which are normally produced within the

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CC      cells and which are toxic to biological systems.
CC      -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC      -1- CORACTOR: Manganese
CC      -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC      -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC      FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; AB001693; BAA76922.1; -.
CC      DR      HSSP; P04179; IABM.
CC      DR      InterPro; IPR001189; SODismutase.
CC      DR      Pfam; PF00081; sodfe_1.
CC      DR      Pfam; PF02777; sodfe_C_1.
CC      DR      ProDom; PD000475; SODismutase; 1.
CC      DR      PROSITE; PS00086; SOD MN; 1.
CC      KM      Oxidoreductase; Manganese; Mitochondrion; Transit peptide.
CC      FT      TRANSIT      1      24      MITOCHONDRION (BY SIMILARITY).
CC      FT      CHAIN      25      222      SUPEROXIDE DISMUTASE [MN].
CC      FT      METAL      50      50      MANGANESE (BY SIMILARITY).
CC      FT      METAL      98      98      MANGANESE (BY SIMILARITY).
CC      FT      METAL      183      183      MANGANESE (BY SIMILARITY).
CC      FT      METAL      187      187      MANGANESE (BY SIMILARITY).
CC      SQ      SEQUENCE      222 AA; 24739 MW; 93A069481944E98C CRC64;
CC
CC      Query Match      55.2%; Score 80; DB 1; Length 222;
CC      Best Local Similarity      46.4%; Pred. No. 7.2e-05;
CC      Matches      13; Conservative %      9; Mismatches      6; Indels      0; Gaps      0;
CC
CC      Qy      1      KYSLPELDYEFSAPEYISQGINEXYT 28
CC      ||:||||:|::|:||||:|:::
CC      Db      25      KHSLEPDLDYGALEPYINQIMOLHMS 52
CC
CC      RESULT 13
CC      SODM_RABIT
CC      ID      _SODM_RABIT      STANDARD;      PRT;      202 AA.
CC      AC      P41982;
CC      DT      01-NOV-1995 (Rel. 32, Created)
CC      DT      01-NOV-1995 (Rel. 32, Last sequence update)
CC      DT      15-JUN-2002 (Rel. 41, Last annotation update)
CC      DE      Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1)
CC      DB      (Fragment).
CC      GN      SOD2.
CC      OS      Oryctolagus cuniculus (Rabbit).
CC      OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC      NX      NCBI_TaxID=9986;
CC      RN      [1]
CC      RP      SEQUENCE FROM N.A.
CC      RA      STRAIN=New Zealand white;
CC      RA      Jackson R.M.;
CC      RL      Submitted (XXX-1994) to the EMBL/GenBank/DBJ databases.
CC      CC      -1- FUNCTION: Destroys radicals which are normally produced within the
CC      CC      cells and which are toxic to biological systems.
CC      CC      -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC      CC      -1- COFACTOR: Manganese (By similarity).
CC      CC      -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC      CC      -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC      CC      -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC      CC      FAMILY.
CC      -----
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RX MEDLINE=90256282; PubMed=1692812;
 RA Thangaraj H.S., Lamb F.I., Davis E.O., Jenner P.J., Jeyakumar L.H.,
 RA Colston M.J.;
 RT "Identification, sequencing, and expression of Mycobacterium leprae
 RT superoxide dismutase, a major antigen.";
 RL Infect. Immun. 58:1937-1942(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=2118732; PubMed=11234002;
 RA Cole S.T., Bigliamer K., Parkhill J., James K.D., Thomson N.R.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthy K., Felwell T., Frazer A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagsis K., Lacroix C., McLean J., Moulé S.,
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Seeger S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrett B.G.;
 RT "Massive gene decay in the leprosy bacillus,"
 RT Nature 409:1007-1011(2001).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
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 CC -----
 CC DR EMBL: X16453; CA34472.1; -;
 CC DR EMBL: AL583917; CAC29580.1; -;
 CC DR PIR: S06599; S06599.
 CC DR PIR: A37212; A37212.
 CC DR HSSP: P17670; 1IDS.
 CC DR Lepidoma: ML0072; -;
 CC DR InterPro: IPR001189; SOD1smutase.
 CC DR Pfam: PF00081; SOD1e, 1.
 CC DR Pfam: PF02777; SOD1e, C1.
 CC DR Prodom: PD000475; SOD1smutase, 1.
 CC DR PROSITE: PS00088; SOD_MN; 1.
 CC DR Oxidoreductase: Manganese; Complete proteome.
 CC INIT MET 0 By SIMILARITY.
 CC METAL 27 MANGANESE (BY SIMILARITY).
 CC METAL 75 MANGANESE (BY SIMILARITY).
 CC METAL 159 MANGANESE (BY SIMILARITY).
 CC METAL 163 MANGANESE (BY SIMILARITY).
 CC SEQUENCE 206 AA; 23027 MW; B02B96EB433F6FF0 CRC64;
 QY 1 KYSLPELDYEFSAEPISGQINFIYXT 28
 DB 2 EYTLPLDMDYALPEPHISGEINFIHHT 29
 Query Match 67.6%; Score 98; DB 1; Length 206;
 Best Local Similarity 57.1%; Pred. No. 1.3e-07;
 Matches 16; Conservative 10; Mismatches 2; Indels 0; Gaps 0;
 RESULT 9
 SODF_MYCTU STANDARD; PRT; 207 AA.
 ID SODF_MYCTU
 AC P17670; P96231;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Fe] (EC 1.15.1.1).
 GN SODB OR SODA OR SOD OR RV3846 OR MT3960 OR MTCT01A6.22C.

OS Mycobacterium tuberculosis, and
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773, 1765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=Erdmann;
 RX MEDLINE=91251768; PubMed=1904126;
 RA Zhang Y.;
 RT "Genetic analysis of superoxide dismutase, the 23 kilodalton antigen
 RT of Mycobacterium tuberculosis.";
 RL Mol. Microbiol. 5:381-391(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC SPECIES=M.tuberculosis; STRAIN=Erdmann;
 RX MEDLINE=99134360; PubMed=9933629;
 RA Harth G., Horwitz M.A.;
 RT "Export of recombinant Mycobacterium tuberculosis superoxide dismutase
 RT is dependent upon both information in the protein and mycobacterial
 RT export machinery. A model for studying export of leaderless proteins
 RT by pathogenic mycobacteria.";
 RL J. Biol. Chem. 274:4281-4292(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=H37Rv;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Bigliamer K., Gas S., Barry C.E. III, Tekle F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagsis K., Krogh A., McLean J., Moulé S., Murphy L.,
 RA Oliver S., Osborne K., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultson J.E., Taylor K., Whitehead S., Barrett B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Hart D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Brimacombe M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.bovis; STRAIN=BCG / Pasteur;
 RA Kimble E., Sanderson R.J., Gill R.E.;
 RT "Superoxide dismutase of M. bovis BCG.";
 RL Submitted (Jul-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RC SPECIES=M.tuberculosis;
 RX MEDLINE=95182461; PubMed=7877174;
 RA Cooper J.B., McIntyre K., Badasso M.O., Wood S.P., Zhang Y.,
 RA Garbe T.R., Young D.;
 RT "X-ray structure analysis of the iron-dependent superoxide dismutase
 RT from Mycobacterium tuberculosis at 2.0-A resolution reveals novel
 RT dimer-dimer interactions.";
 RL J. Mol. Biol. 246:531-544(1995).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF MUTANT ALA-152.
 RC SPECIES=M.tuberculosis;
 RX MEDLINE=96244503; PubMed=8674528;
 RA Cooper J.B., Seward S., Ereline P.T., Badasso M.O., Wood S.P.,
 RA Zhang Y., Young D.;
 RT "X-ray structure analysis of an engineered Fe-superoxide dismutase
 RT Gly-Ala mutant with significantly reduced stability to denaturant.";

OX NCBI_TaxID=1766;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 6841;
 RA MEDLINE=96102872; PubMed=8586279;
 RT Menendez M.C., Domenech P., Prieto J., Garcia M.J.;
 RT "Cloning and expression of the Mycobacterium fortuitum superoxide
 dismutase gene";
 RL FEMS Microbiol. Lett. 134:273-278 (1995).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; X70914; CAA50266.1; -.
 CC HSSP; P17670; 1IDS.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF02777; Sodfe; 1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 KM Oxidoreductase; Manganese.
 FT INIT MET 0 BY SIMILARITY.
 FT METAL 27 27 MANGANESE (BY SIMILARITY).
 FT METAL 75 75 MANGANESE (BY SIMILARITY).
 FT METAL 159 159 MANGANESE (BY SIMILARITY).
 FT METAL 163 163 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 206 AA; 22833 MW; 500625A8B9321246 CRC64;
 Query Match 68.3%; Score 99; DB 1; Length 206;
 Best Local Similarity 57.1%; Pred. No. 8.9e-08;
 Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KYSLPELDYFESATEPYISQGINEIXYT 28
 Db 2 EYTLPLDIDYGALEPHISQGINELHHS 29
 M_MYCSM STANDARD; PRT; 206 AA.
 AC P53643; Q98612;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Mn] (EC 1.15.1.1).
 OS SODA OR SOD
 OS Mycobacterium smegmatis.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1772;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=1-2C;
 RA MEDLINE=99134360; PubMed=9933629;
 RA Harth G., Horwitz M.A.;
 RT "Export of recombinant Mycobacterium tuberculosis superoxide dismutase
 RT is dependent upon both information in the protein and mycobacterial
 RT export machinery. A model for studying export of leaderless proteins
 RT by pathogenic Mycobacterium";
 RL J. Biol. Chem. 274:4281-4292 (1999).
 RP REVISIONS TO 116 AND 201.

RA Tullius M.V., Harth G., Horwitz M.A.;
 RN Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP SEQUENCE OF 27-164 FROM N.A.
 RC STRAIN=NCTC 10265 / ATCC 14468 / W-113;
 RA Bull T.J., Shanson D.C., Archard L.C.;
 RT "Rapid identification of mycobacteria from AIDS patients by capillary
 RT electrophoretic profiling of amplified SOD gene";
 RL J. Clin. Pathol. Clin. Mol. Pathol. 48:124-132 (1995).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: PARTIALLY SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
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 CC -----
 CC EMBL; AF061031; AAD15825.2; -.
 CC HSSP; Z48214; CAA8247.1; -.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF02777; Sodfe; 1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 KM Oxidoreductase; Manganese.
 FT INIT MET 0 BY SIMILARITY.
 FT METAL 27 27 MANGANESE (BY SIMILARITY).
 FT METAL 75 75 MANGANESE (BY SIMILARITY).
 FT METAL 159 159 MANGANESE (BY SIMILARITY).
 FT METAL 163 163 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 206 AA; 22804 MW; B997A1AD0374AEC9 CRC64;
 Query Match 68.3%; Score 99; DB 1; Length 206;
 Best Local Similarity 57.1%; Pred. No. 8.9e-08;
 Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KYSLPELDYFESATEPYISQGINEIXYT 28
 Db 2 EYTLPLDIDYGALEPHISQGINELHHS 29
 RESULT 8
 SODM MYCLB STANDARD; PRT; 206 AA.
 AC P13367;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Mn] (EC 1.15.1.1).
 OS SODA OR ML0072.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90045970; PubMed=2682526;
 RA Thangaraj H.S., Lamb F.I., Davis E.O., Colston M.J.;
 RT "Nucleotide and deduced amino acid sequence of Mycobacterium leprae
 RT manganese superoxide dismutase";
 RL Nucleic Acids Res. 17:8378-8378 (1989).
 RP REVISIONS TO 116 AND 201.

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CC      cells and which are toxic to biological systems.
CC      -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC      -1- COFACTOR: Manganese (By similarity).
CC      -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC      FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: D13288; BAA28850.1; -.
CC      DR HSSP: P17670; 1IDS.
CC      DR InterPro: IPR001189; SODismutase.
CC      DR Pfam: PF000081; sodfe, 1.
CC      DR Pfam: PF02777; sodfe_C, 1.
CC      DR ProDom: PD000475; SODismutase; 1.
CC      DR PROSITE: PS00088; SOD_MN; 1.
CC      KW Oxidoreductase; Manganese.
CC      KW INIT MET 0
CC      FT METAL 27 0 BY SIMILARITY.
CC      FT METAL 75 75 MANGANESE (BY SIMILARITY).
CC      FT METAL 159 159 MANGANESE (BY SIMILARITY).
CC      FT METAL 163 163 MANGANESE (BY SIMILARITY).
CC      SQ SEQUENCE 206 AA; 23031 MW; 92A063471FA9F22F CRC64;

Query Match 69.0%; Score 100; DB 1; Length 206;
Best Local Similarity 60.7%; Pred. No. 6.3e-08;
Matches 17; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KYSLPELDYFSATEPYISGQINEIXYT 28
Db 2 EYTLPLDKMDFGALPEYISGQINEIHYT 29

RESULT 5
SODM_YEAST STANDARD; PRT; 233 AA.
AC P00457;
DT 21-UTL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2 OR YHR008C.
NC Sacccharomyces cerevisiae (Baker's yeast).
NC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
NC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NC NCB1_TaxID=4932;
OX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85127011; Pubmed=3882422;
RX Harris C.A.M., van Loon A.P.G.M., Oudehoorn P., van Steeg H.,
RX Grivell L.A., Slater E.C.;
RA "Nucleotide sequence analysis of the nuclear gene coding for
RA manganese superoxide dismutase of yeast mitochondria, a gene
RA previously assumed to code for the Rieske iron-sulphur protein.";
RL Eur. J. Biochem. 147:153-161(1985).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=S288c / AB972;
RX MEDLINE=94378003; Pubmed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucada T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
RA Nham M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII.";
```

```

RL Science 265:2077-2082(1994).
RN [3]
RP SEQUENCE OF 1-39 FROM N.A.
RX MEDLINE=89211942; Pubmed=3072251;
RA Schrank I.S., Sims P.F., Oliver S.G.;
RT "Functional expression of the yeast Mn-superoxide dismutase gene in
RT Escherichia coli requires deletion of the signal peptide sequence.";
RL Gene 73:121-130(1988).
RN [4]
RP SEQUENCE OF 27-233.
RA Dtlow C., Johansen J.T., Martin B.W., Svendsen I.;
RT "The complete amino acid sequence of manganese-superoxide dismutase
RT from Saccharomyces cerevisiae.";
RL Carlsberg Res. Commun. 47:81-91(1982).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Manganese.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: X02156; CAA26092.1; -.
CC      DR EMBL: U10400; AAB68939.1; -.
CC      DR EMBL: M24079; AAA35065.1; -.
CC      DR PIR: A00521; DSBVN.
CC      DR PIR: S46785; S46785.
CC      DR HSSP: P04179; 1AEM.
CC      DR SGD: S0001050; SOD2.
CC      DR InterPro: IPR001189; SODismutase.
CC      DR Pfam: PF00081; sodfe, 1.
CC      DR Pfam: PF02777; sodfe_C, 1.
CC      DR ProDom: PD000475; SODismutase; 1.
CC      DR PROSITE: PS00088; SOD_MN; 1.
CC      KW Oxidoreductase; Manganese; Mitochondrion; Transit peptide.
CC      KW TRANSIT 1 26 MITOCHONDRION.
CC      FT CHAIN 27 233 SUPEROXIDE DISMUTASE [MN].
CC      FT METAL 52 52 MANGANESE (BY SIMILARITY).
CC      FT METAL 107 107 MANGANESE (BY SIMILARITY).
CC      FT METAL 194 194 MANGANESE (BY SIMILARITY).
CC      FT METAL 198 198 MANGANESE (BY SIMILARITY).
CC      SQ SEQUENCE 233 AA; 25774 MW; 88A9391FBB31D06E CRC64;

Query Match 69.0%; Score 100; DB 1; Length 233;
Best Local Similarity 64.3%; Pred. No. 7.2e-08;
Matches 18; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KYSLPELDYFSATEPYISGQINEIXYT 28
Db 27 KYTLPLDKMDFGALPEYISGQINEIHYT 54

RESULT 6
SODM_MYCFO STANDARD; PRT; 206 AA.
AC O59519;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1).
GN SOD4 OR SOD.
NC Mycobacterium fortuitum.
NC Bacteria; Actinobacteria; Actinobacteridae; Actinobacteriales;
NC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
```

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KYSLPELDYERFATEPYISGOINEIXYT 28
 DB 35 KYSLPELDYERFATEPYISGOINEIHYT 62

RESULT 2

SODM_NOCAS STANDARD; PRT; 206 AA.
 AC P53651;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Mn] (EC 1.15.1.1).
 GN SODA OR SOD.
 OS Nocardiasteroides.
 OS Bacteria; Actinobacteria; Actinobacteridae (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Nocardiaceae; Nocardia.
 NCBI_TaxID=1824;
 [1]
 SEQUENCE FROM N.A.

CC STRAIN=GUH2;
 CC MEDLINE=96060854; PubMed=7590304;
 CC RA Alcendor D.J., Chapman G.D., Beaman B.L.;
 CC RT "Isolation, sequencing and expression of the superoxide dismutase-
 CC encoding gene (sod) of Nocardiasteroides strain GUH-2.";
 CC RL Gene 164:143-147(1995).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.

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DR EMBL; U02341; AAA91964.1; -.
 DR HSSP; P17670; IIDS.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD MN; 1.

FT INIT MET 0 BY SIMILARITY.
 FT METAL 27 MANGANESE (BY SIMILARITY).
 FT METAL 75 MANGANESE (BY SIMILARITY).
 FT METAL 159 MANGANESE (BY SIMILARITY).
 FT METAL 163 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 206 AA; 22823 MW; FA2BCF27EB22CBDCD CRC64;

Query Match 71.0%; Score 103; DB 1; Length 206;
 Best Local Similarity 60.7%; Pred. No. 2.2e-08;
 Matches 17; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYSLPELDYERFATEPYISGOINEIXYT 28
 DB 2 EYLPDLDYALPHISGOINEIHYT 29

RESULT 3

SODM_MYCAV STANDARD; PRT; 206 AA.
 AC P47201;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Mn] (EC 1.15.1.1).
 GN SODA OR SOD.
 OS Mycobacterium avium.
 OS Bacteria; Actinobacteria; Actinobacteridae (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 NCBI_TaxID=1764;
 [1]
 SEQUENCE FROM N.A.

RP STRAIN=HMC 724;
 RX MEDLINE=96276149; PubMed=8692009;
 RX Escuyer V.E., Haddad N., Frenel C., Berche P.;
 RT "Molecular characterization of a surface-exposed superoxide dismutase
 RT of Mycobacterium avium.";
 CC Microb. Pathog. 20:41-55(1996).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.

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DR EMBL; U11550; AAB08770.1; -.
 DR HSSP; P17670; IIDS.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD MN; 1.

FT INIT MET 0 BY SIMILARITY.
 FT METAL 27 MANGANESE (BY SIMILARITY).
 FT METAL 75 MANGANESE (BY SIMILARITY).
 FT METAL 159 MANGANESE (BY SIMILARITY).
 FT METAL 163 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 206 AA; 22912 MW; D6B49083AEBF3C98 CRC64;

Query Match 69.7%; Score 101; DB 1; Length 206;
 Best Local Similarity 60.7%; Pred. No. 4.4e-08;
 Matches 17; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYSLPELDYERFATEPYISGOINEIXYT 28
 DB 2 EYLPDLDYALPHISGOINEIHYT 29

RESULT 4

SODM_MYCLP STANDARD; PRT; 206 AA.
 AC O86165;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Mn] (EC 1.15.1.1).
 GN SODA OR SOD.
 OS Mycobacterium lepraeaurum.
 OS Bacteria; Actinobacteria; Actinobacteridae (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 NCBI_TaxID=64667;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN=Hawaiian.
 RA Nakamura M.;
 RL Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Destroys radicals which are normally produced within the

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 9, 2003, 13:38:54 ; Search time 3.85321 Seconds

(without alignments)
322.923 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 145

Sequence: 1 KYSLPELDYEPSPATEPYISQINEIXYTX 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	141	97.2	234 1 SODM_CANAL	O13401 candida alb
2	103	71.0	206 1 SODM_NOCAS	P33651 nocardia as
3	101	69.7	206 1 SODM_MYCAV	P47201 mycobacteri
4	100	69.0	206 1 SODM_MYCLP	O86165 mycobacteri
5	100	69.0	233 1 SODM_YEAST	P00447 saccharomyc
6	99	68.3	206 1 SODM_MYCFO	O59519 mycobacteri
7	99	68.3	206 1 SODM_MYCSM	P33649 mycobacteri
8	98	67.6	206 1 SODM_MYCLE	P13367 mycobacteri
9	94	64.8	207 1 SODM_MYCTU	P17670 mycobacteri
10	91	62.8	201 1 SODM_PROFR	P80293 propionibac
11	83	57.2	245 1 SODM_NEUCR	O97073 neuropeptid
12	80	55.2	222 1 SODM_HORSE	O95641 equus cabal
13	77	52.4	202 1 SODM_RABIT	P41982 erythrocyte
14	76	52.4	202 1 SODF_METU	P23744 methylomona
15	74	51.0	211 1 SODF_ACIAM	O91913 aciditans a
16	74	51.0	222 1 SODM_BOVIN	P41976 bos taurus
17	74	51.0	222 1 SODM_HUMAN	P09671 mus musculu
18	74	51.0	222 1 SODM_MOUSE	P07885 ratuus norv
19	74	51.0	222 1 SODM_RAT	P07885 ratuus norv
20	73	50.3	210 1 SODF_SULSO	P08057 sulfolobus
21	72	49.7	211 1 SODF_PYRAE	O93724 pyrobaculum
22	72	49.7	228 1 SODM_CAPAN	O90666 capsicum an
23	71	49.0	210 1 SODM_ASFPU	O92450 aspergillus
24	71	49.0	233 1 SODM_HEYBR	P35017 hevea brasl
25	70	48.3	203 1 SODM_BORBU	O30563 borrelia bu
26	70	48.3	207 1 SODM_CHLPN	O92964 chlamydia p
27	70	48.3	231 1 SODM_ARATH	O81235 arabidopsis
28	70	48.3	233 1 SODM_PEA	P27084 pisum sativ
29	69	47.6	281 1 SODF_BACSC	O35023 bacillus su
30	69	47.6	238 1 SODM_NICPL	P11796 nicotiana p
31	68	46.9	200 1 SODM_AGABI	O94466 agavecacti
32	68	46.9	210 1 SODF_SULAC	O08713 sulfolobus
33	68	46.9	211 1 SODM_CAVPO	P49114 cavia porce

34	68	46.9	212 1 SODF_STRCO	O51917 streptomyce
35	68	46.9	232 1 SODM_MAIZE	P41978 zea mays (m
36	68	46.9	233 1 SODM_MAIZE	P41979 zea mays (m
37	67	46.2	23 1 SODM_RANCA	P36125 rana catesb
38	67	46.2	203 1 SODM_RANCP	P36125 rana catesb
39	67	46.2	214 1 SODM_HAEIN	P43725 haemophilus
40	67	46.2	224 1 SODM_CHAFE	O96347 charybdidis f
41	67	46.2	233 1 SODM_MAIZE	P41980 zea mays (m
42	67	46.2	235 1 SODM_MAIZE	P09233 zea mays (m
43	66	45.5	207 1 SODM_YEREN	P53655 yerinia en
44	65	44.8	200 1 SODM_YEREN	O92429 ganderma m
45	65	44.8	202 1 SODF_METTM	O60036 methanobact

ALIGNMENTS

RESULT 1
ID SODM_CANAL STANDARD; PRT; 234 AA.
AC O13401;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE=9177423; PubMed=10076057;
RA Rile G.E., Hwang C.S., Brady M.J., Kim S.T., Kim Y.R., Huh W.K.,
RA Baek Y.U., Lee B.H., Lee J.S., Kang S.O.,
RT "Manganese-containing superoxide dismutase and its gene from Candida
albicans.";
RL Biochim. Biophys. Acta 1426:409-419 (1999).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Manganese.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.
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CC
CC EMBL; AF031478; AAB86583.1; -.
DR HSSP; P04179; IABM.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR Pfam; PF02777; sodfe_C; 1.
DR ProDom; PD000475; SODismutase; 1.
KW Oxidoreductase; Manganese; Mitochondrion; Transit peptide.
FT TRANSIT 1 34
FT CHAIN 35 234
FT METAL 60 60
FT METAL 108 108
FT METAL 198 198
FT METAL 202 202
SQ SEQUENCE 234 AA; 26173 MW; EBFPC2D765CID9C1 CR664;
Query Match 97.2%; Score 141; DB 1; Length 234;
Best Local Similarity 96.4%; Pred. No. 4.5e-14;

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 8, 2003, 02:09:43 ; Search time 278.532 Seconds

(without alignments)
1744.376 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 145

Sequence: 1 KYSLEPDYEPFATEPPIYSGQINIXYTX 30

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xli
-O=/cgn2.1/USPFO_spool/US09987190/runat_02042003_092633_19234/app_query.fasta_1.526
-DB=BS -QFMT=fastap -SUFFIX=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -STAR1=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -MODE=LOCAL
-DOCALLIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=ptc -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09987190 @CGN 1.1 2013 @runat_02042003_092633_19234 -NCPU=6 -ICPU=3
-NO_XIPXY -NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estcin:*
4: em_estmu:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_hc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	97.2	862	17	CNS07DTU
2	92	63.4	519	17	A2929307
3	90	62.1	464	14	B0087025
4	83	57.2	231	9	A1319465
5	83	57.2	265	9	A1320309
6	83	57.2	265	9	AW171655
7	83	57.2	267	9	A1318805
8	83	57.2	267	10	AW723904
9	83	57.2	269	9	A1321638
10	83	57.2	336	9	A1320505
11	83	57.2	339	9	A1318710
12	83	57.2	339	9	A1319577
13	83	57.2	340	10	AW715499
14	83	57.2	343	10	AW724497
15	83	57.2	401	10	AW724781
16	83	57.2	429	10	AW715120
17	83	57.2	429	10	AW715952
18	82	56.6	592	13	B1321452
19	82	56.6	689	13	BM266232
20	80	55.2	466	13	BM367690
21	79	54.5	306	10	AW733168
22	79	54.5	419	13	B1498255
23	79	54.5	420	10	AW756619
24	79	54.5	425	10	BE210200
25	79	54.5	448	9	A1460811
26	79	54.5	448	9	A1460823
27	79	54.5	470	10	AM099772
28	79	54.5	463	10	AM099772
29	79	54.5	521	12	BE802643
30	79	54.5	552	10	BE211438
31	79	54.5	564	13	B1973216
32	79	54.5	571	13	BM521591
33	79	54.5	578	14	B0094786
34	79	54.5	592	10	BE210646
35	79	54.5	592	13	BM521797
36	79	54.5	597	12	BF067640
37	79	54.5	598	10	AM234447
38	79	54.5	670	10	BE330334
39	79	54.5	675	13	B1263359
40	79	54.5	683	13	B1942249
41	79	54.5	706	10	AM184867
42	78	53.8	423	10	AM099781
43	78	53.8	447	10	BE122013
44	78	53.8	476	12	BE726243
45	78	53.8	599	13	B1531113

ALIGNMENTS

RESULT 1
CNS07DTU 862 bp DNA linear GSS 08-JUL-2001
LOCUS T7 end of clone BD0AA015F01 of library BD0AA from strain CBS 94 of
DEFINITION Candida tropicalis, genomic survey sequence.
ACCESSION AL440909.1 GI:12224320
VERSION
KEYWORDS
SOURCE
ORGANISM
Candida tropicalis.
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
1 (bases 1 to 862)
Soucie,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Biolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,

de-Montigny, J., Dujon, B., Duret, P., Lepingle, A., Llorente, B., Malpertuy, A., Neugebäude, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekle, F., Toffano-Nioche, C., Weslowski-Louvel, M., Wincker, P., and Weissbach, J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL
MEDLINE
20584711
FEB5 Lett. 487 (1), 3-12 (2000)

REFERENCE
PUBMED
1152876

TITLE
2 (bases 1 to 862)

AUTHORS
Blandin, G., Ozier-Kalogeropoulos, O., Wincker, P., Artiguenave, F., and Dujon, B.

COMMENT
Genomic exploration of the hemiascomycetous yeasts: 16. Candida tropicalis

JOURNAL
MEDLINE
20584726
FEB5 Lett. 487 (1), 91-94 (2000)

REFERENCE
PUBMED
1152891

TITLE
3 (bases 1 to 862)

AUTHORS
Genoscope.

COMMENT
Direct Submission

JOURNAL
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 Evry cedex, FRANCE. (E-mail: sequef@genoscope.cns.fr - Web: This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermocolarans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

misc_feature

1..862
/organism="Candida tropicalis"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone_1b="BD0A015F01"
/clone_1lb="BD0A"
/note="end: T7"
<124..>726
/note="similar to Saccharomyces cerevisiae ORF YHR008C [SOD2: superoxide dismutase (Mn) precursor, mitochondrial]"
/evidence="not experimental"
BASE COUNT 278 a 117 c 140 g 322 t
ORIGIN

Alignment Scores:

d. No.: 4.5e-13 length: 862
Score: 141.00 Matches: 27
Percent Similarity: 96.43% Conservative: 0
Best Local Similarity: 96.43% Mismatches: 1
Query Match: 97.24% Indels: 0
DB: 17 Gaps: 0

US-09-987-190-2 (1-30) x CNS07DTJ (1-862)

QY 1 LyeTySerleuProGluLeuAspTYrGluPheSerAlaThrGluProTYrIleSerGly 20
DB 130 AATTAATAGTTTACAGAAATTAAGATTATTTCTCTACTGAAACATATATTTGGA 169
QY 21 GlnIleAsnGluIle***TYrThr 28
DB 190 CAAATTAATGAAATTCATTAATCT 213

RESULT 2
LOCUS AZ929307 519 bp DNA linear GSS 01-APR-2001
DEFINITION 479.dif24g04.s1 Saccharomyces kluyveri Saccharomyces kluyveri
ACCESSION genomic clone 479.dif24g04.s1, DNA sequence.
AZ929307

VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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Washington University Medical School
Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
Tel: 314 362 2735
Fax: 314 362 7855
Email: mje@genetics.wustl.edu
Class: random plasmid subclone.

FEATURES

source

1..519
/organism="Saccharomyces kluyveri"
/strain="NRRL Y-12651 (CBS 3082)"
/db_xref="taxon:4934"
/clone="479.dif24g04.s1"
/clone_1b="Saccharomyces kluyveri"
/note="Random genomic sequence"

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 3.15e-05 length: 519
Score: 92.00 Matches: 16
Percent Similarity: 82.14% Conservative: 7
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 63.45% Indels: 0
DB: 17 Gaps: 0

US-09-987-190-2 (1-30) x AZ929307 (1-519)

QY 1 LyeTySerleuProGluLeuAspTYrGluPheSerAlaThrGluProTYrIleSerGly 20
DB 371 AAGGTACCTTGGCAGAAATTAAGATTATTTCTCTACTGAAACCATCTCGGCT 430
QY 21 GlnIleAsnGluIle***TYrThr 28
DB 431 CAAATCAACGAGTTGCATCTCG 454

RESULT 3

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Ceratopteris richardii.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Filicophyta; Filicopsida; Filicales; Pteridaceae; Ceratopteris.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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Fax: 512 232 3402
Email: sroux@uts.cc.utexas.edu
Plate: Crl_9 row: A column: 14

FEATURES Seq primer: SP6.
Location/Qualifiers

source

1..464
/organism="Ceratopteris richardii"

/cultivar="Brogan"

/db_xref="taxon:49495"

/clone_1ib="Ceratopteris Spore Library"

/tissue_type="Gametophyte"

/cell_type="Spore"

/note="Vector: 20 hours after germination initiation"

/note="CDNA library constructed from mRNA isolated from C. richardii spores that had developed for 20 hours after their germination had been initiated by white light."

BASE COUNT 120 a 106 c 116 g 122 t

ORIGIN

Alignment Scores:

Pred. No.: 5.76e-05 Length: 464

Score: 90.00 Matches: 16

Percent Similarity: 81.48% Conservative: 6

Best Local Similarity: 59.26% Mismatches: 5

Query Match: 62.07% Indels: 0

DB: 14 Gaps: 0

US-09-987-190-2 (1-30) x BQ087025 (1-464)

QY 2 TySerLeuProGluLeuSerAlaThrGluProTyrIleSerGlyGln 21

DB 154 TACTCTTACCCGAGCTAGCTTACGATTATGGGCGCTTAGAGCCGTACATCAGTCGCGAA 213

QY 22 IleAsnGluIle**TyrThr 28

DB 214 ATTATGAGCTGCATCAGAC 234

RESULT 4

LOCUS A1319465 231 bp mRNA linear EST 18-DEC-1998

DEFINITION b2a04nm.f1 Neurospora crassa morning CDNA library Neurospora crassa

ACCESSION A1319465.1 GI:4035447

VERSION A1319465.1

KEYWORDS EST.

SOURCE Neurospora crassa

ORGANISM Neurospora crassa

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

AUTHORS Sordariales; Sordariaceae; Neurospora.

TITLE 1 (bases 1 to 231)

JOURNAL Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.

Unpublished (1998)

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We anticipate the future release of the CDNA clones to the Fungal

Genetics Stock Center

Seq primer: Universal Forward Primer

High quality sequence stop: 50.

Location/Qualifiers

1..231

/organism="Neurospora crassa"

/strain="bd, frq7 A"

/db_xref="taxon:5141"

/clone="b2a04nm"

/clone_1ib="Neurospora crassa morning CDNA library"

/tissue_type="tissue harvested following 22hr growth in dark"

/note="Vector: pBluescript SK-; Site_1: XbaI; Site_2: EcoRI; See: Bell-Pedersen, D., et al. PNAS 93:13096, 1996.

5' end of CDNA cloned into XbaI site of pBluescript; 3' end of CDNA cloned into EcoRI site of pBluescript"

BASE COUNT 63 a 105 c 49 g 48 t

ORIGIN

Alignment Scores:

Pred. No.: 0.000372 Length: 265

Score: 83.00 Matches: 15

Percent Similarity: 77.78% Conservative: 6

Best Local Similarity: 55.56% Mismatches: 6

Best Match: 55.56%

BASE COUNT 55 a 91 c 41 g 44 t

ORIGIN

Alignment Scores:

Pred. No.: 0.000304 Length: 231

Score: 83.00 Matches: 15

Percent Similarity: 77.78% Conservative: 6

Best Local Similarity: 55.56% Mismatches: 6

Query Match: 57.24% Indels: 0

DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x A1319465 (1-231)

QY 2 TySerLeuProGluLeuSerAlaThrGluProTyrIleSerGlyGln 21

DB 65 TATTCCTTCCGAGCTACATATGCTTACGAGCCGTACATCAGCCAG 124

QY 22 IleAsnGluIle**TyrThr 28

DB 125 ATCATGAGCTTACACACAGC 145

RESULT 5

LOCUS A1320309 265 bp mRNA linear EST 18-DEC-1998

DEFINITION c3b05nm.f1 Neurospora crassa morning CDNA library Neurospora crassa

ACCESSION A1320309

VERSION A1320309.1 GI:4036291

KEYWORDS EST.

SOURCE Neurospora crassa

ORGANISM Neurospora crassa

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

AUTHORS Sordariales; Sordariaceae; Neurospora.

TITLE 1 (bases 1 to 265)

JOURNAL Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.

Unpublished (1998)

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We anticipate the future release of the CDNA clones to the Fungal

Genetics Stock Center

Seq primer: Universal Forward Primer

High quality sequence stop: 187.

Location/Qualifiers

1..265

/organism="Neurospora crassa"

/strain="bd, frq7 A"

/db_xref="taxon:5141"

/clone="c3b05nm"

/clone_1ib="Neurospora crassa morning CDNA library"

/tissue_type="tissue harvested following 22hr growth in dark"

/note="Vector: pBluescript SK-; Site_1: XbaI; Site_2: EcoRI; See: Bell-Pedersen, D., et al. PNAS 93:13096, 1996.

5' end of CDNA cloned into XbaI site of pBluescript; 3' end of CDNA cloned into EcoRI site of pBluescript"

BASE COUNT 63 a 105 c 49 g 48 t

ORIGIN

Alignment Scores:

Pred. No.: 0.000372 Length: 265

Score: 83.00 Matches: 15

Percent Similarity: 77.78% Conservative: 6

Best Local Similarity: 55.56% Mismatches: 6

Best Match: 55.56%

Query Match: 57.24% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x A1320309 (1-265)

QY 2 TySerLeuProGluLeuAapTYrGluPhseSerAlaThrGluProTYrIleSerGlyIn 21

DB 65 TATTCCCTCCGAGCTACATATGCTTACATGCTCGAGCCCTACATCTCAGCCAG 124

QY 22 IleAsnGluIle***TYrThr 28

DB 125 ATCATGAGCTTCACACAGC 145

RESULT 6 265 bp mRNA linear EST 19-APR-2000

LOCUS h9g04nm.f1 Neurospora crassa morning cDNA library Neurospora crassa

DEFINITION CDNA clone h9g04nm 5', mRNA sequence.

ACCESSION AW717655

VERSION AW717655.1 GI:7606896

KEYWORDS EST.

ORGANISM Neurospora crassa.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariales; Sordariaceae; Neurospora.

1 (bases 1 to 265)

Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.

Two Neurospora crassa EST Databases

Unpublished (1998)

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We anticipate the future release of the cDNA clones to the Fungal

Genetics Stock Center

Seq primer: Universal Forward Primer

High quality sequence stop: 188.

Location/Qualifiers

1..265

/organism="Neurospora crassa"

/strain="bd, frq7 A"

/db_xref="taxon:5141"

/clone="h9g04nm"

/clone_lib="Neurospora crassa morning cDNA library"

/tissue_type="tissue harvested following 22hr growth in

dark"

/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:

EcoRI; See: Bell-Pedersen, D., et al. PNAS 93:13096, 1996.

5' end of cDNA cloned into XbaI site of pBluescript; 3'

end of cDNA cloned into EcoRI site of pBluescript"

BASE COUNT 63 a 105 c 49 g 48 t

ORIGIN

Alignment Scores:

Pred. No.: 0.000372 Length: 265

Score: 83.00 Matches: 15

Percent Similarity: 77.78% Conservative: 6

Best Local Similarity: 55.56% Mismatches: 6

Query Match: 57.24% Indels: 0

DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x AW717655 (1-265)

QY 2 TySerLeuProGluLeuAapTYrGluPhseSerAlaThrGluProTYrIleSerGlyIn 21

DB 65 TATTCCCTCCGAGCTACATATGCTTACATGCTCGAGCCCTACATCTCAGCCAG 124

QY 22 IleAsnGluIle***TYrThr 28

DB 125 ATCATGAGCTTCACACAGC 145

RESULT 7

LOCUS A1318805

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariales; Sordariaceae; Neurospora.

1 (bases 1 to 267)

Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.

Two Neurospora crassa EST Databases

Unpublished (1998)

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We anticipate the future release of the cDNA clones to the Fungal

Genetics Stock Center

Seq primer: Universal Forward Primer

High quality sequence stop: 192.

Location/Qualifiers

1..267

/organism="Neurospora crassa"

/strain="bd, frq7 A"

/db_xref="taxon:5141"

/clone="a2d06nm"

/clone_lib="Neurospora crassa morning cDNA library"

/tissue_type="tissue harvested following 22hr growth in

dark"

/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:

EcoRI; See: Bell-Pedersen, D., et al. PNAS 93:13096, 1996.

5' end of cDNA cloned into XbaI site of pBluescript; 3'

end of cDNA cloned into EcoRI site of pBluescript"

BASE COUNT 63 a 105 c 51 g 48 t

ORIGIN

Alignment Scores:

Pred. No.: 0.000376 Length: 267

Score: 83.00 Matches: 15

Percent Similarity: 77.78% Conservative: 6

Best Local Similarity: 55.56% Mismatches: 6

Query Match: 57.24% Indels: 0

DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x A1318805 (1-267)

QY 2 TySerLeuProGluLeuAapTYrGluPhseSerAlaThrGluProTYrIleSerGlyIn 21

DB 65 TATTCCCTCCGAGCTACATATGCTTACATGCTCGAGCCCTACATCTCAGCCAG 124

QY 22 IleAsnGluIle***TYrThr 28

DB 125 ATCATGAGCTTCACACAGC 145

RESULT 8

LOCUS AW723904

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

REFERENCE
1 (bases 1 to 267)
Sordariales; Sordariaceae; Neurospora.
AUTHORS
Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
TITLE
Two Neurospora crassa EST Databases
JOURNAL
Unpublished (1998)
COMMENT
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We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 223.

FEATURES
source
1..267
Location/Qualifiers

BASE COUNT 63 a 105 c 51 g 48 t
ORIGIN
/organism="Neurospora crassa"
/strain="bd, frq7 A"
/db_xref="taxon:5141"
/clone="f2d01nm"
/clone_1ib="Neurospora crassa morning cDNA library"
/tissue_type="tissue harvested following 22hr growth in
dark"
/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:
EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
5' end of cDNA cloned into XbaI site of pBluescript; 3'
end of cDNA cloned into EcoRI site of pBluescript"

Alignment Scores:

Pred. No.: 0.000376 Length: 267
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x AW723904 (1-267)

QY 2 TysSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
|||||
Db 65 TATTCCTTCGAGCATCATATGCTCAATGCTCTGAGCCCTCATCTCAGCCAG 124
|||||

22 TleAsnGluIle**TyrThr 28
|||||

125 ATCATGAGCTTCACCAACG 145
|||||

RESULT 9
AI321638 269 bp mRNA linear EST 18-DEC-1998
LOCUS
DEFINITION
e1d05nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
cDNA clone e1d05nm 5', mRNA sequence.
AI321638
ACCESSION
AI321638.1 GI:4037620
VERSION
EST.
KEYWORDS
Neurospora crassa.
SOURCE
Neurospora crassa
Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
1 (bases 1 to 269)
AUTHORS
Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
TITLE
Two Neurospora crassa EST Databases
JOURNAL
Unpublished (1998)
COMMENT
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We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 229.

FEATURES
source
1..269
Location/Qualifiers

BASE COUNT 63 a 106 c 52 g 48 t
ORIGIN
/organism="Neurospora crassa"
/strain="bd, frq7 A"
/db_xref="taxon:5141"
/clone="e1d05nm"
/clone_1ib="Neurospora crassa morning cDNA library"
/tissue_type="tissue harvested following 22hr growth in
dark"
/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:
EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
5' end of cDNA cloned into XbaI site of pBluescript; 3'
end of cDNA cloned into EcoRI site of pBluescript"

Alignment Scores:

Pred. No.: 0.00038 Length: 269
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x AI321638 (1-269)

QY 2 TysSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
|||||
Db 65 TATTCCTTCGAGCATCATATGCTCAATGCTCTGAGCCCTCATCTCAGCCAG 124
|||||

QY 22 TleAsnGluIle**TyrThr 28
|||||

Db 125 ATCATGAGCTTCACCAACG 145
|||||

RESULT 10

AI320505 336 bp mRNA linear EST 18-DEC-1998
LOCUS
DEFINITION
c5h03nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
cDNA clone c5h03nm 5', mRNA sequence.
AI320505
ACCESSION
AI320505.1 GI:4036487
VERSION
EST.
KEYWORDS
Neurospora crassa.
SOURCE
Neurospora crassa
Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
1 (bases 1 to 336)
AUTHORS
Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
TITLE
Two Neurospora crassa EST Databases
JOURNAL
Unpublished (1998)
COMMENT
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We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 194.

FEATURES
source
1..336
Location/Qualifiers

BASE COUNT 63 a 106 c 52 g 48 t
ORIGIN
/organism="Neurospora crassa"
/strain="bd, frq7 A"
/db_xref="taxon:5141"
/clone="c5h03nm"
/clone_1ib="Neurospora crassa morning cDNA library"
/tissue_type="tissue harvested following 22hr growth in
dark"

dark"
/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:
EcoRI; See: Bell-Pedersen,D., et al., PNAS 93:13096,1996.
5' end of cDNA cloned into XbaI site of pBluescript; 3'
end of cDNA cloned into EcoRI site of pBluescript"

BASE COUNT 80 a 133 c 64 g 59 t

ALIGNMENT Scores:

Pred. No.: 0.000527 Length: 336
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x A1320505 (1-336)

QY 2 TySerLeuProGluLeuAspTYrGluPheSerAlaThrGluProTYrIleSerGlyGln 21

65 TATTCCTTCGCGAGCTACCATATGCTCTGAGAGCCCTACATCTCAGCCAG 124

22 TLeAsnGluIle***TYrThr 28

Db 125 ATCATGAGAGCTTCACACAGC 145

RESULT 11

A1318710 339 bp mRNA linear EST 18-DEC-1998

LOCUS a1b10nm.f1 Neurospora crassa morning cDNA library Neurospora crassa

DEFINITION cDNA clone a1b10nm 5', mRNA sequence.

ACCESSION A1318710

VERSION A1318710.1 GI:4034645

KEYWORDS EST.

SOURCE Neurospora crassa.

ORGANISM Neurospora crassa

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

AUTHORS Sordariales; Sordariaceae; Neurospora.

TITLE 1 (bases 1 to 339)

JOURNAL Two Neurospora crassa EST Databases

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We anticipate the future release of the cDNA clones to the Fungal

Genetics Stock Center

Seq primer: Universal Forward Primer

High quality sequence stop: 309.

FEATURES

source

1. .339

/organism="Neurospora crassa"

/strain="bd, frq7 A"

/db_xref="taxon:5141"

/clone="a1b10nm"

/clone_lib="Neurospora crassa morning cDNA library"

/tissue_type="tissue harvested following 22hr growth in

dark"

/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:

EcoRI; See: Bell-Pedersen,D., et al., PNAS 93:13096,1996.

5' end of cDNA cloned into XbaI site of pBluescript; 3'

end of cDNA cloned into EcoRI site of pBluescript"

BASE COUNT 82 a 133 c 65 g 59 t

ORIGIN

ALIGNMENT Scores:

Pred. No.: 0.000534 Length: 339
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Mismatches: 6
Conservative: 6

Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x A1318710 (1-339)

QY 2 TySerLeuProGluLeuAspTYrGluPheSerAlaThrGluProTYrIleSerGlyGln 21

65 TATTCCTTCGCGAGCTACCATATGCTCTGAGAGCCCTACATCTCAGCCAG 124

QY 22 TLeAsnGluIle***TYrThr 28

Db 125 ATCATGAGAGCTTCACACAGC 145

RESULT 12

A1319577 339 bp mRNA linear EST 18-DEC-1998

DEFINITION b3g06nm.f1 Neurospora crassa morning cDNA library Neurospora crassa

ACCESSION A1319577

VERSION A1319577.1 GI:4035559

KEYWORDS EST.

SOURCE Neurospora crassa.

ORGANISM Neurospora crassa

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

AUTHORS Sordariales; Sordariaceae; Neurospora.

TITLE 1 (bases 1 to 339)

JOURNAL Two Neurospora crassa EST Databases

COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

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620 Parrington Oval, Norman, OK 73019, USA

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Email: broe@ou.edu

We anticipate the future release of the cDNA clones to the Fungal

Genetics Stock Center

Seq primer: Universal Forward Primer

High quality sequence stop: 314.

FEATURES

source

1. .339

/organism="Neurospora crassa"

/strain="bd, frq7 A"

/db_xref="taxon:5141"

/clone="b3g06nm"

/clone_lib="Neurospora crassa morning cDNA library"

/tissue_type="tissue harvested following 22hr growth in

dark"

/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:

EcoRI; See: Bell-Pedersen,D., et al., PNAS 93:13096,1996.

5' end of cDNA cloned into XbaI site of pBluescript; 3'

end of cDNA cloned into EcoRI site of pBluescript"

BASE COUNT 82 a 133 c 65 g 59 t

ORIGIN

ALIGNMENT Scores:

Pred. No.: 0.000534 Length: 339
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x A1319577 (1-339)

QY 2 TySerLeuProGluLeuAspTYrGluPheSerAlaThrGluProTYrIleSerGlyGln 21

65 TATTCCTTCGCGAGCTACCATATGCTCTGAGAGCCCTACATCTCAGCCAG 124

QY 22 TLeAsnGluIle***TYrThr 28

Db 125 ATCATGAGAGCTTCACACAGC 145

Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 394.
Location/Qualifiers

FEATURES

source

1. 401
/organism="Neurospora crassa"
/strain="bd, frq7 A"
/db_xref="taxon:5141"
/clone="f8b07nm"
/clone_lib="Neurospora crassa morning cDNA library"
/tissue_type="tissue harvested following 22hr growth in
dark"
/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:
EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
5' end of cDNA cloned into XbaI site of pBluescript; 3'
end of cDNA cloned into EcoRI site of pBluescript"

BASE COUNT

96 a 145 c 87 g 73 t

ORIGIN

Alignment Scores:

pred. No.: 0.000683 Length: 401
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x AW724781 (1-401)

QY 2 TySerLeuProGluLeuAapTYrGluPheSerAlaThrGluProTYrIleSerGlyGln 21

DB 65 TATTCCTTCGAGCTACCATATGCTTACCAATGCTCTGAGCCCTACATCTCAGCCAG 124

QY 22 IleAsnGluIle**TYrThr 28

DB 125 ATCATGAGCTTCACACAGC 145

RESULT 16

AW715120

LOCUS 429 bp mRNA linear EST 19-APR-2000
DEFINITION g2c12nm.f1 Neurospora crassa morning cDNA library Neurospora crassa

ACCESSION AW715120
CDNA clone g2c12nm 5', mRNA sequence.

VERSION AW715120.1 GI:7604309

KEYWORDS

EST.

SOURCE

Neurospora crassa.

ORGANISM

Neurospora crassa

REFERENCE

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariales; Sordariaceae; Neurospora.

1 (bases 1 to 429)

Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.

Two Neurospora crassa EST Databases

Unpublished (1998)

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma

620 Farrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

We anticipate the future release of the cDNA clones to the Fungal

Genetics Stock Center

Seq primer: Universal Forward Primer

High quality sequence stop: 336.

Location/Qualifiers

1. 429

/organism="Neurospora crassa"

/strain="bd, frq7 A"

/db_xref="taxon:5141"

/clone="g2c12nm"

/clone_lib="Neurospora crassa morning cDNA library"

/tissue_type="tissue harvested following 22hr growth in
dark"
/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:
EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
5' end of cDNA cloned into XbaI site of pBluescript; 3'
end of cDNA cloned into EcoRI site of pBluescript"

BASE COUNT

98 a 154 c 95 g 82 t

ORIGIN

Alignment Scores:

pred. No.: 0.000754 Length: 429
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x AW715120 (1-429)

QY 2 TySerLeuProGluLeuAapTYrGluPheSerAlaThrGluProTYrIleSerGlyGln 21

DB 65 TATTCCTTCGAGCTACCATATGCTTACCAATGCTCTGAGCCCTACATCTCAGCCAG 124

QY 22 IleAsnGluIle**TYrThr 28

DB 125 ATCATGAGCTTCACACAGC 145

RESULT 17

AW715952

LOCUS 429 bp mRNA linear EST 19-APR-2000
DEFINITION g8b12nm.f1 Neurospora crassa morning cDNA library Neurospora crassa

ACCESSION AW715952
CDNA clone g8b12nm 5', mRNA sequence.

VERSION AW715952.1 GI:7605157

KEYWORDS

EST.

SOURCE

Neurospora crassa.

ORGANISM

Neurospora crassa

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariales; Sordariaceae; Neurospora.

1 (bases 1 to 429)

Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.

Two Neurospora crassa EST Databases

Unpublished (1998)

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma

620 Farrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

We anticipate the future release of the cDNA clones to the Fungal

Genetics Stock Center

Seq primer: Universal Forward Primer

High quality sequence stop: 310.

Location/Qualifiers

1. 429

/organism="Neurospora crassa"

/strain="bd, frq7 A"

/db_xref="taxon:5141"

/clone="g8b12nm"

/clone_lib="Neurospora crassa morning cDNA library"

/tissue_type="tissue harvested following 22hr growth in
dark"/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:
EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
5' end of cDNA cloned into XbaI site of pBluescript; 3'
end of cDNA cloned into EcoRI site of pBluescript"

BASE COUNT

98 a 154 c 95 g 82 t

ORIGIN

Alignment Scores:

pred. No.: 0.000754 Length: 429
Score: 83.00 Matches: 15

Alignment Scores:

Pred. No.: 0.00221 Length: 689
 Score: 82.00 Matches: 15
 Percent Similarity: 75.00% Conservative: 6
 Best Local Similarity: 53.57% Mismatches: 7
 Query Match: 56.55% Indels: 0
 DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x BM266232 (1-689)

QY 1 lyeYrserleuProGluLeuAspTYrGluPheserAlathrgluProTYrIleserGly 20

DB 404 AAGTTACTCTTCGGGACATTCGCTTATGATGCGTAGAACCTTACATCTCCGCGC 463

QY 21 Glulleangluile**TYrThr 28

DB 464 CAATTATGCATTCACCATTC 487

RESULT 20 BM367690 466 bp mRNA linear EST 10-JAN-2002

LOCUS NXLV_053_C03_F_NXLV (Nsf Xylem Late wood Vertical) Pinus taeda cDNA
 ACCESSION BM367690
 VERSION BM367690.1 GI:18111080
 KEYWORDS EST.
 SOURCE loblolly pine.
 ORGANISM Pinus taeda
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 1 (bases 1 to 466)
 Sederoff, R.
 Molecular Basis of Wood Formation in the Pine Megagenome
 Unpublished (2000)
 Contact: Johnson, Arthur
 North Carolina State University
 Tel: 919 515 7800
 Fax: 919 515 7801
 Email: a.johnson@uncit.ncsu.edu
 Seq primer: T3.
 Location/Qualifiers
 1..466
 /organism="Pinus taeda"
 /strain="Coastal plain loblolly pine from North Carolina"
 /db_xref="taxon:3352"
 /clone="NXLV_053_C03"
 /clone_1lb="NXLV (Nsf Xylem Late wood Vertical)"
 /tissue_type="primary xylem"
 /dev_stage="late wood"
 /lab_host="XLI-Blue"
 /note="Vector: pTRipleX; Site 1: EcoRI; The library is from late (summer-August) wood, taken from below the crown of a 20 year old tree. The harvested xylem tissue was on the cusp between transitional and mature wood. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATCGGCATATGCGC'."

BASE COUNT 118 a 86 c 126 g 118 t 18 others
 ORIGIN

Alignment Scores:

Pred. No.: 0.00269 Length: 466
 Score: 80.00 Matches: 15
 Percent Similarity: 76.92% Conservative: 5
 Best Local Similarity: 57.69% Mismatches: 6
 Query Match: 55.17% Indels: 0
 DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x BM367690 (1-466)

QY 2 TySerleuProGluLeuAspTYrGluPheserAlathrgluProTYrIleserGly 21
 DB 204 TTATGTTACCGAGCTTCATAGATACAGCGCATTCGACCGTATTATGATGAG 263

QY 22 lIeAsngluile**TYr 27
 DB 264 ATTATGAGCTGCACAC 281

RESULT 21

LOCUS AW733168 306 bp mRNA linear EST 03-DEC-2001
 DEFINITION sk7b06.y1 Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1016-9492 5' similar to SW:SDM_PEA P27084 SUPEROXIDE DISMUTASE [MN] PRECURSOR ;, mRNA sequence.

ACCESSION AW733168
 VERSION AW733168.1 GI:7638902
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 306)
 Shoemaker, R., Kain, P., Vodkin, L., Erpelting, J., Corvett, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, W., Pape, D., Harvey, N., Schurk, R., Ritzer, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: cduoresgen.com
 Insert Length: 1240 Std Error: 0.00
 Seq primer: -40RP from Gibco
 High quality sequence stop: 305.
 Location/Qualifiers
 1..306
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1016-9492"
 /clone_1lb="Gm-c1016"
 /tissue_type="immature flowers of field grown plants"
 /dev_stage="XLI0-Gold"
 /lab_host="XLI0-Gold"
 /note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI. This cDNA library was constructed from mRNA isolated from immature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLI0-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."

BASE COUNT 72 a 102 c 72 g 60 t
 ORIGIN

Alignment Scores:

Pred. No.: 0.00213 Length: 306
 Score: 79.00 Matches: 13
 Percent Similarity: 80.77% Conservative: 8
 Best Local Similarity: 50.00% Mismatches: 5
 Query Match: 54.48% Indels: 0

```

DB:                               10          Gaps:          0
US-09-987-190-2 (1-30) x AM733168 (1-306)

Oy      2  TTTSerLeuProGluLeuAspTYrGluPheSerAlaThrGluProTYrIleSerGlyAln 21
         |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      160 TACAGCGTCCCGCATCTGGATTACGACATATGCGCTCTGGAGCCAGCCATCATCGCGCGCA 219
         |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Oy      22 TleaaGluIle***TYr 27
         |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      220 ATCATGACAGCTGCACCAC 237
         |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 22
BI498255
LOCUS      BI498255              419 bp      mRNA      linear      EST 29-NOV-2001
DEFINITION      saai1h04.y1 Gm-cl080 glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl080-1519 5' similar to SW:SODM_PEA P27084 SUPEROXIDE
DIMUTYASE [NM], MITOCHONDRIAL PRECURSOR ;, mRNA sequence.
BI498255
BI498255.1  GI:1537599
EST.
SOURCE      soybean.
ORGANISM      Glycine max
AUTHORS      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
              Glycine.
REFERENCE      1 (bases 1 to 419)
AUTHORS      Shoemaker,R., Keim,P., Vocklin,L., Erpelting,J., Corvett,V., Khanna
              ,A., Bolla,B., Maritz,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
              Wylie,T., Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers
              ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
              ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
              ,R., Waterston,R. and Wilson,R.
TITLE      Public Soybean EST Project
JOURNAL      Unpublished (1999)
COMMENT      Contact: Shoemaker R/Public Soybean EST Project
              Public Soybean EST Project
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              This clone is available through: Resgen, Invitrogen Corp. 2130
              South Memorial Parkway Huntville, AL 35801 For further information
              call: (800)-533-4363 or contact via email: ccu@resgen.com
              High quality sequence stop: 287.
              location/Qualifiers
              1..419
              /organism="Glycine max"
              /db_xref="taxon:3847"
              /clone="GENOME SYSTEMS CLONE ID: Gm-cl080-1519"
              /clone_1lb="Gm-cl080"
              /tissue_type="Roots of 8 day old 'Bragg' supernodulating
              mutant NT5382 seedlings"
              /dev_stage="8 days old"
              /lab_host="DH10B"
              /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site_2:
              XhoI; The mRNA was isolated from roots of 8 day old
              'Bragg' supernodulating mutant NT5382 seedlings that were
              infected with Bradyrhizobium japonicum, strain USDA 110, 72
              hours prior to harvest. Dr. Gary Stacey generously donated
              the tissue. The roots were flash-frozen in liquid
              nitrogen. Stragene's cDNA Synthesis Kit (catalog number
              200401) was used to synthesize the cDNA. First-strand
              synthesis was performed with 5-methyl dCTP, hence the
              ligated cDNA was hememethylated. A modification of
              Stragene's first-strand synthesis primer was used. An
              'anchor' nucleotide (V=A, C, or G) was added to the 3' end
              of the primer [GAGAGAGAGAGAGAGAGAGACATGCTGAG(T)18V] to
              anchor the primer at the 5' end of the poly(A) tract.
              After second-strand synthesis, the cDNA ends were filled
              in with cloned Pfu DNA, ligated to EcoRI adapters and

```

[illegible]

REFERENCE	AUTHORS	1 (bases 1 to 448) Shoemaker, R., Keim, P., Vocklin, L., Erpelding, J., Corryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kuabab, T., Martin, T., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harrey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
TITLE	PUBLIC Soybean EST Project	
COMMENT	Public Soybean EST Project Contact: Shoemaker R/Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Possible reversed clone: similarity on wrong strand This clone is available through: Resgen, Invitrogen Corp, 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800) 533-4363 or contact via email: cduresgen.com Insert Length: 1069 Std Error: 0.00 Seq primer: -40RP from Gibco High quality sequence stop: 124 POLYA=NO	
FEATURES	Source	Location/Qualifiers 1..448 /organism="Glycine max" /db_xref="taxon:3847" /clone="GENOME SYSTEMS CLONE ID: Gm-cl004-4579" /clone_1id="Gm-cl004" /c1issue_type="root" /lab_host="XL10-Gold" /note="Vector: pBluescript II Xr; Site 1: EcoRI; Site 2: XhoI; Root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratsagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA is hemimethylated. Stratsagene's first-strand synthesis primer was used [GAGGAGAGAGAGAGAGAGACTGATCTCGAG(T)-18]. After second-strand synthesis, the cDNA ends were 'polished' with clone Pfu DNA polymerase, ligated to EcoRI adaptors, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratsagene's pBluescript II Xr Predigested vector (pBluescript II SK(+)) that had been digested with EcoRI and XhoI, and phosphorylated. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. Blue colonies 9n=15 have been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Corryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011, phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Corryell), Fax: 520-523-7500, email: paul.keim@nau.edu, virginia.corryell@nau.edu"
BASE COUNT	108 a	144 c 105 g 90 t 1 others
ORIGIN		
Alignment Scores:	0.00373	Length: 448

Score:	79.00	Matches:	13
Percent Similarity:	80.77%	Conservative:	5
Best Local Similarity:	50.00%	Mismatches:	5
Query Match:	54.48%	Indels:	0
DB:	9	Gaps:	0

US-09-987-190-2 (1-30) x A1460811 (1-448)

Qy	2	TyrsrleuPrgGluLeuAspTyGluPheserAlaThrGluProTyrIleSerGlycIn 21
Db	173	TACAGCGCCCCGATCTGGATTACGACTATGAGCGCTCTGGAGCAGCCATCATGACGCGCGAA 232
Qy	22	IleAsnGluIle***Tyr 27
Db	233	ATCATGCAGCTGCACACC 250

RESULT 26

A1460823

LOCUS

DEFINITION

A1460823 448 bp mRNA linear EST 28-NOV-2001

GM-cl1004-4580 5 similar to SW:SODM_PEA P27084 SUPEROXIDE DISMUTASE

PRECUNSOR ; mRNA sequence.

A1460823

VERSION

KEYWORDS

A1460823.1 GI:4313704

EST.

SOURCE

ORGANISM

soybean.

Glycine max

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 448)

Shoemaker,R., Keim,P., Vodkin,L., Eppelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Strepeou,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuck,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.wustl.edu

Possible reversed clone: similarity on wrong strand. This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com

Insert Length: 1069 Std Error: 0.00

Seq primer: -40RP from Gibco

High quality sequence stop: 284

POLYA=No.

FEATURES

source

location/Qualifiers

1..448

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl1004-4580"

/clone_1b="Gm-cl1004"

/tissue type="root"

/lab host="XL10-Gold"

/note="vector: pBluescript II XR; site 1: EcoRI; site 2: XhoI; Root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stragene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cDNA. First- strand synthesis was performed with 5-methyl dCpP, hence the ligated cDNA is hemimethylated. Stragene's first-strand synthesis primer was used [GAGAGGAGAGAGAGAGAACTAGTCTTGAG(T)-18]. After second-strand synthesis, the cDNA ends were 'polished'

with clone pFu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GIBCOBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+)) that had been digested with EcoRI and XhoI, and phosphorylated. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. Blue colonies 9n-15) have been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax: 520-523-7500, email: Paul.Keim@nau.edu, Virginia.coryell@nau.edu"

BASE COUNT 107 a 143 c 105 g 93 t
 Alignment Scores:
 Pred. No.: 0.00373 Length: 448
 Score: 79.00 Matches: 13
 Percent Similarity: 80.77% Conservative: 8
 Best Local Similarity: 50.00% Mismatches: 5
 Query Match: 54.48% Indels: 0
 DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x A1460823 (1-448)

QY 2 TySerLeuProGluLeuAapTYrGluPheSerAlaThrGluProTYrIleSerGlyGln 21
 Db 173 TACACGCTCCCGCATTCGATTCAGACTATGAGCCCTCTGAGCCAGCATCAGCGCGAA 232
 QY 22 IleAsnGluIle***Tyr 27
 Db 233 ATCATGCACTGCGACAC 250

RESULT 27
 AM099772 463 bp mRNA linear EST 30-NOV-2001
 LOCUS 631C07.Y2 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION Gm-c1012-3301.5' similar to SW:SDOM_PEA P27084 SUPEROXIDE DISMUTASE
 [MN] PRECURSOR ;, mRNA sequence.

ACCESSION AM099772
 VERSION AM099772.1 GI:6070236
 KEYWORDS EST.

ORGANISM

soybean.
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 463)

REFERENCE
 AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
 A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
 R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
 R., Waterston,R. and Wilson,R.
 Public Soybean EST Project
 Unpublished (1999)

TITLE
 JOURNAL

COMMENT
 Contact: Shoemaker R./Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact via email: cdu@resgen.com
 Seq primer: -40RP from Gibco
 High quality sequence stop: 417.
 Location/Qualifiers

FEATURES
 source
 1..463
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1012-3301"
 /clone_1ib="Gm-c1012"
 /tissue_type="Apical shoot tips, 9-10 day old etiolated seedlings"
 /lab_host="X110-Gold"
 /note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from the apical shoots of 9 to 10 day old etiolated seedlings. The shoot tips including any emerged leaves were harvested for mRNA isolation. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into X110-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."

BASE COUNT 109 a 149 c 110 g 95 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.00391 Length: 463
 Score: 79.00 Matches: 14
 Percent Similarity: 77.78% Conservative: 7
 Best Local Similarity: 51.85% Mismatches: 6
 Query Match: 54.48% Indels: 0
 DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x AM099772 (1-463)
 QY 2 TySerLeuProGluLeuAapTYrGluPheSerAlaThrGluProTYrIleSerGlyGln 21
 Db 178 TACACGCTCCCGCATTCGATTCAGACTATGAGCCCTCTGAGCCAGCATCAGCGCGAA 237
 QY 22 IleAsnGluIle***TyrThr 28
 Db 238 ATCATGCACTGCGACAC 258

RESULT 28
 BM892237 470 bp mRNA linear EST 11-MAR-2002
 LOCUS 6am77h1.Y1 Gm-c1069 Glycine max cDNA clone SOYBEAN CLONE ID:
 DEFINITION Gm-c1069-3813.5' similar to SW:SDOM_NICP_P1796 SUPEROXIDE
 DISMUTASE [MN], MITOCHONDRIAL PRECURSOR ;, mRNA sequence.

ACCESSION BM892237
 VERSION BM892237.1 GI:19347357
 KEYWORDS EST.

ORGANISM

soybean.
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 470)

REFERENCE
 AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
 A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
 R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
 R., Waterston,R. and Wilson,R.
 Public Soybean EST Project
 Unpublished (1999)

TITLE
 JOURNAL

Gm-c1036-7603 5' similar to SW:SODM_PEA P27084 SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL PRECURSOR ;, mRNA sequence.

ACCESSION
BM521591
VERSION
BM521591.1 GI:18692743
KEYWORDS
EST.
SOURCE
ORGANISM
soybean.

REFERENCE
AUTHORS

1 (bases 1 to 571)
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccut@resgen.com web site: www.resgen.com
Seq primer: -40RP from gibco
High quality sequence stop: 428.
Location/Qualifiers

FEATURES

source

1..571
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1036-7603"
/clone_1ib="Gm-c1036"
/tissue_type="somatic embryo cultured on MSD 20"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This cDNA library was constructed from mRNA isolated from somatic embryos (age ranging from 2 months to 9 months) cultured on MSD 20. The library was prepared using the Life Technologies superscript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a NotI restriction site. SalI linker adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into B.coli Electromax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Ann Khanna e-mail: l-vodkin@uiuc.edu"
Urbana-Champaign

BASE COUNT 139 a 157 c 147 g 128 t

ORIGIN

Alignment Scores:
Pred. No.: 0.00532 Length: 571
Score: 79.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 54.48% Indels: 0
DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x BM521591 (1-571)

OY 2 TySeSerLeProGluLeuAaPyTyrGluPhSeSerAlaThrGluProTyrIleSeGlyGln 21
DB 155 TACACGCTCCCGATCTGGATTAAGACTATGGCGCTCTGAGCAGCAGCATCAGCGCGAA 214

OY 22 lLeaHGlutlle***Tyr 27
DB 215 ATCATGCACTGCACCCAC 232

RESULT 33
LOCUS
B0094786

DEFINITION
B0094786 578 bp mRNA linear EST 08-APR-2002
san51905.y1 Gm-c1052 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1052-3370 5' similar to SW:SODM_PEA P27084 SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL PRECURSOR ;, mRNA sequence.

ACCESSION
B0094786
VERSION
B0094786.1 GI:20076003
KEYWORDS
EST.
SOURCE
ORGANISM
soybean.

REFERENCE
AUTHORS

1 (bases 1 to 578)
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccut@resgen.com web site: www.resgen.com
Seq primer: -40RP from gibco
High quality sequence stop: 427.
Location/Qualifiers

FEATURES

source

1..578
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1052-3370"
/clone_1ib="Gm-c1052"
/tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="1 week old"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI. The Harosoy NIL was constructed and seed was provided by Dr. U. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from whole seedlings of 1 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a 3' poly(dT) sequence with a XhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). The library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."

BASE COUNT 144 a 160 c 148 g 126 t

ORIGIN

Alignment Scores:
Pred. No.: 0.00541 Length: 578
Score: 79.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8


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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1028-997"
/clone_1lb="Gm-c1028"
/tissue_type="roots of 'Supermod' plants"
/lab_host="DH10B"
/notes="Vector: pBluescript II Xr, Site_1: EcoRI, Site_2:
XhoI; The mRNA was isolated from roots of Glycine max
'Supermod' plants generously donated by Dr. Gary Stacey.
The seedlings were inoculated with Bradyrhizobium
japonicum, strain USDA110 prior to harvest. Stratagene's
cDNA synthesis kit (catalog number 200401) was used to
synthesize the cDNA. First-strand synthesis was performed
with 5-methyl dCTP, hence the ligated cDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An 'anchor'
nucleotide (V=A,C, or G) was added to the 3' end of the
primer (GAGAGACAGACAGACAGACAGACTACTCTCGAG(T18V)) to anchor
the primer at the 5' end of the poly(A) tract. After
second-strand synthesis, the cDNA ends were filled in with
cloned Pfu DNA polymerase, ligated to EcoRI adapters and
subsequently phosphorylated. The XhoI site within the
first-strand synthesis primer was then restricted by
digestion with XhoI; all XhoI sites in the cDNA would be
protected by their hemimethylated status. The cDNA
constructs were size-fractionated with a 500bp cutoff,
using GibcoBRL Life Technologies' cDNA Size Fractionation
column. The column eluent was then ligated into
Stratagene's pBluescript II Xr Predigested vector
(pBluescript II SK(+)) that has been digested with EcoRI
and XhoI, and phosphorylated by Stratagene). Both the
white and blue colonies appear to contain recombinant
plasmids with cDNA inserts, based on size (n=25). This
library was constructed by Dr. Paul Keim and Dr. Virginia
Coryell."

BASE COUNT      147 a      166 c      151 g      132 t      2 others
ORIGIN

Alignment Scores:
Pred. No.:      0.00569      Length:      598
Score:          79.00      Matches:      13
Percent Similarity: 80.77%      Conservative: 8
Best Local Similarity: 50.00%      Mismatches: 5
Query Match:    54.48%      Indels:      0
DB:             10      Gaps:      0

US-09-987-190-2 (1-30) x AM234447 (1-598)

QY      2  TTTSerLeuProGluLeuApyTYrGluPheSerAlaThrGluProTYrIleSerGlyGln 21
      173 TACACGCTCCCGCATCTGATTAAGCATTAAGCGCTCTGAGAGCCAGCATCAGCGGTGAA 232
QY      22 TleAaNGluIle***TYr 27
      233 ATCATGACGCTGCACAC 250

RESULT 38
LOCUS      BE330334      670 bp      mRNA      linear      EST 04-DEC-2001
DEFINITION      B077004.Y1 Gm-c1040 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1040-1664 5', similar to SW:SDOM_PEA P27084 SUPEROXIDE DISMUTASE
[MN] PRECURSOR ;, mRNA sequence.
ACCESSION      BE330334
VERSION        BE330334
KEYWORDS      EST.
SOURCE        soybean.
ORGANISM      Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 670)
REFERENCE      1 (bases 1 to 670)
AUTHORS      Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
,A., Bolla,B., Matra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,

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TITLE
JOURNAL
COMMENT
Wyle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Waller,T., Gibbons,M., Page,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watsn.wustl.edu
This clone is available through: Reggen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cc@wreggen.com
Insert Length: 1066 Std Error: 0.00
High quality sequence stop: 470.
Location/Qualifiers
1..670
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1040-1664"
/clone_1lb="Gm-c1040"
/tissue_type="Hypocotyl and Plumule, germinating seeds"
/lab_host="DH10B"
/notes="Vector: pT7T3Pac (Pharmacia); Site_1: EcoRI;
Site_2: NotI; This cDNA library was constructed from mRNA
isolated from hypocotyl and plumule tissues of seeds
germinated for three days of the cultivar Williams 82.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a NotI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by digestions with EcoRI and NotI. The
cDNA fragments were directionally cloned into the
EcoRI-NotI restriction site of the pT7T3-Pac vector. The
ligated cDNA fragments were transformed into DH10B host
cells (Gibco BRL). This library was constructed by Dr.
Randy Shoemaker."

BASE COUNT      162 a      177 c      178 g      151 t      2 others
ORIGIN

Alignment Scores:
Pred. No.:      0.00672      Length:      670
Score:          79.00      Matches:      13
Percent Similarity: 80.77%      Conservative: 8
Best Local Similarity: 50.00%      Mismatches: 5
Query Match:    54.48%      Indels:      0
DB:             10      Gaps:      0

US-09-987-190-2 (1-30) x BE330334 (1-670)

QY      2  TTTSerLeuProGluLeuApyTYrGluPheSerAlaThrGluProTYrIleSerGlyGln 21
      173 TACACGCTCCCGCATCTGATTAAGCATTAAGCGCTCTGAGAGCCAGCATCAGCGGTGAA 232
QY      22 TleAaNGluIle***TYr 27
      233 ATCATGACGCTGCACAC 250

RESULT 39
LOCUS      BI263359      675 bp      mRNA      linear      EST 18-JUL-2001
DEFINITION      NF089FP09P1F1079 Phosphate starved leaf Medicago truncatula cDNA
clone NF089FP09PL 5', mRNA sequence.
ACCESSION      BI263359
VERSION        BI263359
KEYWORDS      EST.
SOURCE        barrel medic.
ORGANISM      Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

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TITLE
JOURNAL
COMMENT
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 483.
FEATURES
source
1. .683
/organism="Glycine max"
/db xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1025-681"
/clone_1db="Gm-c1025"
/tissue_type="Hypocotyl, 3 day seedlings"
/lab host="DH10B"
/notes="Vector: pTR73Pac (PT73, Pharmacia); Site 1: EcoRI;
Site 2: NotI. This cDNA library was constructed from mRNA
isolated from hypocotyl tissue of 3 day old seedlings.
Complementary DNA was synthesized from mRNA using a poly
(dT) primer with a NotI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
digestion with EcoRI and NotI. The cDNA fragments were
directionally cloned into the EcoRI-NotI restriction site
of the pTR73-Pac vector. The ligated cDNA fragments were
transformed into DH10B host cells (Gibco BRL). This
library was constructed by Dr. Randy Shoemaker."
BASE COUNT 174 a 183 c 175 g 151 t
ORIGIN
Alignment Scores:
Pred. No.: 0.00691 Length: 683
Score: 79.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best local Similarity: 50.00% Mismatches: 5
Query Match: 54.48% Indels: 0
DB: 13 Gaps: 0
US-09-387-190-2 (1-30) x B1942249 (1-683)
QY 2 TyrsenleuPFGGluLeuAspTYrGluPheseraLathGluProTYrIleSerGlyGln 21
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 150 TACACGGCTCCCGCATTCGGATTACGACTATGCGCTCTGAGCAGCCATCATGCGGCGAA 209
QY 22 IleAsnGluIle***Tyr 27
||| :|||| :|||
Db 210 ATCATGCAAGCTGCACAC 227

```


GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 8, 2003, 03:17:18 ; Search time 18.1651 Seconds

(without alignments)
1448.656 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 145

Sequence: 1 KXSLELDYFSGATEPIYSGQINEXYTX 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-CG=cg2_1/USPTO_spool/US09987190/runat_02042003_092634_19348/app.query.fasta_1.526
-DB=Published Applications_NA -QWTS=fastcat -SUFFIX=rmpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USRR=US09987190 @CGN 1.1 89 @runat 02042003_092634_19348
-NCPU=6 -ICPU=3 -NO_XLPEXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-BEV_TIMEOUT=120 -WRRN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:*

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14: /cg2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	54.5	360	10	US-09-878-574-2556
2	79	54.5	390	10	US-09-878-574-503
3	77	53.1	600	9	US-09-738-626-3227
4	77	53.1	1143	10	US-09-818-564-1

5	74	51.0	224	10	US-09-960-352-5895	Sequence 5895, Ap
6	74	51.0	259	10	US-09-960-352-3021	Sequence 3021, Ap
7	74	51.0	325	9	US-09-993-333-11	Sequence 11, Appl
8	74	51.0	424	10	US-09-960-352-14744	Sequence 14744, A
9	74	51.0	972	12	US-10-044-090-836	Sequence 836, Ap
10	74	51.0	1026	10	US-09-954-456-1822	Sequence 1822, Ap
11	74	51.0	1492	10	US-09-917-800A-1627	Sequence 1627, Ap
12	71	49.0	721	10	US-09-987-190-8	Sequence 8, Appl
13	70	48.3	817	10	US-09-770-445-745	Sequence 745, Ap
14	67	46.2	597	9	US-09-727-855B-6	Sequence 6, Appl
15	66	45.5	669	9	US-09-727-855B-4	Sequence 4, Appl
16	66	45.5	838	10	US-09-974-300-2052	Sequence 2052, Ap
17	62	42.8	767	10	US-09-070-927A-425	Sequence 425, Ap
18	56	38.6	640681	10	US-09-790-988-1	Sequence 1, Appl
19	54	37.2	757	10	US-09-770-445-976	Sequence 976, Ap
20	54	37.2	1145	7	US-08-781-986A-777	Sequence 777, Ap
21	54	37.2	1290	9	US-09-938-842A-2090	Sequence 2090, Ap
22	54	37.2	3393	7	US-08-781-986A-426	Sequence 426, Ap
23	53	36.6	1044	9	US-09-948-820-29	Sequence 29, Appl
24	52	35.9	385	10	US-09-974-300-6347	Sequence 6347, Ap
25	51	35.2	2454	10	US-09-822-849A-208	Sequence 208, Ap
26	51	35.2	32249	9	US-10-091-504-2314	Sequence 2314, Ap
27	51	35.2	32249	10	US-09-764-869-2314	Sequence 2314, Ap
28	50	34.5	1203	9	US-10-012-896-851	Sequence 851, Ap
29	50	34.5	1203	9	US-09-895-793-851	Sequence 851, Ap
30	50	34.5	1203	9	US-09-895-814-851	Sequence 851, Ap
31	50	34.5	1203	10	US-09-759-143-851	Sequence 851, Ap
32	50	34.5	1203	10	US-09-760-669-851	Sequence 851, Ap
33	50	34.5	1203	10	US-09-822-827-851	Sequence 851, Ap
34	50	34.5	2904	9	US-10-012-896-703	Sequence 703, Ap
35	50	34.5	2904	9	US-09-895-793-703	Sequence 703, Ap
36	50	34.5	2904	9	US-09-895-814-703	Sequence 703, Ap
37	50	34.5	2904	10	US-09-759-143-703	Sequence 703, Ap
38	50	34.5	2904	10	US-09-760-669-703	Sequence 703, Ap
39	50	34.5	2904	10	US-09-822-827-703	Sequence 703, Ap
40	50	34.5	3320	10	US-09-838-785-1	Sequence 1, Appl
41	50	34.5	3320	9	US-09-232-880-110	Sequence 110, Ap
42	50	34.5	3410	9	US-10-012-896-110	Sequence 110, Ap
43	50	34.5	3410	9	US-09-895-799-110	Sequence 110, Ap
44	50	34.5	3410	9	US-09-895-814-110	Sequence 110, Ap
45	50	34.5	3410	10	US-09-745-288-100	Sequence 100, Ap

ALIGNMENTS

RESULT 1
US-09-878-574-2556
; Sequence 2556, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 2556
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-023-Q1-B1-D6
US-09-878-574-2556

Alignment Scores:
Pred. No.: 6.18e-06
Score: 79.00
Percent Similarity: 80.77%
Best Local Similarity: 50.00%
Length: 360
Matches: 13
Conservative: 8
Mismatches: 5

Query Match: 54.48% Indels: 0
DB: 10 Gaps: 0
US-09-987-190-2 (1-30) x US-09-878-574-2556 (1-360)
QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
DB 150 TACACGCTCCCGATCGATTCGACTATGCGCTCTGGAGCCAGCATCAGCGCGAA 209
QY 22 IleAsnGluIle**Tyr 27
DB 210 ATCATGCACTGCACAC 227
RESULT 2
US-09-878-574-503
Sequence 503, Application US/09878574
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 503
LENGTH: 390
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-050-Q1-B1-C12
US-09-878-574-503
Alignment Scores:
Pred. No.: 6.85e-06 Length: 390
Score: 79.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 54.48% Indels: 0
DB: 10 Gaps: 0
US-09-987-190-2 (1-30) x US-09-878-574-503 (1-390)
QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
DB 140 TACACGCTCCCGATCGATTCGACTATGCGCTCTGGAGCCAGCATCAGCGCGAA 199
QY 22 IleAsnGluIle**Tyr 27
DB 200 ATCATGCACTGCACAC 217
RESULT 3
US-09-738-626-3227
Sequence 3227, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIHO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHITO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 3227
LENGTH: 600
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-3227
Alignment Scores:
Pred. No.: 2.82e-05 Length: 600
Score: 77.00 Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
DB: 9 Gaps: 0
US-09-987-190-2 (1-30) x US-09-738-626-3227 (1-600)
QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
DB 10 TACGAAGCTCCAGAACTCAGATCGATCGACGCTCTGAGCCACACATCCCGCTGAA 69
QY 22 IleAsnGluIle**TyrThr 28
DB 70 ATCATGAGCTTCACCATCC 90
RESULT 4
US-09-818-564-1
Sequence 1, Application US/09818564
Patent No. US20020137151A1
GENERAL INFORMATION:
APPLICANT: MERKAM, MURIEL
APPLICANT: GUYONVARCH, ARMEI
APPLICANT: MARX, ACHIM
TITLE OF INVENTION: A PROCESS FOR THE FERMENTATIVE PREPARATION OF METABOLIC
TITLE OF INVENTION: PRODUCTS AND FOR THE NUCLEOTIDE SEQUENCES ENCODING FOR
FILE REFERENCE: 21123/27841/MAS
CURRENT APPLICATION NUMBER: US/09/818,564
CURRENT FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 09/373,731
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1143
TYPE: DNA
ORGANISM: Corynebacterium melassecola
FEATURE:
NAME/KEY: CDS
LOCATION: (338)..(937)
OTHER INFORMATION: ATCC 17965
US-09-818-564-1
Alignment Scores:
Pred. No.: 6.51e-05 Length: 1143
Score: 77.00 Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
DB: 10 Gaps: 0
US-09-987-190-2 (1-30) x US-09-818-564-1 (1-1143)
QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
DB 347 TACGAAGCTCCAGAACTCAGATCGATCGACGCTCTGAGCCACACATCCCGCTGAA 406


```

Oy      22  ileaenglile**TyrThr 28
          |||||: : : : :
Db      407  ATCATGAGCTTCACCACTCC 427

RESULT 5
US-09-960-352-5895
; Sequence 5895, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengping
; APPLICANT: Byatt, John C.
; APPLICANT: Machialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5895
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 25-LIB34-057-Q1-E1-G1
US-09-960-352-5895

Alignment Scores:
Pred. No.:      2.85e-05      Length:      224
Score:          74.00         Matches:     12
Percent Similarity: 78.57%    Conservative: 10
Best Local Similarity: 42.86%  Mismatches:   6
Query Match:    51.03%        Indels:      0
DB:             10           Gaps:         0

US-09-987-190-2 (1-30) x US-09-960-352-5895 (1-224)

Oy      1  lvsTyrSerLeuProGluIleuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
          |||||: : : : :
Db      140  AAGCAGACGCTCCCGACCTGCCGACACATCGAGCGCCCTGAGCGCAGCATCAACGCG 199

Oy      21  gniIleaenglile**TyrThr 28
          |||||: : : : :
Db      200  CAGATCATGACGCTGCACCAACGC 223

RESULT 6
US-09-960-352-3021
; Sequence 3021, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengping
; APPLICANT: Byatt, John C.
; APPLICANT: Machialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 3021
; LENGTH: 259
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 13-LIB34-076-Q1-E1-D1
US-09-960-352-3021

Alignment Scores:
Pred. No.:      3.44e-05      Length:      259
Score:          74.00         Matches:     12
Percent Similarity: 78.57%    Conservative: 10
Best Local Similarity: 42.86%  Mismatches:   6
Query Match:    51.03%        Indels:      0

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DB: 10 Gaps: 0
US-09-987-190-2 (1-30) x US-09-960-352-3021 (1-259)

OY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 142 AAGCAGACAGCTCCCGACCTCGCGTACGACTACGAGCGCGCTGAGCGCACATCAGCG 201
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

OY 21 GlnIleAsnGluIle**TyrThr 28
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 202 CAGATCATGACGCTGCACACACG 225
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 7
US-09-993-333-11
/ Sequence 11, Application US/09993333
/ Patent No. US20020156040A1
/ GENERAL INFORMATION:
/ APPLICANT: Oberley, Larry Wayne
/ APPLICANT: Weydert, Christine J.
/ APPLICANT: Smith, Benjamin Barnes
/ TITLE OF INVENTION: Reduction of antioxidant enzyme levels in tumor cells using antisense
/ FILE REFERENCE: 875.042US1
/ CURRENT APPLICATION NUMBER: US/09/993,333
/ CURRENT FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: US 60/248,328
/ PRIOR FILING DATE: 2000-11-14
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 11
/ LENGTH: 325
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-993-333-11

Alignment Scores:
Pred. No.: 4.61e-05 Length: 325
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-09-993-333-11 (1-325)

OY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 113 AAGCAGACAGCTCCCGACCTCGCGTACGACTACGAGCGCGCTGAGCGCACATCAGCG 172
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

OY 21 GlnIleAsnGluIle**TyrThr 28
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 173 CAGATCATGACGCTGCACACACG 196
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 8
US-09-960-352-14744
/ Sequence 14744, Application US/09960352
/ Patent No. US20020137139A1
/ GENERAL INFORMATION:
/ APPLICANT: Warren, Wesley C.
/ APPLICANT: Tao, Nengping
/ APPLICANT: Byatt, John C.
/ APPLICANT: Mahalingam, Nagappan
/ TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
/ TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
/ FILE REFERENCE: 16511.006/37-21(10298)C
/ CURRENT APPLICATION NUMBER: US/09/960,352
/ CURRENT FILING DATE: 2001-09-24
/ NUMBER OF SEQ ID NOS: 15112
/ SEQ ID NO 14744
/ LENGTH: 424
/ TYPE: DNA
/ ORGANISM: Bos taurus
/ OTHER INFORMATION: Clone ID: 63-LIB3057-022-Q1-K1-H4

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US-09-960-352-14744
Alignment Scores:
Pred. No.: 6.51e-05 Length: 424
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x US-09-960-352-14744 (1-424)
QY 1 LyeTySerIeuProGluLeuApyTyGluPhSeSerAlaThrgIuProTyRlleSerGly 20
Db 121 AAGCAGAGCCCTCCCGACCTGCGACTACGACGCGCCCTGAGCCGACATCAACGCG 180
QY 21 GlnIleAenGluIle**TyThr 28
Db 181 CAGATCATGCACTGCACACACAGC 204

RESULT 9
US-10-044-090-836
Sequence 836 Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 836
LENGTH: 972
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 010001CB1
US-10-044-090-836

Alignment Scores:
Pred. No.: 0.000191 Length: 972
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 12 Gaps: 0

US-09-987-190-2 (1-30) x US-10-044-090-836 (1-972)
QY 1 LyeTySerIeuProGluLeuApyTyGluPhSeSerAlaThrgIuProTyRlleSerGly 20
Db 166 AAGCAGAGCCCTCCCGACCTGCGACTACGACGCGCCCTGAGCCGACATCAACGCG 225
QY 21 GlnIleAenGluIle**TyThr 28
Db 226 CAGATCATGCACTGCACACACAGC 249

RESULT 10
US-09-954-456-1822
Sequence 1822 Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
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PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1822
LENGTH: 1026
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-1822

Alignment Scores:
Pred. No.: 0.000205 Length: 1026
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x US-09-954-456-1822 (1-1026)
QY 1 LyeTySerIeuProGluLeuApyTyGluPhSeSerAlaThrgIuProTyRlleSerGly 20
Db 77 AAGCAGAGCCCTCCCGACCTGCGACTACGACGCGCCCTGAGCCGACATCAACGCG 136
QY 21 GlnIleAenGluIle**TyThr 28
Db 137 CAGATCATGCACTGCACACACAGC 160

RESULT 11
US-09-917-800A-1627
Sequence 1627 Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
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[illegible]

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1  APPLICANT: Gorlach, Jörn
2  APPLICANT: An, Yong-Qiang
3  APPLICANT: Hamilton, Carol M.
4  APPLICANT: Price, Jennifer L.
5  APPLICANT: Raine, Tracy M.
6  APPLICANT: Yu, Yang
7  APPLICANT: Rameaka, Joshua G.
8  APPLICANT: Page, Amy
9  APPLICANT: Matthew, Abraham V.
10 APPLICANT: Ledford, Brooke L.
11 APPLICANT: Moessner, Jeffrey P.
12 APPLICANT: Haas, William David
13 APPLICANT: Garcia, Carlos A.
14 APPLICANT: Krickler, Maja
15 APPLICANT: Slader, Ted
16 APPLICANT: Davis, Keith R.
17 APPLICANT: Allen, Keith
18 APPLICANT: Hoffman, Neil
19 APPLICANT: Hurban, Patrick
20 TITLE OF INVENTION: Expressed Sequences of Arabidopsis
21 FILE REFERENCE: thaliana
22 FILE REFERENCE: 2023US (PARA-012PRV)
23 CURRENT APPLICATION NUMBER: US/09/770,445
24 CURRENT FILING DATE: 2001-01-26
25 PRIOR APPLICATION NUMBER: US 60/178,472
26 PRIOR FILING DATE: 2000-01-27
27 NUMBER OF SEQ ID NOS: 999
28 SOFTWARE: FastSeq for Windows Version 4.0
29 SEQ ID NO 745
30 LENGTH: 817
31 TYPE: DNA
32 ORGANISM: Arabidopsis thaliana
33 US-09-770-445-745
34
35 Alignment Scores:
36 Pred. No.: 0.000846 Length: 817
37 Score: 70.00 Matches: 12
38 Percent Similarity: 76.92% Conservative: 8
39 Best Local Similarity: 46.15% Mismatches: 6
40 Query Match: 48.28% Indels: 0
41 DB: Gaps: 0
42
43 US-09-987-190-2 (1-30) x US-09-770-445-745 (1-817)
44
45 Cy 2 TyserleupProgiuLeuaspTyrgluPheserelathrgiuProTyrlleSerglycin 21
46 Db 48 TTTAGCGCTCTGTACTCTTCCTTACGATTATGCGCATTTGGAACGGCCATTAGTGAAG 107
47
48 Cy 22 llaangluile***Tyr 27
49 Db 108 ATCATGCAGATTCATCAC 125
50
51 RESULT 14
52 US-09-727-855B-6
53 Sequence 6, Application US/09727855B
54 Patent No. US20020168703A1
55 GENERAL INFORMATION:
56 APPLICANT: HOSHINO, Tatsuo
57 APPLICANT: OIIMA, Kazuyuki
58 APPLICANT: SETOGUCHI, Yutaka
59 TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
60 FILE REFERENCE: C38435/111694
61 CURRENT APPLICATION NUMBER: US/09/727,855B
62 CURRENT FILING DATE: 2000-12-01
63 NUMBER OF SEQ ID NOS: 17
64 SOFTWARE: PatentIn version 3.1
65 SEQ ID NO 6
66 LENGTH: 597
67 TYPE: DNA
68 ORGANISM: Phaffia rhodozyma
69 FEATURE:
70 NAME/KEY: CDS

```

```
/ LOCATION: (1)..(594)
/ OTHER INFORMATION:
US-09-727-855B-6

Alignment Scores:
Pred. No.: 0.00204 Length: 597
Score: 67.00 Matches: 12
Percent Similarity: 76.19% Conservative: 4
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 46.21% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-09-727-855B-6 (1-597)

QY 2 TySerleupProgluLeuAapTyGluPheserAlaThrgluProTyrlleSerglyGln 21
Db 10 TACACTCTCCCGACCTTCCTTACGCTTACGATGCTTGAGCCTTACATCTTAAGAA 69
QY 22 1le 22
Db 70 ATC 72

RESULT 15
US-09-727-855B-4
/ Sequence 4, Application US/09727855B
/ Patent No. US20020168703A1
/ GENERAL INFORMATION:
/ APPLICANT: HOSHINO, Tatsuo
/ APPLICANT: OJIMA, Kazuyuki
/ APPLICANT: SETOGUCHI, Yutaka
/ TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
/ FILE REFERENCE: C38435/111694
/ CURRENT APPLICATION NUMBER: US/09/727, 855B
/ CURRENT FILING DATE: 2000-12-01
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 669
/ TYPE: DNA
/ ORGANISM: Phaeofila rhodozyma
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(666)
/ OTHER INFORMATION: n or X = A, C, G or T
US-09-727-855B-4

Alignment Scores:
Pred. No.: 0.00363 Length: 669
Score: 66.00 Matches: 13
Percent Similarity: 67.86% Conservative: 6
Best Local Similarity: 46.43% Mismatches: 9
Query Match: 45.52% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-09-727-855B-4 (1-669)

QY 1 TySerleupProgluLeuAapTyGluPheserAlaThrgluProTyrlleSerglyGln 20
Db 76 AAGCATACCTCGAGCTTCCTTACGCTTACGATGCTTGAGCCTTCATCTCAAG 135
QY 21 GlnleAangluile**TyThr 28
Db 136 GAGATCATGACCTTACACACACC 159

RESULT 16
US-09-974-300-2052
/ Sequence 2052, Application US/09974300
/ Patent No. US20020146721A1
/ GENERAL INFORMATION:
/ APPLICANT: Berka, Randy M.
/ APPLICANT: Clausen, Ib Groth
/ TITLE OF INVENTION: Methods For Monitoring Multiple Gene
```

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/ TITLE OF INVENTION: Expression
/ FILE REFERENCE: 10085.500-US
/ CURRENT APPLICATION NUMBER: US/09/974,300
/ CURRENT FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: 09/680,598
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 60/279,526
/ PRIOR FILING DATE: 2001-03-27
/ NUMBER OF SEQ ID NOS: 8481
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2052
/ LENGTH: 838
/ TYPE: DNA
/ ORGANISM: Bacillus licheniformis
US-09-974-300-2052

Alignment Scores:
Pred. No.: 0.00485 Length: 838
Score: 66.00 Matches: 13
Percent Similarity: 66.67% Conservative: 5
Best Local Similarity: 48.15% Mismatches: 9
Query Match: 45.52% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x US-09-974-300-2052 (1-838)

QY 2 TySerleupProgluLeuAapTyGluPheserAlaThrgluProTyrlleSerglyGln 21
Db 238 CATCGCTGCCAGCCTCCCTGATCTGATTCAGCCTTGAGCCTTAATTTAAAGAA 297
QY 22 1leAangluile**TyThr 28
Db 298 ATTATGTTCTTCATCATACA 318

RESULT 17
US-09-070-927A-425
/ Sequence 425, Application US/09070927A
/ Patent No. US20020120116A1
/ GENERAL INFORMATION:
/ APPLICANT: Charles A. Kunsch
/ Patrick J. Dillon
/ Steven Barash
/ TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
/ NUMBER OF SEQUENCES: 982
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/070,927A
/ FILING DATE: 04-May-2000
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/046,655
/ FILING DATE: 1997-05-16
/ APPLICATION NUMBER: 60/044,031
/ FILING DATE: 1997-05-06
/ APPLICATION NUMBER: 60/066,009
/ FILING DATE: 1997-11-14
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kenley K. Hoover
/ REGISTRATION NUMBER: 40,302
/ REFERENCE/DOCKET NUMBER: PB369
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
```

```
TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 425:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 767 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 425:
US-09-070-927A-425

Alignment Scores:
Pred. No.: 0.024      Length: 767
Score: 62.00         Matches: 11
Percent Similarity: 76.47%  Conservative: 2
Best Local Similarity: 64.71%  Mismatches: 4
Query Match: 42.76%      Indels: 0
DB: 10               Gaps: 0

09-987-190-2 (1-30) x US-09-070-927A-425 (1-767)

QY 2 TySerleupProgluLeuAapTyrgluPheserAlathrgluProtyrIleSerglyIn 18
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 TAGACATTACCAAGATTACCATATGCTTATGATGACATTAGACCTTACATT 174

RESULT 18
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:
; APPLICANT: SHIGEMOBU, SHUJI
; APPLICANT: MATANABE, HIDEKI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
; US-09-790-988-1

Alignment Scores:
Pred. No.: 1.93e+03      Length: 640681
Score: 56.00            Matches: 10
Percent Similarity: 59.26%  Conservative: 6
Best Local Similarity: 37.04%  Mismatches: 11
Query Match: 38.62%      Indels: 0
DB: 10               Gaps: 0

US-09-987-190-2 (1-30) x US-09-790-988-1 (1-640681)

QY 2 TySerleupProgluLeuAapTyrgluPheserAlathrgluProtyrIleSerglyIn 21
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 204469 TAGGTTTCCTCTTCACTTATCAATGCAATGCGTTAGAACATTTTTGTGAAGA 204528

QY 22 IleasnGluIle**TyThr 28
   ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 204529 ACTATGAATAATTCATCTACT 204549

RESULT 19
US-09-770-445-976
; Sequence 976, Application US/09770445
; Patent No. US2002002381A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
```

```
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hubban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2023US (PAPA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 976
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(757)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-445-976

Alignment Scores:
Pred. No.: 0.729      Length: 757
Score: 54.00         Matches: 10
Percent Similarity: 75.00%  Conservative: 5
Best Local Similarity: 50.00%  Mismatches: 5
Query Match: 37.24%      Indels: 0
DB: 10               Gaps: 0

US-09-987-190-2 (1-30) x US-09-770-445-976 (1-757)

QY 1 TySerleupProgluLeuAapTyrgluPheserAlathrgluProtyrIleSergly 20
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 236 AAGAAGACATTAGAGAGCTTCCACACATCTCACATCCGACCCGTTATTTCGGGT 295

RESULT 20
US-08-781-986A-777/C
; Sequence 777, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
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; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US/09/565,391
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: PCT/US99/26409
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/108,207
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-948-820-29

Alignment Scores:
Pred. No.: 1 7
Score: 53.00 Length: 1044
Percent Similarity: 58.33% Matches: 11
Best Local Similarity: 45.83% Conservative: 3
Query Match: 36.55% Mismatches: 8
DB: Gaps: 2
Indels: 1

US-09-987-190-2 (1-30) x US-09-948-820-29 (1-1044)

QY 1 TySerLeuProGluLeuAspTyr-----GluPheSerAlaThrGluProTyrIle 18
Db 642 AATAGTGTGATGCTGATTTGACCACTCCTCATTCATTCACCATCTCCACCATATATT 701

QY 19 SerGlyGlnIle 22
Db 702 TCAGGTGCTCTT 713

RESULT 24
US-09-974-300-6347
; Sequence 6347, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6347
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-6347

Alignment Scores:
Pred. No.: 0.715 Length: 385
Score: 52.00 Matches: 10
Percent Similarity: 70.59% Conservative: 2
Best Local Similarity: 58.82% Mismatches: 5
Query Match: 35.86% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x US-09-974-300-6347 (1-385)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIle 18
Db 7 TACAACTACAGATTGCTTAGCGGCAATGCACTTGACCGCATATT 57

RESULT 25
US-09-822-849A-208
```

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; Sequence 208, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 208
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-849A-208

Alignment Scores:
Pred. No.: 12.1 Length: 2454
Score: 51.00 Matches: 10
Percent Similarity: 60.00% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 8
Query Match: 35.17% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x US-09-822-849A-208 (1-2454)

QY 1 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 1797 AGATATAGCTCCAGAGAAATTCCTATATGCAATCGTGAAAGAACCATPCCAGCAGGA 1856

RESULT 26
US-10-091-504-2314
; Sequence 2314, Application US/10091504
; Publication No. US20030059908A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C1
; CURRENT APPLICATION NUMBER: US/10/091,504
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2442
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2314
; LENGTH: 32249
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-091-504-2314

Alignment Scores:
Pred. No.: 341 Length: 32249
Score: 51.00 Matches: 9
Percent Similarity: 68.18% Conservative: 6
Best Local Similarity: 40.91% Mismatches: 7
Query Match: 35.17% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x US-10-091-504-2314 (1-32249)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 31767 TATAGCTCCACATCATTCATTATATATATGAGAGCCCTTTATCTCTCCAA 31826
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QY      22 Ileaen 23          :
DB      31827 GTRAGC 31832          .

RESULT 27
US-09-764-869-2314
; Sequence 2314, Application US/09764869
; Patent No. US20020065521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764, 869
; PRIORITY FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2314
; LENGTH: 32249
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-869-2314

Alignment Scores:
Pred. No.:           341             Length:           32249
Score:              51.00            Matches:           9
Percent Similarity: 68.18%           Conservative:       6
Best Local Similarity: 40.91%         Mismatches:        7
Query Match:         35.17%           Indels:            0
DB:                  10               Gaps:              0

US-09-987-190-2 (1-30) x US-09-764-869-2314 (1-32249)

QY      2 TysSerLeuProGluIleuAspTyrGlnPheSerAlaThrGluProTyrIleSerGlyGln 21
Db      31767 TADAGCTCCACATCATCATTTTCATTATAATAGAGAGACCCTTTTATCTCCGA 31826
      |||||
      ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
      QY      22 Ileaen 23          :
DB      31827 GTRAGC 31832          .

RESULT 28
US-10-012-896-851
; Sequence 851, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqichun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, David X.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Heptier, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Baesols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27

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US-09-987-190-2 (1-30) x US-09-895-793-851 (1-1203)
DB:
Alignment Scores:
Pred. No.: 7.38 Length: 1203
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-10-012-896-851 (1-1203)
OY 2 TySerLeuPProGluLeuAspTYrGlnPheserLathrgtUpPrOTyIleSerglyGln 21
Db 832 TACCTCCTGCCTGCCATTGACTGGAGCACACAGTCCCTGCCGCCCTTA CTGGGACCACAG 891
RESULT 29
US-09-895-793-851
; Sequence 851, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jjiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Basols, Carloca
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534CZ
; CURRENT APPLICATION NUMBER: US/09/895.793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-851
Alignment Scores:
Pred. No.: 7.38 Length: 1203
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 9 Gaps: 0

```



```
Qy 2 TySerLeuProGluLeuApyTyrgLupheSerAlaThrGluProTyrlleSerglyGln 21
Db 832 TACCTCGTGCCTGCATTGACTGGACACACAGTGCCTGGCCCCCTACCTGGGACCCAG 891

RESULT 30
US-09-895-814-851
; Sequence 851, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-851

Alignment Scores:
Pred. No.: 7.38 Length: 1203
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-09-895-814-851 (1-1203)
Qy 2 TySerLeuProGluLeuApyTyrgLupheSerAlaThrGluProTyrlleSerglyGln 21
Db 832 TACCTCGTGCCTGCATTGACTGGACACACAGTGCCTGGCCCCCTACCTGGGACCCAG 891

RESULT 31
US-09-759-143-851
; Sequence 851, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
```

```
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-851

Alignment Scores:
Pred. No.: 7.38 Length: 1203
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x US-09-759-143-851 (1-1203)
Qy 2 TySerLeuProGluLeuApyTyrgLupheSerAlaThrGluProTyrlleSerglyGln 21
Db 832 TACCTCGTGCCTGCATTGACTGGACACACAGTGCCTGGCCCCCTACCTGGGACCCAG 891

RESULT 32
US-09-780-669-851
; Sequence 851, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-851
```

```
Alignment Scores:
Pred. No.: 7.38 Length: 1203
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x US-09-780-669-851 (1-1203)

QY 2 TySerleuprogIuLeuApTYrGluPhseSerAlaThrgluProTYrIleSerGlyGln 21
DB 832 TACTCTGCTGCTGCATTGACGTGGACACACAGTCCCTGGCCCCCTTACTGGGACCCAG 891

RESULT 33
US-09-822-827-851
; Sequence 851, Application US/09822827
; Patent No. US2002008160A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-851

Alignment Scores:
Pred. No.: 7.38 Length: 1203
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x US-09-822-827-851 (1-1203)

QY 2 TySerleuprogIuLeuApTYrGluPhseSerAlaThrgluProTYrIleSerGlyGln 21
DB 832 TACTCTGCTGCTGCATTGACGTGGACACACAGTCCCTGGCCCCCTTACTGGGACCCAG 891

RESULT 34
US-10-012-896-703
Sequence 703, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Huxal, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
```

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; APPLICANT: Fanger, Gary R.
; APPLICANT: Mantanabe, Yoshihiro
; APPLICANT: Meagher, Madeline Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-703

Alignment Scores:
Pred. No.: 23.1 Length: 2904
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-10-012-896-703 (1-2904)

QY 2 TySerleuprogIuLeuApTYrGluPhseSerAlaThrgluProTYrIleSerGlyGln 21
DB 40 TACTCTGCTGCTGCATTGACGTGGACACACAGTCCCTGGCCCCCTTACTGGGACCCAG 99

RESULT 35
US-09-895-793-703
Sequence 703, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-703

Alignment Scores:
Pred. No.: 23.1 Length: 2904
Score: 50.00 Matches: 9
```

```
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-09-895-793-703 (1-2904)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
   |||||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 40 TACCTCTGCTGCTGCATGTGACGACACCAAGTGCCTGCGCCCTGACTGCGGACCCAG 99

RESULT 36
US-09-895-814-703
; Sequence 703, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carloca
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-703

Alignment Scores:
Pred. No.: 23.1 Length: 2904
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-09-895-814-703 (1-2904)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
   |||||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 40 TACCTCTGCTGCTGCATGTGACGACACCAAGTGCCTGCGCCCTGACTGCGGACCCAG 99

RESULT 37
US-09-759-143-703
; Sequence 703, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
```

```
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-703

Alignment Scores:
Pred. No.: 23.1 Length: 2904
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x US-09-759-143-703 (1-2904)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
   |||||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 40 TACCTCTGCTGCTGCATGTGACGACACCAAGTGCCTGCGCCCTGACTGCGGACCCAG 99

RESULT 38
US-09-780-669-703
; Sequence 703, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
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/ SEQ ID NO 703
/ LENGTH: 2904
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-780-669-703

Alignment Scores:
Pred. No.: 23.1 Length: 2904
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x US-09-780-669-703 (1-2904)

Qy 2 TySerLeuProGluLeuAlaPheSerAlaThrGluProTyrIleSerGlyIn 21
Db 40 TACCTCCTGCTGCCTGACATTGACGTGGACACACAGTGCCTGGCCCTTACTGGGACCCAG 99

RESULT 39
US-09-822-827-703
Sequence 703, Application US/09822827
Patent No. US2002008180A1

/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.534C1
/ CURRENT APPLICATION NUMBER: US/09/822,827
/ CURRENT FILING DATE: 2001-03-28
/ NUMBER OF SEQ ID NOS: 982
/ SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 703
LENGTH: 2904
TYPE: DNA

ORGANISM: Homo sapiens
US-09-822-827-703

Alignment Scores:
Pred. No.: 23.1 Length: 2904
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x US-09-822-827-703 (1-2904)

Qy 2 TySerLeuProGluLeuAlaPheSerAlaThrGluProTyrIleSerGlyIn 21
Db 40 TACCTCCTGCTGCCTGACATTGACGTGGACACACAGTGCCTGGCCCTTACTGGGACCCAG 99

RESULT 40
US-09-838-785-1

/ Sequence 1, Application US/09838785
/ Patent No. US20020009455A1

/ GENERAL INFORMATION:
/ APPLICANT: Lau, Ted
/ APPLICANT: Lin, Rick
/ APPLICANT: Parkes, Debbie
/ APPLICANT: Parry, Gordon
/ APPLICANT: Schneider, Douglas
/ APPLICANT: Steinhilber, Renate
/ APPLICANT: Van Heule, Pam T
/ APPLICANT: Wu, John

/ TITLE OF INVENTION: DNA Encoding a No. US20020009455A1e1 PROST 03
/ FILE REFERENCE: 51831AUSM1

/ CURRENT APPLICATION NUMBER: US/09/838,785

/ CURRENT FILING DATE: 2001-04-20

/ PRIOR APPLICATION NUMBER: 60/200,065

/ PRIOR FILING DATE: 2000-04-27
/ NUMBER OF SEQ ID NOS: 26

/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 3320
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (282) .. (1943)
US-09-838-785-1

Alignment Scores:
Pred. No.: 27.5 Length: 3320
Score: 50.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 34.48% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x US-09-838-785-1 (1-3320)

Qy 2 TySerLeuProGluLeuAlaPheSerAlaThrGluProTyrIleSerGlyIn 21
Db 807 TACCTCCTGCTGCCTGACATTGACGTGGACACACAGTGCCTGGCCCTTACTGGGACCCAG 866

Search completed: April 8, 2003, 05:00:28
Job time : 72.1651 secs

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: April 9, 2003, 13:51:49 ; Search time 14.8624 Seconds
(without alignments)
415.910 Million cell updates/sec

Title: US-09-987-190-2
Perfect score: 145
Sequence: 1 KXSLPELDYFSGATEPYISQJNEIXYTX 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

rchd: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	73.8	237	3	P79022
2	101	69.7	207	2	Q9F9R1
3	101	69.7	210	2	Q9AM00
4	91	62.8	189	2	Q59673
5	80	55.2	32	8	Q9T2Q1
6	80	55.2	201	5	Q8TA63
7	77	53.1	200	2	Q9APY3
8	76	52.4	216	10	Q9FY32
9	75	51.7	216	3	Q8XIN7
10	74	51.0	140	4	Q96AM7
11	74	51.0	165	4	Q9UG59
12	74	51.0	218	11	Q8VEM5
13	74	51.0	222	4	Q96RE6
14	74	51.0	231	10	Q65324
15	74	51.0	231	10	Q947R3
16	73	50.3	203	2	Q9MWG7

17	73	50.3	206	3	Q96UT6	Q96UT6 candida alb
18	72	49.7	211	17	Q96Y84	Q96Y84 sulfobus
19	71	49.0	203	5	Q93K55	Q93K55 frankia sp.
20	71	49.0	205	10	Q9STB5	Q9STB5 hevea bras
21	71	49.0	205	10	Q9FSJ2	Q9FSJ2 hevea bras
22	71	49.0	208	3	Q96UR1	Q96UR1 colletoic
23	71	49.0	213	2	Q9X6N3	Q9X6N3 streptomye
24	71	49.0	220	3	Q74200	Q74200 pneumocyst
25	71	49.0	224	10	Q9FY33	Q9FY33 digitalis 1
26	71	49.0	224	13	Q9DDJ1	Q9DDJ1 gallus gall
27	71	49.0	224	13	Q90Y34	Q90Y34 gallus gall
28	71	49.0	227	10	Q9M532	Q9M532 euphorbia e
29	69	47.6	223	3	Q9E945	Q9E945 emericella
30	68	46.9	201	2	Q9F326	Q9F326 staphylococ
31	68	46.9	203	16	Q9PAA4	Q9PAA4 xylella fas
32	68	46.9	206	3	Q96W28	Q96W28 phanerocha
33	68	46.9	215	16	Q9X469	Q9X469 streptomye
34	68	46.9	211	10	P93606	P93606 triticum ae
35	68	46.9	240	10	Q82584	Q82584 zantedesch
36	67	46.2	202	2	Q9KW85	Q9KW85 vibrio vuln
37	67	46.2	211	16	Q9RUV2	Q9RUV2 deinococcus
38	67	46.2	218	5	Q9NB66	Q9NB66 callinectes
39	67	46.2	228	10	Q9SM64	Q9SM64 prunus pers
40	67	46.2	235	10	Q43273	Q43273 zea mays (m
41	66	45.5	25	8	Q9T2Q0	Q9T2Q0 solanum tub
42	66	45.5	206	3	Q9Y773	Q9Y773 paxillus in
43	66	45.5	207	16	Q829X6	Q829X6 yersinia pe
44	65	44.8	224	10	Q82571	Q82571 triticum ae
45	65	44.8	231	10	Q96185	Q96185 triticum ae

ALIGNMENTS

RESULT 1

P79022 PRELIMINARY; PRT; 227 AA.
AC P79022;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Superoxide dismutase (EC 1.15.1.1) precursor.
GN MNSOD.
OS Candida sp. HN95.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_taxid=159257;
RN [1]
RP SEQUENCE FROM N.A.
RA Choi S.-Y., Nam Y.-S., Hong Y.M.;
RT "Molecular cloning and characterization of Mn-superoxide dismutase
RT gene from Candida sp.";
RL Korean J. Microbiol. 35:309-314(1997).
CC -I- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -I- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -I- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR EMBL; Y11598; CA72335.1; -.
DR HSSP; P04179; IAP6.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodef; 1.
DR Pfam; PF02777; sodef; C; 1.
DR Prodom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase; Signal.
FT SIGNAL
FT CHAIN 31 227 POTENTIAL.
SQ SEQUENCE 227 AA; 25227 MW; 2987F6E3C7743DB0 CRC64;

Query Match 73.8%; Score 107; DB 3; Length 227;
Best Local Similarity 71.4%; Pred. No. 2.1e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

RESULT 5

Q9T201 PRELIMINARY; PRT; 32 AA.
 ID Q9T201
 AC Q9T201
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE Mangnese superoxide dismutase, MN-SOD (EC 1.15.1.1) (Fragment).
 OS Pinus sylvestris (Scots pine).
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxId=3349;
 RN 11
 RP SEQUENCE.
 RX MEDLINE=95072927; PubMed=7981961;
 RA Streller S., Kromer S., Winkler G.;
 "Isolation and purification of mitochondrial Mn-superoxide dismutase from the gymnosperm Pinus sylvestris L.";
 Plant Cell Physiol. 35:859-867(1994).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sodfe; 1.
 DR Prodom: PD000475; SODismutase; 1.
 KM Mangnese; Oxidoreductase.
 SQ SEQUENCE 32 AA; 3681 MW; 7A6826DC1427092C CRC64;

Query Match

Best Local Similarity 55.2%; Score 80; DB 8; Length 32;
 Matches 15; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISQINEIXYT 27

Db 4 FSLPELDYFSATEPYISQINEIXYT 29

RESULT 6

Q8TA63 PRELIMINARY; PRT; 201 AA.
 ID Q8TA63
 AC Q8TA63
 DT 01-JUN-2002 (TEMBLrel. 21, Created)
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE Superoxide dismutase like protein.
 OS SOD-1.
 OS Penaeus japonicus (Kuruma prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Marsupenaeus.
 OX NCBI_TaxId=27405;
 RN 11
 RP SEQUENCE FROM N.A.
 RP Soma G., Inagawa H., Nishizawa T., Honda T., Nomura Y., Uenobe M.,
 RA Takahashi Y., Itami T., Yokomizo Y.;
 "Kuruma shrimp cDNA similar to superoxide dismutase protein.";
 Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB079877; BAB85211.1; -
 SQ SEQUENCE 201 AA; 21485 MW; 3317CBEF5FDA9A52 CRC64;

Query Match

Best Local Similarity 55.2%; Score 80; DB 5; Length 201;
 Matches 15; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISQINEIXYT 28

Db 87 HALPLKIDYDALEPHISGIMWEIHT 113

RESULT 7

Q9APY3 PRELIMINARY; PRT; 200 AA.
 ID Q9APY3
 AC Q9APY3
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE Mangnese superoxide dismutase (EC 1.15.1.1).
 OS SODA.
 OS Corynebacterium melassecola, and
 OC Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;
 OC Corynebacterium.
 OX NCBI_TaxId=41643, 1718;
 RN 11
 RP SEQUENCE FROM N.A.
 RC SPECIES=C.melassecola; STRAIN=ATCC17965;
 RX MEDLINE=21101811; PubMed=11157941;
 RA Merkamm M., Guyonvarch A.;
 "Cloning of the soda gene from Corynebacterium melassecola and Role of
 RT Superoxide dismutase in Cellular Viability.";
 J. Bacteriol. 183:1284-1295(2001).
 RL 12
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=C.glutamicum; STRAIN=ATCC 13032;
 RA Nakagawa S., Mizoguchi H., Ando S., Hayashi M., Hattori M., Shiba T.,
 RA Sakaki Y., Yokoi H., Ozaki A.;
 "SOD of Corynebacterium glutamicum ATCC 13032.";
 Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.

EMBL; AF236111; AA01490.1; -
 EMBL; AB055218; BAB62412.1; -
 DR HSSP; P17670; 1IDS.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sodfe; 1.
 DR Pfam: PF02777; sodfe; C; 1.
 DR Prodom: PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 KM Oxidoreductase.
 SQ SEQUENCE 200 AA; 22101 MW; D236A2C3F291CE13 CRC64;

Query Match

Best Local Similarity 53.1%; Score 77; DB 2; Length 200;
 Matches 13; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISQINEIXYT 28

Db 4 YELPELDYDALEPHIAEIMELHNS 30

RESULT 8

Q9FY32 PRELIMINARY; PRT; 216 AA.
 ID Q9FY32
 AC Q9FY32
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE Mangnese superoxide dismutase (EC 1.15.1.1) (Fragment).
 OS MN-SOD.
 OS Digitalis lanata (Foxglove).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Veronicaceae; Digitalis.
 OX NCBI_TaxId=49450;
 RN 11
 RP SEQUENCE FROM N.A.
 RP Gruner B., Reva V.A., Mueller-Urli F.;
 "Stress-induction of Mn-dependent SOD and CAT in Digitalis lanata

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RT (shrh.) during somatic embryogenesis."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR EMBL: AJ278864; CAC05260.1; -.
DR HSSP: P04179; IAP6.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; sodfe; 1.
DR Pfam: PF02777; sodfe_C; 1.
DR Prodom: PD000475; SODismutase; 1.
DR PROSITE: PS00088; SOD_MN; 1.
KM Oxidoreductase.
FT NON TER 1
SQ SEQUENCE 216 AA; 23923 MW; 5CDD6EF9FC73077 CRC64;

Query Match 52.4%; Score 76; DB 10; Length 216;
Best Local Similarity 51.9%; Pred. No. 0.0012;
Matches 14; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

1 KXSLPDLPEYDYGALPEVIGSIMQIHH 41
Db |||:|||||:|||||:
15 KXSLPDLPEYDYGALPEVIGSIMQIHH 41

RESULT 9
OBX1N7 PRELIMINARY; PRT; 216 AA.
AC 08X1N7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Superoxide dismutase.
GN SOD1.
OS Blumeria graminis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
OC Erysiphales; Erysiphaceae; Blumeria.
OX NCBI_TaxId=34373;
[1]
RN SEQUENCE FROM N.A.
RA Zhang Z., Gurr S.J.;
RT "Isolation and characterization of a Blumeria graminis superoxide
RT dismutase gene involved in antioxidant action in barley/powdery mildew
RT interactions."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF227338; AAL56985.1; -.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; sodfe; 1.
DR Pfam: PF02777; sodfe_C; 1.
DR Prodom: PD000475; SODismutase; 1.
DR PROSITE: PS00088; SOD_MN; UNKNOWN 1.
DR PROSITE: PS00088; SOD_MN; UNKNOWN 1.
SQ SEQUENCE 216 AA; 24194 MW; 20EB6F1A027AA9C CRC64;

Query Match 51.7%; Score 75; DB 3; Length 216;
Best Local Similarity 50.0%; Pred. No. 0.0017;
Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

1 KXSLPDLPEYDYGALPEVIGSIMQIHH 28
Db |||:|||||:|||||:
4 KXNIPPLPYAYDALEPHISSQIMNIHHT 31

RESULT 10
Q96AM7 PRELIMINARY; PRT; 140 AA.
AC Q96AM7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 15.7 kDa protein.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
[1]
RN SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR EMBL: BC016934; AAH16934.1; -.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; sodfe; 1.
DR Prodom: PD000475; SODismutase; 1.
KM Hypothetical protein; Oxidoreductase.
SQ SEQUENCE 140 AA; 15745 MW; 499AC0467EF5C451 CRC64;

Query Match 51.0%; Score 74; DB 4; Length 140;
Best Local Similarity 42.9%; Pred. No. 0.0015;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

1 KXSLPDLPEYDYGALPEVIGSIMQIHH 28
Db |||:|||||:|||||:
25 KXSLPDLPEYDYGALPEVIGSIMQIHH 52

RESULT 11
Q9UG59 PRELIMINARY; PRT; 165 AA.
AC Q9UG59;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 18.6 kDa protein (Fragment).
GN DKFZP64W2422.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
[1]
RN SEQUENCE FROM N.A.
RA Mambour R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR EMBL: AL050388; CAB62521.1; -.
DR HSSP: P04179; IAP6.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; sodfe; 1.
DR Prodom: PD000475; SODismutase; 1.
DR PROSITE: PS00088; SOD_MN; UNKNOWN 1.
FT NON TER 1
SQ SEQUENCE 165 AA; 18605 MW; C7F2C078AD127205 CRC64;

Query Match 51.0%; Score 74; DB 4; Length 165;
Best Local Similarity 42.9%; Pred. No. 0.0018;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

1 KXSLPDLPEYDYGALPEVIGSIMQIHH 28
Db |||:|||||:|||||:
50 KXSLPDLPEYDYGALPEVIGSIMQIHH 77

RESULT 12
Q8VEM5 PRELIMINARY; PRT; 218 AA.
ID Q8VEM5

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DR PROSITE; PS00088; SOD_MN; UNKNOWN_1.
KM Oxidoreductase.
SQ SEQUENCE 231 AA; 25454 MW; 9805F5D53B949BEC CRC64;

Query Match 51.0%; Score 74; DB 10; Length 231;
Best Local Similarity 50.0%; Pred. No. 0.0026;
Matches 13; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAPEYISGQINEIXY 27
DB 31 FTLPDLPIYDALPDAISGEIMQIH 56

RESULT 16

Q9WMG7 PRELIMINARY; PRT; 203 AA.

AC Q9WMG7; (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Manganese superoxide dismutase.

SODA.
Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OC Pseudomonas.
OX NCBI_TaxID=321;

RP SEQUENCE FROM N.A.

RC STRAIN=B728A.

RA Kim Y.C., Miller C.D., Anderson A.J.

RT "Transcriptional regulation and mutational analysis of genes encoding

iron- and manganese-superoxide dismutases from the phytopathogenic

RT bacterium, Pseudomonas syringae pv. syringae B728A."

Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE

CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).

CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE

CC FAMILY.

DR EMBL; AF121078; AAD24796.1; -.

DR HSSP; P00448; IYEW.

DR InterPro; IPR001189; SODismutase.

DR Pfam; PF00081; sodfe, 1.

DR Pfam; PF02777; sodfe, C, 1.

DR ProDom; PD000475; SODismutase; 1.

DR PROSITE; PS00088; SOD_MN; 1.

KM Oxidoreductase.

SQ SEQUENCE 203 AA; 22628 MW; BAF6DA34642F155B CRC64;

Query Match 50.3%; Score 73; DB 2; Length 203;
Best Local Similarity 51.9%; Pred. No. 0.0032;
Matches 14; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAPEYISGQINEIXY 28
DB 3 YTLPALPYADALPDAISGEIMQIH 29

RESULT 17
Q96UT6 PRELIMINARY; PRT; 206 AA.

AC Q96UT6; (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Manganese-containing superoxide dismutase.

GN SOD3.

OS Candida albicans (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; mitosporic Saccharomycetales; Candida.

OX NCBI_TaxID=3476;

RP SEQUENCE FROM N.A.

RA Lamarre C., LeMay J.-D., Deslauriers N., Bourbonnais Y.;
RT "Candida albicans expresses an unusual cytoplasmic manganese-
containing superoxide dismutase SOD3 upon entry and during stationary

RT phase."

CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE

CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).

CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE

CC FAMILY.

DR EMBL; AF16340; AA09560.1; -.

DR InterPro; IPR001189; SODismutase.

DR Pfam; PF00081; sodfe, 1.

DR Pfam; PF02777; sodfe, C, 1.

DR ProDom; PD000475; SODismutase; 1.

DR PROSITE; PS00088; SOD_MN; UNKNOWN_1.

KM Oxidoreductase.

SQ SEQUENCE 206 AA; 22734 MW; 303FA3503417F332 CRC64;

Query Match 50.3%; Score 73; DB 3; Length 206;
Best Local Similarity 52.0%; Pred. No. 0.0033;
Matches 13; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISGQINEI 25
DB 7 KISLPKIDWALDAPYISKEINDL 31

RESULT 18
Q96Y84 PRELIMINARY; PRT; 211 AA.

AC Q96Y84; (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 21, Last annotation update)
DE Putative superoxide dismutase.

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Putative superoxide dismutase.

GN ST283.

OS Sulfolobus tokodaii.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

OC Sulfolobus.

OX NCBI_TaxID=111955;

RP SEQUENCE FROM N.A.

RC STRAIN=JCM 10545 / 7;

RX PubMed=11572479;

RA Karabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

RA Sekine M., Baba S.-I., Anka A., Kosugi H., Hosoyama A., Fukui S.,

RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

RA Yoshizawa T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,

RA Aoki K.-I., Maeda S., Yanagii M., Nishimura M., Yamagishi A.,

RA Oshima T., Kikuchi H.;

RT "Complete genome sequence of an aerobic thermophilic

RT Crenarchaeon, Sulfolobus tokodaii strain7."

RT DNA Res. 8:123-140(2001).

DR EMBL; AP000989; BAB67393.1; -.

DR InterPro; IPR001189; SODismutase.

DR Pfam; PF00081; sodfe, 1.

DR Pfam; PF02777; sodfe, C, 1.

DR ProDom; PD000475; SODismutase; 1.

KM Hypothetical protein; Complete proteome.

SQ SEQUENCE 211 AA; 24302 MW; 0EEAC4A76938002 CRC64;

Query Match 49.7%; Score 72; DB 17; Length 211;
Best Local Similarity 51.9%; Pred. No. 0.0048;
Matches 14; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISGQINEIXY 27
DB 9 KYELPPLPYVDALPYSKIDIVHY 35

RESULT 19
Q93K55

OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
 OC Glomerella.
 OX NCBI_TaxID=31870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fang G., Hanau R., Vallancourt L.;
 RT "Molecular characterization of the SOD2 gene, encoding a manganese
 type superoxide dismutase in the plant-pathogenic fungus
 RT Colletotrichum graminicola."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL: AF430836; AAL27457.1; -.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sodefe; 1.
 DR Pfam: PF02777; sodefe_C; 1.
 DR Prodom: PD000475; SODismutase; 1.
 DR PROSITE: PS00088; SOD_MN; UNKNOWN_1.
 DR Oxidoreductase.
 SEQUENCE 208 AA; 23026 MW; COB22E4AE66E225E CRC64;

Query Match 49.0%; Score 71; DB 3; Length 208;
 Best Local Similarity 46.4%; Pred. No. 0.0068;
 Matches 13; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KYSLPELDYFSATEPYISQINEXYT 28
 Db 5 QYILPELPYAYDALEPHISQIMELHHS 32

RESULT 23

09X6N3 PRELIMINARY; PRT; 213 AA.
 ID 09X6N3;
 AC 09X6N3;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Re-Zn-superoxide dismutase.
 GN SODF.
 OS Streptomyces griseus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20435297; PubMed=10978523;
 RA Kim J.-S., Jang J.-H., Lee J.-W., Kang S.-O., Kim K.-S., Lee J.K.;
 RT "Identification of cis site involved in nickel-responsive
 transcriptional repression of sodef gene coding for Fe- and Zn-
 containing superoxide dismutase of Streptomyces griseus."
 RL Biochim. Biophys. Acta 1493:200-207(2000).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL: AF141866; AAD30139.1; -.
 DR HSPSP; P17670; 1IDS.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sodefe; 1.
 DR Pfam: PF02777; sodefe_C; 1.
 DR Prodom: PD000475; SODismutase; 1.
 DR PROSITE: PS00088; SOD_MN; 1.
 DR Oxidoreductase.
 SEQUENCE 213 AA; 23476 MW; 57989919447C7583 CRC64;

Query Match 49.0%; Score 71; DB 2; Length 213;
 Best Local Similarity 50.0%; Pred. No. 0.007;
 Matches 13; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 2 YSLPELDYFSATEPYISQINEXYT 27
 Db 4 YTLPELPYAYDALEPHISQIMELHHS 29

RESULT 24

074200 PRELIMINARY; PRT; 220 AA.
 ID 074200;
 AC 074200;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Manganese superoxide dismutase precursor.
 GN MNSOD.
 OS Pneumocystis carinii.
 OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
 OC Pneumocystis.
 OX NCBI_TaxID=4754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Denis C.M., Guyot K., Del-Cas E., Camus D., Odberg-Ferragut C.;
 RT "Mn SOD gene from rat derived P. carinii."
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL: AF036321; AAC24764.1; -.
 DR HSPSP; P04179; 1ABW.
 DR InterPro: IPR001189; SODismutase.
 DR InterPro: IPR000834; Zn_cardozept.
 DR Pfam: PF00081; sodefe; 1.
 DR Pfam: PF02777; sodefe_C; 1.
 DR Prodom: PD000475; SODismutase; 1.
 DR PROSITE: PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
 DR PROSITE: PS00088; SOD_MN; 1.
 DR Oxidoreductase; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 220
 FT POTENTIAL.
 SEQUENCE 220 AA; 25869 MW; 73B1F1C98929E18 CRC64;

Query Match 49.0%; Score 71; DB 3; Length 220;
 Best Local Similarity 44.4%; Pred. No. 0.0072;
 Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 KYSLPELDYFSATEPYISQINEXYT 27
 Db 24 KHVLPSPYDYQALEPYLSADLIELHY 50

RESULT 25

09FY33 PRELIMINARY; PRT; 224 AA.
 ID 09FY33;
 AC 09FY33;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Manganese superoxide dismutase (EC 1.15.1.1) (Fragment).
 GN MN-SOD.
 OS Digitalis lanata (Foxglove).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Veroniceae; Digitalis.
 OX NCBI_TaxID=49450;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gruner B., Reva V.A., Mueller-Urli F.;
 RT "Stress-induction of Mn-dependent SOD and CAT in Digitalis lanata
 (Bhrh.) during somatic embryogenesis."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL; AJ276863; CAC05259.1; -.
 DR HSSP; P04179; IABM.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR Pfam; PF02777; sodfe_C; 1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 KW Oxidoreductase.
 FT NON_TER 1 1
 SQ SEQUENCE 224 AA; 24757 MW; DD569F3F62C66E08 CRC64;
 Query Match 49.0%; Score 71; DB 10; Length 224;
 Best Local Similarity 46.2%; Pred. No. 0.0074;
 Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

RESULT 26
 Q9DDJ1 PRELIMINARY; PRT; 224 AA.
 ID Q9DDJ1
 AC Q9DDJ1
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Manganese-containing superoxide dismutase precursor (EC 1.15.1.1).
 GN MNSOD.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RA Bu Y.Q., Luo X.G., Li S.F., Lu C., Li Y.W., Kuang X., Liu B., Li J.F.,
 RA Yu S.X.;
 RT "Cloning and Sequence Analysis of Manganese-containing Superoxide
 RT Dismutase (Mnsod) cDNA of Chicken."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC EMBL; AF329270; AAG46055.1; -.
 DR HSSP; P04179; IABM.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR Pfam; PF02777; sodfe_C; 1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 KW Oxidoreductase; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 224
 SQ SEQUENCE 224 AA; 24946 MW; 119211AC7266687F CRC64;

Query Match 49.0%; Score 71; DB 13; Length 224;
 Best Local Similarity 39.3%; Pred. No. 0.0074;
 Matches 11; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXSLPELDYEFSAPEYISQINEIXY 28
 Db 27 KHTLPDLPYDYGALPEHISAEMQLHHS 54

RESULT 27

Q90Y34
 ID Q90Y34 PRELIMINARY; PRT; 224 AA.
 AC Q90Y34
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Mnsod.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kim H., You S., Foster L.K., Farris J., Foster D.N.;
 RT "Expression of antioxidant genes in primary and immortal chicken
 RT embryo fibroblast cells."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC EMBL; AF299388; AAK97214.1; -.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR Pfam; PF02777; sodfe_C; 1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; UNKNOWN_1.
 KW Oxidoreductase.
 SQ SEQUENCE 224 AA; 24770 MW; A1B570FC736BD3DD CRC64;
 Query Match 49.0%; Score 71; DB 13; Length 224;
 Best Local Similarity 39.3%; Pred. No. 0.0074;
 Matches 11; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXSLPELDYEFSAPEYISQINEIXY 28
 Db 27 KHTLPDLPYDYGALPEHISAEMQLHHS 54

RESULT 28
 Q9M532 PRELIMINARY; PRT; 237 AA.
 ID Q9M532
 AC Q9M532
 DT 01-OCT-2000 (T-EMBLrel. 15, Created)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Manganese superoxide dismutase.
 OS Euphorbia esula (leafy spurge).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosid 1; Malvidiales; Euphorbiaceae; Euphorbia.
 OX NCBI_TaxID=3993;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=UNDERGROUND ADVENTITIOUS BUDS;
 RA Anderson J.V., Horvath D.P.;
 RT "Identification of mRNAs expressed in underground adventitious buds of
 RT Euphorbia esula (leafy spurge)."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC EMBL; AF242310; AAF65768.1; -.
 DR HSSP; P04179; IAP6.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR Pfam; PF02777; sodfe_C; 1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.

RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsunako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*.";
 RL Nature 406:151-159(2000).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL: AF004068; AA85411.1; -.
 DR HSSP: P00446; IVEW.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sodfe; 1.
 DR Pfam: PF02777; sodfe_C; 1.
 DR Prodom: PD000475; SODismutase; 1.
 DR PROSITE: PS00088; SOD_MN; 1.
 DR OXidoreductase; Complete proteome.
 DR SEQUENCE 203 AA; 22643 MW; F339B9D93CDCBA7F CRC64;

Query Match 46.9%; Score 68; DB 16; Length 203;
 Best Local Similarity 48.1%; Pred. No. 0.019;
 Matches 13; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 YSLPDLFEFATPEYISQIINEIXYT 28
 ID 096W28 PRELIMINARY; PRT; 206 AA.
 AC 096W28;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE Manganese superoxide dismutase.
 DE MNSOD1.
 OS Phanerochaete chrysosporium.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Corticiaceae; Phanerochaete.
 OX NCBI_TaxID=5306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BKM-F-1767;
 RA Dosoretz C.G., Goldberg D., Belinky P.A., Rothschild N., Krinfeld B.,
 RA Kalati O., Burger M.;
 RT "The manganese superoxide dismutase of *Phanerochaete chrysosporium*:
 RT its function, expression and gene structure.";
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL: AF388395; AA82369.1; -.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sodfe; 1.
 DR Pfam: PF02777; sodfe_C; 1.
 DR Prodom: PD000475; SODismutase; 1.
 DR PROSITE: PS00088; SOD_MN; UNKNOWN_1.
 DR OXidoreductase.
 DR SEQUENCE 206 AA; 22860 MW; 63625CCFBDA4A290 CRC64;

Query Match 46.9%; Score 68; DB 3; Length 206;
 Best Local Similarity 44.4%; Pred. No. 0.019;
 Matches 12; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 KYSPLDYEFATPEYISQIINEIXY 27
 ID 096W28 PRELIMINARY; PRT; 206 AA.
 AC 096W28;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE Manganese superoxide dismutase.
 DE MNSOD1.
 OS Phanerochaete chrysosporium.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Corticiaceae; Phanerochaete.
 OX NCBI_TaxID=5306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BKM-F-1767;
 RA Dosoretz C.G., Goldberg D., Belinky P.A., Rothschild N., Krinfeld B.,
 RA Kalati O., Burger M.;
 RT "The manganese superoxide dismutase of *Phanerochaete chrysosporium*:
 RT its function, expression and gene structure.";
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL: AF388395; AA82369.1; -.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sodfe; 1.
 DR Pfam: PF02777; sodfe_C; 1.
 DR Prodom: PD000475; SODismutase; 1.
 DR PROSITE: PS00088; SOD_MN; UNKNOWN_1.
 DR OXidoreductase.
 DR SEQUENCE 206 AA; 22860 MW; 63625CCFBDA4A290 CRC64;

RESULT 33
 Q9X469 PRELIMINARY; PRT; 215 AA.
 ID Q9X469;
 DT 01-NOV-1999 (TEMBLrel. 12, Created)
 DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE Superoxide dismutase (EC 1.15.1.1).
 DE SODF2 OR SC00999 OR 2SCG2.12C.
 GN Streptomyces coelicolor.
 OS Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomyces; Streptomyces; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=99250253; PubMed=10231572;
 RA Chung H.-U., Kim E.-U., Suh B., Choi J.-H., Roe J.-H.;
 RA "Duplicate genes for Fe-containing superoxide dismutase in
 RA Streptomyces coelicolor A3(2).";
 RT Gene 231:87-93(1999).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Brown S.P., Harris D.;
 RA Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RA Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8943436;
 RA Redenbach M., Kleiser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Frazer A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleiser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wierczek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RT *coelicolor* A3(2).";
 RL Nature 417:141-147(2002).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL: AF099015; AA03130.1; -.
 DR EMBL: AL445963; CA014367.1; -.
 DR HSSP: P80293; IAVM.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sodfe; 1.
 DR Pfam: PF02777; sodfe_C; 1.
 DR Prodom: PD000475; SODismutase; 1.
 DR PROSITE: PS00088; SOD_MN; 1.
 DR OXidoreductase.
 DR SEQUENCE 215 AA; 23599 MW; 3D7FA9524CA3264B CRC64;

Query Match 46.9%; Score 68; DB 16; Length 215;

Best Local Similarity 50.0%; Pred. No. 0.02;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATEPYISGOINEIXY 27
Db 4 YTLPELDYISALPAVISEIIEIHLH 29

RESULT 34
P3606 PRELIMINARY; PRT; 231 AA.
AC P3606;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Manganese superoxide dismutase (EC 1.15.1.1).
GN SOD3.2.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Triticum.
NCBI_TaxId=4565;
[1]

SEQUENCE FROM N.A.
RA Wu G., Robertson A., Wilen R., Gust L.;
RT "Isolation and characterization of two cDNAs (Accession Nos. U72212 and U73172) encoding mitochondrial manganese superoxide dismutases in wheat (PGR97-023)."
RL Plant Physiol. 113:664-664(1997).
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
DR EMBL: U73172; AAB68036.1; -.
DR HSSP; P04179; IABW.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sode; 1.
DR Pfam; PF02777; sode; C; 1.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KM Oxidoreductase.
SQ SEQUENCE 231 AA; 25299 MW; 01C5B547E2F8FFD0 CRC64;

Query Match 46.9%; Score 68; DB 10; Length 231;
Best Local Similarity 42.3%; Pred. No. 0.022;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATEPYISGOINEIXY 27
Db 31 FTLPLDLYFGALPAVSGEIMRLH 56

RESULT 35
082584 PRELIMINARY; PRT; 240 AA.
AC 082584;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Manganese superoxide dismutase (EC 1.15.1.1).
GN MNSOD.
OS Zantedeschia aethiopica (White calla lily).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Zantedeschia.
OK NCBI_TaxId=69721;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RA Lino-Neto T., Tavares R.M., Palme K., Pais M.S.S.;
RT "Expression of superoxide dismutases during senescence and regreening of Zantedeschia aethiopica spathe."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
DR EMBL; AF094832; AAC63379.1; -.
DR HSSP; P04179; IABW.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sode; 1.
DR Pfam; PF02777; sode; C; 1.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KM Oxidoreductase.
SQ SEQUENCE 240 AA; 26276 MW; 3D0479B8F38F4FDF CRC64;

Query Match 46.9%; Score 68; DB 10; Length 240;
Best Local Similarity 46.2%; Pred. No. 0.023;
Matches 12; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATEPYISGOINEIXY 27
Db 40 FSLPLDLYGSLPAISGEIMRLH 65

RESULT 36
09KM85 PRELIMINARY; PRT; 202 AA.
AC 09KM85;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Manganese superoxide dismutase.
GN SODA.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.
OK NCBI_TaxId=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M2799;
RA Yamamoto S., Kimoto R.;
RT "Identification and characterization of the soda genes in some Vibrio species."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
DR EMBL; AB041847; BAA97807.1; -.
DR HSSP; P09214; IMNG.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sode; 1.
DR Pfam; PF02777; sode; C; 1.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KM Manganese; Oxidoreductase.
SQ SEQUENCE 202 AA; 22972 MW; 6177B5CF62CA700A CRC64;

Query Match 46.2%; Score 67; DB 2; Length 202;
Best Local Similarity 40.7%; Pred. No. 0.027;
Matches 11; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATEPYISGOINEIXY 28
Db 3 HTPELDYISALPAVISEIIEIHLH 29

RESULT 37
09RUV2 PRELIMINARY; PRT; 211 AA.
AC 09RUV2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (T-EMBLrel. 21, last annotation update)
 DE Superoxide dismutase (SOD), MN family.
 GN DRI279.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 NC NCB1_TaxID=1299;
 RX MEDLINE=20036896; PubMed=10567266;
 RC STRAIN=RI;
 RP SEQUENCE FROM N.A.
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
 Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 Fraser C.M.;
 "Genome sequence of the radioresistant bacterium Deinococcus
 radiodurans RI.";
 RL Science 286:1571-1577(1999).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY)
 CC -1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 FAMILY.
 CC EMBL: AE001975; AAF10851.1; -.
 DR HSSP: P00448; IVEW.
 DR TIGR: DRI279; -.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sodfe, 1.
 DR Pfam: PF02777; sodfe_C, 1.
 DR ProDom: PD000475; SODismutase; 1.
 DR PROSITE: PS00088; SOD MN; 1.
 KM Oxidoreductase; Complete proteome.
 SQ SEQUENCE 211 AA; 25478 MW; A71P22F516A1897E CRC64;
 QY Query Match 46.2%; Score 67; DB 16; Length 211;
 Best Local Similarity 44.4%; Pred. No. 0.029;
 Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 DB 3 YSLPDLPPYVDALEPHIDARMEIHT 29
 QY 2 YSLPDLPPYVDALEPHIDARMEIHT 28
 ID Q9NB66 PRELIMINARY; PRT; 218 AA.
 AC Q9NB66;
 DT 01-OCT-2000 (T-EMBLrel. 15, Created)
 DT 01-OCT-2000 (T-EMBLrel. 15, last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, last annotation update)
 DE Mitochondrial manganese superoxide dismutase precursor.
 OS Callinectes sapidus (Blue crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Callinectes.
 NC NCB1_TaxID=6763;
 RX MEDLINE=20036896; PubMed=10567266;
 RC STRAIN=RI;
 RP SEQUENCE FROM N.A.
 RA Browner M., Browner T.H.;
 RT "cDNA sequence of the mitochondrial manganese superoxide dismutase
 from the blue crab, Callinectes sapidus.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 FAMILY.
 CC EMBL: AF264029; AAF74770.1; -.
 DR HSSP: P04179; IAP6.
 DR InterPro: IPR001189; SODismutase.

DR Pfam: PF00081; sodfe, 1.
 DR Pfam: PF02777; sodfe_C, 1.
 DR ProDom: PD000475; SODismutase; 1.
 DR PROSITE: PS00088; SOD MN; 1.
 KM Oxidoreductase; Transferrin peptide.
 FT TRANSIT 1 22
 SQ SEQUENCE 218 AA; 24125 MW; A7FC617E8908CF0 CRC64;
 QY Query Match 46.2%; Score 67; DB 5; Length 218;
 Best Local Similarity 39.3%; Pred. No. 0.03;
 Matches 11; Conservative 10; Mismatches 7; Indels 0; Gaps 0;
 DB 23 KHTLPDLPYVDALEPHIDARMEIHT 50
 QY 1 KHTLPDLPYVDALEPHIDARMEIHT 28
 ID Q9SM64 PRELIMINARY; PRT; 228 AA.
 AC Q9SM64;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, last annotation update)
 DE Manganese superoxide dismutase 1 precursor (BC 1.15.1.1).
 GN SOD.
 OS Prunus persica (Peach).
 OC Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid 1; Rosales; Rosaceae; Amygdaloidae; Prunae.
 NC NCB1_TaxID=3760;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF.
 RA Bagnoli F., Racchi M.L.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 FAMILY.
 CC EMBL: AJ238316; CAB56851.1; -.
 DR HSSP: P04179; IAP6.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sodfe, 1.
 DR Pfam: PF02777; sodfe_C, 1.
 DR ProDom: PD000475; SODismutase; 1.
 DR PROSITE: PS00088; SOD MN; 1.
 KM Manganese; Mitochondrion; Oxidoreductase; Transferrin peptide.
 FT TRANSIT 1 24
 FT CHAIN 25 228
 SQ SEQUENCE 228 AA; 25455 MW; A32DA57F552F18AB CRC64;
 QY Query Match 46.2%; Score 67; DB 10; Length 228;
 Best Local Similarity 46.2%; Pred. No. 0.031;
 Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 DB 28 FSLPDLPPYVDALEPHIDARMEIHT 53
 QY 2 FSLPDLPPYVDALEPHIDARMEIHT 27
 ID Q43273 PRELIMINARY; PRT; 235 AA.
 AC Q43273;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, last annotation update)
 DE Manganese superoxide dismutase (SOD-3).
 OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxId=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89051020; PubMed=2461225;
 RA White J.A., Scandalios J.G.;
 RT "Isolation and characterization of a cDNA for mitochondrial manganese
 superoxide dismutase (SOD-3) of maize and its relation to other
 RT manganese superoxide dismutases.";
 RL Biochim. Biophys. Acta 951:61-70(1988).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC DR EMBL; M33119; AAA33512.1; -.
 DR HSSP; P04179; 1ABM.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sode; 1.
 DR Pfam; PF02777; sode; C; 1.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 DR K01doreductase.
 KW OXidoreductase.
 SQ SEQUENCE 235 AA; 25579 MW; AD5CDAD992FD336 CRC64;

Query March 46.2% Score 67; DB 10; Length 235;
 Best Local Similarity 48.0%; Pred. No. 0.032; 7; Indels 0; Gaps 0;
 Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 QY 3 SLPELDYFSATPYISQINEIXY 27
 Db 36 TLPLSYDFGALPAISGEIMRLH 60

Search completed: April 9, 2003, 13:59:51
 Job time : 17.8624 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 9, 2003, 13:38:19 ; Search time 14.3119 Seconds

(without alignments)
279.314 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 145
Sequence: 1 KYSLEPDIYEFSTPEYISQINEIXYTX 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
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9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
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12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
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14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	97.2	30	19 AAM53252	Candida albicans a
2	100	69.0	233	23 ABB05612	S. cerevisiae mang
3	79	54.5	30	18 AAM29762	Malassezia fungus
4	79	54.5	224	18 AAM29771	Malassezia fungus
5	77	53.1	200	22 AAC92973	C. glutamicum prote
6	77	53.1	200	22 AAU00514	C. melaleucola sup
7	74	51.0	101	21 AAG02172	Human secreted pro
8	74	51.0	155	22 AAU03130	Novel human secret
9	74	51.0	183	20 AA129656	Human manganese su
10	74	51.0	198	9 AAP80602	Sequence of polype

11	74	51.0	198	9 AAP80603	Sequence of polype
12	74	51.0	198	16 AAR75191	Human manganese su
13	74	51.0	198	16 AAR75192	Human manganese su
14	74	51.0	198	21 AAY55846	Human manganese su
15	74	51.0	199	13 AAR20015	Mn-SOD (1159Thr) .
16	74	51.0	199	15 AAR60359	MnSOD N-terminal.
17	74	51.0	222	8 AAP71701	Recombinant human
18	74	51.0	222	14 AAR44801	MnSOD cDNA. Homo
19	74	51.0	222	15 AAR61337	Human manganese-co
20	74	51.0	222	16 AAR75193	Human manganese su
21	74	51.0	222	17 AAW00018	Human manganese su
22	74	51.0	222	17 AAW00453	Human manganese su
23	74	51.0	222	17 AAR90713	Human manganese su
24	74	51.0	222	20 AAW98173	Human manganese su
25	74	51.0	222	20 AAW98173	Human manganese su
26	74	51.0	222	20 AAW98175	Human manganese su
27	74	51.0	222	20 AAW98175	Human manganese su
28	74	51.0	222	20 AAW98176	Human manganese su
29	74	51.0	222	20 AAW98177	Human manganese su
30	74	51.0	222	20 AAW98169	Human native manga
31	74	51.0	222	20 AAW98170	Human native manga
32	74	51.0	222	20 AAW98171	Human manganese su
33	74	51.0	222	20 AAW96317	Human manganese co
34	74	51.0	222	20 AAW82446	Human mSOD protein
35	74	51.0	222	21 AAB08204	Amino acid sequenc
36	74	51.0	222	21 AAB08205	Q143N modified hum
37	74	51.0	222	21 AAB08206	A modified human m
38	74	51.0	222	23 ABB07330	Human manganese su
39	74	51.0	223	9 AAP80551	Human manganese su
40	74	51.0	226	21 AAY55849	Human manganese su
41	74	49.7	44	22 AAB78878	C. glutamicum SRT
42	71	49.0	188	19 AAM53253	Candida albicans f
43	71	49.0	207	19 AAB61476	A. fumigatus aller
44	70	48.3	46	9 AAP80604	Sequence of human
45	70	48.3	161	21 AAC33605	Arabidopsis thalia

ALIGNMENTS

RESULT 1	
AAW53252	
ID	AAW53252 standard; Protein; 30 AA.
XX	
AC	AAW53252;
XX	
DT	30-JUL-1998 (first entry)
XX	
DE	Candida albicans allergen - antigenic protein SEQ ID NO:2.
XX	
KW	Candida albicans; vaccine; allergen; antigenic protein; fungal antigen;
KW	immune response; infection; insoluble.
XX	
OS	Candida albicans.
XX	
FH	Key
FT	Misc-difference 26
FT	Misc-difference 29
FT	Misc-difference 30
FT	Misc-difference 30
XX	
PN	WO9809990-A1.
XX	
PD	12-MAR-1998.
XX	
PF	29-AUG-1997; 97MO-JP03041.
XX	
PR	31-MAR-1997; 97JP-0099775.
PR	04-SEP-1996; 96JP-0255400.
XX	
PA	(TAKI) TAKARA SHUZO CO LTD.

XX Endo M, Kato I, Mizutani S, Takesako K;
XX
XX WPI; 1998-193553/17.
XX
XX Fungal antigens comprising insoluble fraction of fungal cells -
PT useful for, e.g. stimulating immune response and treatment and
PT diagnosis of fungal infection(s)
XX
XX Claim 26; Page 75; 108pp; Japanese.
XX
XX The present sequence represents an active vaccine component or allergen
CC derived from *Candida albicans*, which is an antigenic protein. The
CC present invention describes fungal antigens, comprising the insoluble
CC fraction of fungal cells having completely/partially removed cell walls.
CC Also described are nucleic acids encoding the antigens and a method for
CC producing the antigens. The antigens can be used for preparing
CC therapeutic compositions for stimulating immune response, e.g. as a
CC vaccine. They can be used for treatment of fungal infections, treatment
CC and prevention of allergies and diagnosis of fungal infections in
CC vertebrates. The vaccines are not live, and have low toxicity.
SQ
SQ Sequence 30 AA;
Query Match 97.2%; Score 141; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.2e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KYSLPELDYEFSEATEPYISQINEIXYT 28
DB 1 KYSLPELDYEFSEATEPYISQINEIXYT 28
RESULT 2
ABB05612
ID ABB05612 standard; Protein; 233 AA.
XX
XX ABB05612;
AC
XX 24-APR-2002 (first entry)
DT
XX
XX S. cerevisiae manganese superoxide dismutase protein SEQ ID NO:31.
DE
XX
XX *Aspergillus oryzae*; mutant; modified; reduced transcription; hormone;
KM reduced translation; reduced secretion; receptor; antibody; reporter;
KM enzyme; lipase; manganese superoxide dismutase.
XX
XX Saccharomyces cerevisiae.
OS Synthetic.
XX
XX US6323002-B1.
XX
XX 27-NOV-2001.
PD
XX
XX 25-JUN-1999; 99US-0339972.
PF
XX
XX 12-SEP-1997; 97US-0928692.
PR
XX 13-SEP-1996; 96US-0713312.
PR
XX
XX (NOVO) NOVOSYMS BIOTECH INC.
PA
XX
XX Brody H, Yaver DS, Lamsa M, Hansen K;
PI
XX WPI; 2002-163017/21.
DR
XX
XX Producing a polypeptide using a cell for reducing the production of the
PT polypeptide, comprises inserting DNA into the genome of the cell at a
PT position not within the polypeptide coding sequence or a regulatory
PT sequence -
XX
XX Example 17; Column 125-128; 129pp; English.
PS
XX The present invention describes a method for producing a polypeptide (P1)
CC

CC comprising cultivating a mutant cell whose parent cell comprises a DNA
CC sequence encoding P1, by introducing a nucleic acid construct into the
CC genome of the parent cell at a locus not within the P1 sequence, so
CC that P1 transcription, translation or secretion is reduced, and
CC recovering P1. The method is used to produce a polypeptide, such as a
CC recombinant or heterologous hormone, hormone variant, receptor, antibody,
CC reporter or enzyme, particularly an oxidoreductase, transferase,
CC hydrolase, lyase, isomerase or ligase. The present sequence represents
CC a Saccharomyces cerevisiae manganese superoxide dismutase protein which
CC shares significant identity with the mutant *Aspergillus oryzae* DB9Y1058
CC protein, which is used in an example from the present invention.
XX
XX
SQ
SQ Sequence 233 AA;
Query Match 69.0%; Score 100; DB 23; Length 233;
Best Local Similarity 64.3%; Pred. No. 3.8e-08;
Matches 18; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 KYSLPELDYEFSEATEPYISQINEIXYT 28
DB 27 KVTLPDLKMDFGALPEPYISQINEIXYT 54
RESULT 3
AAW29762
ID AAW29762 standard; peptide; 30 AA.
XX
XX AAW29762;
AC
XX
XX 20-FEB-1998 (first entry)
DT
XX
XX *Malassezia* fungus MF-4 antigenic peptide.
DE
XX
XX *Malassezia*; fungus; antigenic; human; IGE; immunoglobulin E;
KM antibody; allergy; antigen.
KM
XX
XX *Malassezia* sp.
OS
XX
XX WO9721817-A1.
PN
XX
XX 19-JUN-1997.
PD
XX
XX 10-DEC-1996; 96WO-JP03602.
PF
XX
XX 05-SEP-1996; 96JP-0257613.
PR
XX 12-DEC-1995; 95JP-0346627.
PR
XX 05-SEP-1996; 96JP-0257612.
PR
XX
XX (TAKI) TAKARA SHUZO CO LTD.
PA
XX
XX Akiyama K, Kato I, Kuroda M, Okado T, Onishi Y;
PI
XX Takesako K, Yagihara T, Yamaguchi H, Yasueda H;
PI
XX WPI; 1997-332788/30.
DR
XX
XX Antigenic proteins from the fungus *Malassezia* - bind to IGE
PT antibodies present in patients with *Malassezia* allergies, useful for
PT diagnosis, treatment and prevention of such conditions
PT
XX
XX Claim 8; Page 113; 162pp; Japanese.
PS
XX
XX The present sequence represents a specifically claimed antigenic
CC peptide isolated from the fungus *Malassezia*. The antigenic peptide
CC can bind to IGE antibodies present in patients with allergic
CC conditions. Antigenic proteins, peptides and nucleic acids from the
CC fungus *Malassezia* can be used in the diagnosis, treatment and
CC prevention of allergic conditions due to *Malassezia* organisms (such
CC as *M. furfur*, *M. sympodialis* and *M. pachydermatitis*).
XX
XX
SQ
SQ Sequence 30 AA;
Query Match 54.5%; Score 79; DB 18; Length 30;
Best Local Similarity 55.6%; Pred. No. 8.4e-06;
CC

XX 21-FEB-2001.
PD
XX
PF 02-AUG-2000; 2000EP-0116669.
XX
PR 13-AUG-1999; 99US-0373731.
XX
PA (DEGS) DEGUSSA-HUELS AG.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Merkamm M, Guyonvarch A, Marx A;
XX WPI; 2001-212718/22.
DR N-PSDB; AAS00520.
XX
PT New DNA encoding superoxide dismutase of *Corynebacterium*, useful for
PT producing transformants with increased production of metabolites,
PT particularly lysine -
XX
PS Claim 3; Page 14-15; 19pp; English.
XX
CC The sequence represents *Corynebacterium melasscola* superoxide dismutase
CC (sod) polypeptide. *Corynebacterium* microorganisms may be transformed with a
CC sod DNA sequence and the sod gene can be amplified. Sod is then often
CC overexpressed in *Corynebacterium* bacteria. *Corynebacterium* that overexpress sod
CC are used for production of metabolites, particularly nucleotides,
CC vitamins and amino acids, especially D-pantoic acid or, specifically,
CC L-lysine. These metabolites are useful in human or animal nutrition and
CC as pharmaceuticals. Overexpression of sod in *Corynebacterium* increases the
CC yield of particular metabolites.
XX
SQ Sequence 200 AA;
XX
Query March 53.1%; Score 77; DB 22; Length 200;
Best Local Similarity 48.1%; Pred. No. 0.00019;
Matches 13; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 2 YSLPELDYFSAPEYISQINEIXYT 28
DB 4 YELPELDYADYDLEPHIAEIMELHHS 30
XX
RESULT 7
AAG02172
ID AAG02172 standard; Protein; 101 AA.
XX
AC AAG02172;
XX
OT 06-OCT-2000 (first entry)
XX
E Human secreted protein, SEQ ID NO: 6253.
XX
E Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
XX EP1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-0200610.
XX
XX 26-FEB-1999; 99US-0122487.
XX
XX (GEST) GENSET.
XX
XX Dunas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX
XX N-PSDB; AAC02178.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX
PS Claim 13; SEQ ID 6253; 71pp + CD-ROM; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC were prepared from total human RNAs or polyA+ RNAs derived from 30
CC different tissues. EST sequences usually correspond mainly to the 3'
CC untranslated region (UTR) of the mRNA because they are often obtained
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC those cases where longer cDNA sequences have been obtained, the full 5'
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC ends and can therefore be used to obtain full length cDNAs and genomic
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC chromosome mapping procedures. They are used to obtain upstream
CC regulatory sequences and to design expression and secretion vectors.
XX
SQ Sequence 101 AA;
XX
Query March 51.0%; Score 74; DB 21; Length 101;
Best Local Similarity 42.9%; Pred. No. 0.00026;
Matches 13; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY 1 KYSLPELDYFSAPEYISQINEIXYT 28
DB 25 KHSPLDLPDYDYGALPHINQIMQLHHS 52
XX
RESULT 8
AAU30130
ID AAU30130 standard; Protein; 155 AA.
XX
AC AAU30130;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #621.
XX
XX Human; vaccination; gene therapy; nutritional supplement;
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200179449-A2.
XX
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-US08656.
XX
XX 18-APR-2000; 2000US-0552929.
XX
XX 26-JAN-2001; 2001US-0770160.
XX
XX (HYSB-) HYSBQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-611725/70.
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy -
XX
XX Claim 20; Page 248; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or

CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation, to regulate haematopoiesis, and in
CC bone, cartilage, tendon, and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.

XX Sequence 155 AA;

Query Match 51.0%; Score 74; DB 22; Length 155;
Best Local Similarity 42.9%; Pred. No. 0.00044;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KYSLPDLDFSAPEPTISQGINEIXYT 28
Db 50 KHSLPDLDFYGALEPHINQIMQLHHS 77

RESULT 9

AA29656 ID AAY29656 standard; protein; 183 AA.

XX AC AAY29656;

DT 03-NOV-1999 (first entry)

DE Human manganese superoxide dismutase exon 3-deleted isoform protein.

XX Human, manganese superoxide dismutase; MnSOD; exon 3 deleted isoform;

KM MnSOD E3(-); diagnosis; viral infection; HIV; oncogenesis; tumour;

KM UV-induced damage; post ischemia reperfusion damage; anti-inflammatory;

XX cytotoxic; cardiotoxic; cancer.

OS Homo sapiens.

OS Synthetic.

XX WO9943697-A1.

XX 02-SEP-1999.

XX 25-FEB-1999; 99WO-US04129.

XX 25-FEB-1998; 98US-0075948.

XX (UYCO-) UNIV & COMMUNITY COLLEGE.

XX Anziano FQ;

XX WPI; 1999-527592/44.

XX N-PSDB; AA208755.

XX A new isoform useful for diagnosing oxidative stress, and treating

PT viral infections

XX Claim 1; Page 12; 64pp; English.

XX The present sequence represents an isoform of manganese superoxide

CC dismutase (MnSOD), which is a splice-variant lacking exon 3 of the full

CC length MnSOD (i.e. MnSOD E3(-)). MnSOD E3(-) may be useful in the

CC treatment of a wide variety of disorders including viral infections,

CC particularly HIV, and may be used for the prevention of oncogenesis,

CC tumour promotion and invasiveness, and UV-induced damage, for protection

CC of cardiac tissue against post ischemia reperfusion damage, as an

CC anti-inflammatory agent, to reduce the cytotoxic and cardiotoxic effects

CC of anti-cancer drugs, and to improve the longevity of living cells.

XX Sequence 183 AA;

Query Match 51.0%; Score 74; DB 20; Length 183;

Best Local Similarity 42.9%; Pred. No. 0.00054;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KYSLPDLDFSAPEPTISQGINEIXYT 28
Db 25 KHSLPDLDFYGALEPHINQIMQLHHS 52

RESULT 10

AA80602 ID AAP80602 standard; protein; 198 AA.

XX AC AAP80602;

DT 03-OCT-1990 (first entry)

DE Sequence of polypeptide of Formula IVA encoding modified portion of

DE human manganese superoxide dismutase (MnSOD).

XX Human manganese superoxide dismutase derivative; clone BS8;

XX formula IVA; enzyme; EC-1.15.1.1.

XX OS Homo sapiens.

XX EP282899-A.

XX 21-SEP-1988.

XX 10-MAR-1988; 88EP-0103754.

XX 24-DEC-1987; 87DE-3744038.

XX 14-MAR-1987; 87DE-3708306.

XX (BOEH) BOEHRINGER INGELHEIM.

XX Heckl K, Spevak W, Ostermann E, Zophel A, Krystek E, Maurer-Fogy I;

PI White-Castanon MJ, Stratowa C, Hauptmann R;

XX WPI; 1988-265361/38.

XX N-PSDB; AAN61218.

XX Prodn. of human manganese superoxidizedismutase peptide(s) -

PT and DNA coding sequences, for control and diagnosis of eg

XX inflammatory diseases

XX Disclosure; Page 8; 57pp; German.

XX The patent is for polypeptides, esp. non-glycosylated, having the

CC enzymatic, biological and immunological properties of MnSOD that are

CC prep. by genetic engineering methods. Also new are DNA sequences

CC encoding all or part of the polypeptides and replicating vectors,

CC expression plasmids and transformed host cells contg. these sequences.

CC MnSOD catalyses disproportionation of the superoxide radical and can be

CC used in the prevention, diagnosis and treatment of inflammatory,

CC degenerative, neoplastic and rheumatoid disorders; for wound healing; in

CC autoimmune disease and in organ transplantation. It can also be used to

CC improve the storage stability of liq. and solid foods.

XX Sequence 198 AA;

Query Match 51.0%; Score 74; DB 9; Length 198;
Best Local Similarity 42.9%; Pred. No. 0.0006;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KYSLPDLDFSAPEPTISQGINEIXYT 28
Db 1 KHSLPDLDFYGALEPHINQIMQLHHS 28

RESULT 11

AA80603 ID AAP80603 standard; protein; 198 AA.

XX

XX Key Location/Qualifiers
 FH Modified-site 39...41
 FT /label= "N-glycosylation_site"
 FT /note= "potential"
 FT Modified-site 73...75
 FT /label= "N-glycosylation_site"
 FT /note= "potential"
 FT Modified-site 80...82
 FT /label= "N-glycosylation_site"
 FT /note= "potential"
 FT Modified-site 188...190
 FT /label= "N-glycosylation_site"
 FT /note= "potential"
 EP676472-A1.
 11-OCT-1995.
 10-MAR-1988; 88EP-0107460.
 24-DEC-1987; 87DE-3744038.
 14-MAR-1987; 87DE-3708306.
 26-MAY-1987; 87DE-3717685.
 10-JUL-1987; 87DE-3722884.
 (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 Hauptmann R, Heckl K, Krystek E, Maurer-Fogy I,
 Ostermann E, Spevak W, Stratowa C, Wiche-Castanon M,
 Zepherl A;
 WPI; 1995-346092/45.
 N-PSDB; AAQ94272.
 Genes encoding recombinant human manganese superoxide dismutase -
 for treatment, prevention and diagnosis of inflammatory diseases
 Claim 1; Page 9-10; 54pp; German.
 The present sequence is that of the 198 amino acid long hMn-SOD
 mature polypeptide having a Gln residue at position 29. The protein
 is produced with an N-terminal Met residue which is then removed, e.g.
 by treatment with CNBr or CNCl, to release mature hMn-SOD. The mature
 recombinant protein is useful for treating, preventing or diagnosing
 inflammatory, degenerative, neoplastic and rheumatic disorders; in
 wound healing and in autoimmune diseases.
 Sequence 198 AA;
 Query Match 51.0%; Score 74; DB 16; Length 198;
 Best Local Similarity 42.9%; Pred. No. 0.0006;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KXSLPELDYEFSAPEYISQGINEIXYT 28
 1 KXSLPELDYEFSAPEYISQGINEIXYT 28
 1 KXSLPELDYEFSAPEYISQGINEIXYT 28
 RESULT 14
 ID AAY55846
 AC AAY55846; Protein; 198 AA.
 AC AAY55846;
 DT 06-MAR-2000 (first entry)
 XX Human manganese superoxide dismutase (MnSOD) protein.
 XX Manganese superoxide dismutase; MnSOD; proteoglycan; human;
 KM endothelial; oxidative damage; pulmonary inflammatory injury; cancer;
 KM lung disease; hypoxia; ischemia; reperfusion injury; arthritis;
 KM hyperoxia; atherosclerosis; lupus erythematosus; hypertension;

KM neutrophil-mediated inflammation.
 XX OS Homo sapiens.
 XX WO9958547-A1.
 XX 18-NOV-1999.
 XX 06-MAY-1999; 99WO-US09921.
 XX 08-MAY-1998; 98US-0075019.
 (WEBB-) WEBB-MARING INST BIOMEDICAL RES.
 McCord JW, Gao B, Flores SC;
 WPI; 2000-062283/05.
 N-PSDB; AA239779.
 Modified manganese superoxide dismutase, methods of production and
 antibodies -
 Claim 29; Page 71-72; 83pp; English.
 The invention provides a nucleic acid molecule encoding a genetically
 modified manganese superoxide dismutase (MnSOD). The nucleic acid
 comprises: a first nucleic acid sequence encoding an enzymatically active
 portion of MnSOD; and a second nucleic acid sequence encoding a peptide
 (ECSD) that binds to polyanionic polysaccharides or proteoglycans on
 endothelial cell surfaces. The protein protects a mammal, especially
 humans, from oxidative damage and especially from conditions consisting
 of pulmonary inflammatory injury, lung disease, cancer, hypoxia, ischemia
 reperfusion injury, hyperoxia, atherosclerosis, arthritis, lupus
 erythematosus, hypertension and neutrophil-mediated inflammation. The
 lung disease is infant or adult respiratory distress syndrome.
 interstitial lung disease or asthma. The mutant MnSOD also protects
 organs of mammals from pre- and post-transplantation oxidative damage.
 MnSOD is positively charged at physiological pH and has a longer plasma
 half-life of about 4 hours compared to 6-15 minutes for cytosolic Cu,Zn
 SOD (following intravenous injection). ECSD has a substantial advantage
 over both Cu,ZnSOD and MnSOD because of its ability to bind to the
 endothelium. ECSD is hard to produce in mammalian cell culture systems,
 so a fusion of ECSD and MnSOD therefore overcomes these problems. The
 present sequence represents the human MnSOD protein.
 Sequence 198 AA;
 Query Match 51.0%; Score 74; DB 21; Length 198;
 Best Local Similarity 42.9%; Pred. No. 0.0006;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KXSLPELDYEFSAPEYISQGINEIXYT 28
 1 KXSLPELDYEFSAPEYISQGINEIXYT 28
 1 KXSLPELDYEFSAPEYISQGINEIXYT 28
 RESULT 15
 ID AAR20015
 AC AAR20015; Protein; 199 AA.
 AC AAR20015;
 DT 01-APR-1992 (first entry)
 XX Mn-SOD (Ile59Thr).
 XX Manganese superoxide dismutase; vector; anti-inflammatory.
 KM Homo sapiens.
 XX OS Homo sapiens.
 KM Key Location/Qualifiers
 FH Msc-difference 59
 FT /label= Ile->THR

QY 1 KVSLEPDLDFEFSATEPYISGOINEIXYT 28
 DB 25 KHSLEPDLDFYDYGALPEPHINAQIMQLHHS 52

RESULT 18

AAAR44801
 ID AAR44801 standard; Protein; 222 AA.

AC AAR44801;

DT 21-JUN-1994 (first entry)

DE MnSOD cDNA.

MnSOD; manganese superoxide dismutase; N-terminal; catalytic;
 Km reperfusion injury; ischaemia; superoxide; SO; molecular oxygen;
 Km anti-inflammatory; ss.

OS Homo sapiens.

PN USS270195-A.

PD 14-DEC-1993.

PF 22-NOV-1985; 85US-0801090.

PR 29-OCT-1986; 86IE-0002851.

PA (BIOT-) BIO-TECHNOLOGY GENERAL CORP.

PI Beck Y, Hartman JR;

DR WPI; 1993-404931/50.

DR N-PSDB; AAQ53193.

PT Expression plasmid in Escherichia coli host system - encodes

PT human manganese superoxidisedismutase analogue, useful for e.g.

PT treating inflammation

PS Claim 1; Fig 1a-1c; 27pp; English.

CC The sequence is of a manganese superoxide dismutase which can be used

CC to catalyse the reduction of superoxide (SO) radicals to hydrogen

CC peroxide and molecular oxygen. It can be used to reduce

CC reperfusion injury following ischaemia and prolong the survival of

CC excised organs. It can also be used as a long acting

CC anti-inflammatory drug.

QY 1 KVSLEPDLDFEFSATEPYISGOINEIXYT 28
 DB 25 KHSLEPDLDFYDYGALPEPHINAQIMQLHHS 52

RESULT 19

AAAR61337
 ID AAR61337 standard; Protein; 222 AA.

AC AAR61337;

DT 31-MAY-1995 (first entry)

DE Human manganese-contg. superoxide dismutase SOD-2.

KM human superoxide dismutase; hSOD2; mSOD; neurodegeneration;
 KM Alzheimer's disease; Parkinson's disease; Huntington's disease;

KM Hallervorden-Spatz disease; olivopontocerebellar atrophy;
 KM familial amyotrophic lateral sclerosis; FALS; diagnosis; mutant SOD;
 KM reverse transcription polymerase chain reaction; SSCP analysis.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Peptide 1..18

FT Protein /label= signal peptide

FT 19..222

FT /label= mature_mSOD

PN W09419493-A.

PD 01-SEP-1994.

PF 28-FEB-1994; 94MO-US02089.

PR 26-FEB-1993; 93US-0023980.

PA (GENO) GEN HOSPITAL CORP.

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

PI Brown R, Horvitz HR, Rosen DR;

DR WPI; 1994-294353/36.

DR N-PSDB; AAQ57474.

PT Diagnosis, treatment and prevention of diseases of cell death -

PT e.g. amyotrophic lateral sclerosis, which are the result of e.g.

PT decreased SOD activity

PS Claim 22; Fig 3; 94pp; English.

CC The presence of a mutation in a gene encoding a superoxide

CC dismutase (SOD1, SOD2 or SOD3) indicates an increased likelihood of

CC developing a cell death disease, specifically a neurodegenerative

CC disease. The use of SOD polypeptides to treat amyotrophic lateral

CC sclerosis and diseases involving a deleterious mutation in the

CC glutathione peroxidase-encoding gene, the catalase-encoding gene

CC and the nitric oxide-encoding gene is claimed. The specification

CC includes the sequences of human SOD1, hSOD2 and hSOD3 (AAR61336-
 AAR61338, respectively).

RESULT 20

AAAR75193
 ID AAR75193 standard; Protein; 222 AA.

AC AAR75193;

DT 23-MAY-1996 (first entry)

DE Human manganese superoxide dismutase (lys29) preproteoin.

KM hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;
 KM autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;
 KM osteoarthritis; wound healing; leader peptide; precursor.
 OS Homo sapiens.
 FX Key Location/Qualifiers
 FT Peptide 1..24

FT /label= leader
FT Protein 25..222
FT /label= mature_hmnSOD_(lys29)
XX
XX Epe76472-A1.
XX
XX 11-OCT-1995.
XX
XX 10-MAR-1988; 88EP-0107460.
XX
XX 24-DEC-1987; 87DE-3744038.
XX 14-MAR-1987; 87DE-3708306.
XX 26-MAY-1987; 87DE-3717695.
XX 10-JUL-1987; 87DE-3722884.
XX
XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX
XX Hauptmann R, Heckl K, Krystek E, Maurer-Fogy I,
XX Ostermann E, Spevak W, Stralow C, Wiche-Castanon M,
XX Zoepfel A;
XX WPI; 1995-346092/45.
XX N-PSDB; AAQ94284.
XX
XX Genes encoding recombinant human manganese superoxide dismutase -
XX for treatment, prevention and diagnosis of inflammatory diseases
XX
XX Claim 8; Page 3-4 and Page 19-20; 54pp; German.
XX
XX The present sequence is that of the 198 amino acid long hmn-SOD
XX mature polypeptide having a Lys residue at position 29, preceded
XX by a 24 amino acid residue leader peptide. Mature, recombinant
XX hmn-SOD is useful for treating, preventing or diagnosing
XX inflammatory, degenerative, neoplastic and rheumatic disorders; in
XX wound healing and in autoimmune diseases.
XX
XX Sequence 222 AA;
XX
XX Query Match 51.0%; Score 74; DB 16; Length 222;
XX Best Local Similarity 42.9%; Pred. No. 0.00069;
XX Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
XX
XX 1 KYSLPELDYFSAEPYISGQINEIXYT 28
XX
XX 25 KHSLPDLPYDYGALPHTNAQIMQLHHS 52
XX
XX
XX RESULT 21
XX AAW00018
XX ID AAW00018 standard; Protein; 222 AA.
XX
XX AAW00018;
XX
XX 24-OCT-1996 (first entry)
XX
XX Human manganese superoxide dismutase.
XX
XX Manganese superoxide dismutase; MnSOD; reperfusion injury;
XX ischaemia; bronchial pulmonary dysplasia; inflammation;
XX antiinflammatory.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..24
XX /label= Sig_peptide
XX Protein 25..222
XX /label= Mat_protein
XX
XX US5540911-A.
XX
XX 30-JUL-1996.
XX

PF 22-NOV-1985; 85US-0801090.
XX
XX 29-OCT-1986; 86IE-0002851.
XX
XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
XX
XX Beck Y, Hartman JR;
XX
XX WPI; 1996-361912/36.
XX N-PSDB; AAT34277.
XX
XX Use of recombinant human manganese superoxide dismutase - for
XX treating inflammation or bronchial pulmonary dysplasia, reducing
XX reperfusion injury or prolonging organ survival
XX
XX Claim 1; Fig 1A-1C; 27pp; English.
XX
XX Human manganese superoxide dismutase (MnSOD) (AAW00018) catalyses
XX the reduction of superoxide radicals to H2O2 and O2. Recombinant
XX MnSOD can be obtd. using transformed host cells, esp. Escherichia
XX coli cells contg. a plasmid carrying e.g. a cDNA clone (AAT34277)
XX obtd. from a human T cell library. The MnSOD is useful for reducing
XX reperfusion injury, treating inflammation or bronchial pulmonary
XX dysplasia and for prolonging survival of excised organs.
XX
XX Sequence 222 AA;
XX
XX Query Match 51.0%; Score 74; DB 17; Length 222;
XX Best Local Similarity 42.9%; Pred. No. 0.00069;
XX Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
XX
XX 1 KYSLPELDYFSAEPYISGQINEIXYT 28
XX
XX 25 KHSLPDLPYDYGALPHTNAQIMQLHHS 52
XX
XX
XX RESULT 22
XX AAW00453
XX ID AAW00453 standard; Protein; 222 AA.
XX
XX AAW00453;
XX
XX 26-SEP-1996 (first entry)
XX
XX Human manganese superoxide dismutase.
XX
XX Gene therapy; hypoxia related enhancer element; HREB; ischaemia;
XX reperfusion; promoter; superoxide dismutase.
XX
XX Homo sapiens.
XX
XX W09620276-A1.
XX
XX 04-JUL-1996.
XX
XX 13-NOV-1995; 95WO-1B00996.
XX
XX 23-DEC-1994; 94US-0365486.
XX (STRI) SRI INT.
XX
XX Bishopric NH, Green CJ, Laderoute KR, Murphy B;
XX Webster KA;
XX WPI; 1996-321849/32.
XX N-PSDB; AAT31018.
XX
XX Chimeric gene contg. therapeutic gene linked to HREB - partic. for
XX expressing SOD etc. in hypoxic tissue to reduce tissue injury caused
XX by ischaemia or reperfusion
XX
XX Disclosure; Page 94-95; 118pp; English.
XX

CC Human manganese superoxide dismutase (AAW00453) catalyzes the
 CC decomposition of the superoxide anion to peroxide. Agents such as
 CC superoxide dismutase are able to increase the salvage of heart muscle
 CC cells. The SOD gene (AAT1018) can be used in novel therapeutic
 CC constructs also contg. a tissue-specific promoter and a hypoxia
 CC response enhancer element. Expression of the gene is enhanced in the
 CC target tissue under hypoxic conditions, such as those encountered
 CC during ischemia and reperfusion.

XX
 SQ Sequence 222 AA;
 Query Match 51.0%; Score 74; DB 17; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.00069;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

OY 1 KXSLPELDYERFATPEYISQGINEIXYT 28
 DB 25 KXSLPDLPYDYGALPHINAQIMQLHRS 52

RESULT 23
 AAR90713
 ID AAR90713 standard; Protein; 222 AA.
 AC AAR90713;
 XX
 DT 06-APR-1996 (first entry)
 XX
 DE Human manganese superoxide-dismutase.
 KW Human; manganese superoxide-dismutase; T-lymphocyte; probe; cDNA;
 KW Escherichia coli; plasmid pMS8-4; N-terminal truncation; cloning;
 KM aminopeptidase; antiinflammatory; oxygen free radical scavenger;
 KM synovial inflammation; arthritis; lung fibrosis.

XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /note= "Pre-peptide"
 FT Region 39..48
 FT /note= "Region used to construct probe AAT15591"
 FT Misc-difference 66
 FT /note= "Gln in previously published sequence"
 FT Misc-difference 112
 FT /note= "Gln in previously published sequence"
 FT Misc-difference 132
 FT /note= "Gln in previously published sequence"
 FT Misc-difference 147..148
 FT /note= "Residues not present in previously
 FT published sequence"
 FT Region 203..213
 FT /note= "Region used to construct probe AAT15592"
 XX
 PN EP691401-A1.
 PD 10-JAN-1996.
 XX
 PF 25-MAR-1988; 88EP-0106995.
 XX
 PR 26-FEB-1988; 88US-0161117.
 PR 27-MAR-1987; 87US-0032734.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
 XX
 PI Beck Y, Hartman JR, Nimrod A;
 XX
 DR WPI; 1996-059735/07.
 DR N-PSDB; AAT15589.
 XX
 PT New human manganese superoxide dismutase analogues - having a Lys
 PT and Opt. His residue absent from the N-terminus, useful for treating
 PT e.g. synovial inflammation, arthritis or lung fibrosis

XX
 PS Example 1; Fig 1; 45pp; English.
 XX
 CC The sequence represents a human manganese superoxide-dismutase
 CC (MnSOD), and is encoded by a human T-lymphocyte cDNA isolated from
 CC a library in phage lambda-gt10 in Escherichia coli, by screening
 CC with a 5'-probe (AAT15591) and a 3'-probe (AAT15592), followed by
 CC subcloning in plasmid pBR322 to give plasmid pMS8-4. The cDNA may
 CC be expressed in e.g. E. coli for production of recombinant MnSOD.
 CC The MnSOD product may be cleaved with Aeromonas proteolytica
 CC aminopeptidase to produce an N-terminally truncated analogue with
 CC lysine and optionally histidine residues removed. The MnSOD
 CC analogue may be used in therapy of conditions associated with
 CC generation of oxygen free radicals, particularly synovial
 CC inflammation, arthritis and lung fibrosis (claimed).

XX
 SQ Sequence 222 AA;
 Query Match 51.0%; Score 74; DB 17; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.00069;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

OY 1 KXSLPELDYERFATPEYISQGINEIXYT 28
 DB 25 KXSLPDLPYDYGALPHINAQIMQLHRS 52

RESULT 24
 AAW98172
 ID AAW98172 standard; Protein; 222 AA.
 AC AAW98172;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human manganese superoxide dismutase Q143A mutant.
 KW Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
 KW inflammation; reperfusion injury; therapy; mutant.

XX
 OS Homo sapiens.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /note= "signal peptide"
 FT Protein 25..222
 FT /note= "mature protein"
 FT Active-site 50
 FT /note= "His-26"
 FT Active-site 54
 FT /note= "His-30"
 FT Active-site 58
 FT /note= "Tyr-58"
 FT Active-site 98
 FT /note= "Tyr-74"
 FT Active-site 167
 FT /note= "Gln-143"
 FT Active-site 183
 FT /note= "Asp-159"
 FT Active-site 185
 FT /note= "Trp-161"
 FT Active-site 187
 FT /note= "His-163"
 FT Misc-difference 155
 FT /label= Gln, Gln
 FT Misc-difference 167
 FT /note= "Gln replaces Ala in wild-type hMnSOD"
 XX
 PN W09913088-A1.
 PN 18-MAR-1999.
 XX

XX 10-SEP-1998; 98WO-US18842.
 XX 10-SEP-1997; 97US-0927230.
 XX (UYFL) UNIV FLORIDA.
 XX Nick HS, Silverman DN;
 XX WPI; 1999-229242/19.
 FT New recombinant human manganese superoxide dismutase proteins
 XX
 PS Claim 14; Page -: 61pp; English.
 CC This protein is a Q143A mutant of human manganese superoxide
 CC dismutase (hmnSOD, see also AAW98170). Novel modified hmnSOD
 CC proteins having catalytic activity which differs from natural
 CC hmnSOD are claimed. The modified proteins (see also AAW98171-77)
 CC exhibit reduced or no product inhibition, or have greater
 CC activity, or both, compared to natural hmnSOD. The modifications
 CC involve one or amino acid substitutions within the active site of
 CC the enzyme, especially at residues His-26, His-30, Tyr-34, His-74,
 CC Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-34 and His-30
 CC are located near the active site metal, are highly conserved, and
 CC are involved in a hydrogen bond relay which links the active site
 CC metal-bound hydroxyl group to ordered solvent, and are thus all
 CC potentially involved in catalytic activity, product inhibition
 CC and/or enzyme stability. Modified hmnSODs, or expression vectors
 CC in which a modified hmnSOD nucleic acid is linked to a promoter
 CC (preferably mammalian), are used to protect a cell line from damage
 CC caused by superoxide radicals (claimed). They can also be used to
 CC treat subjects suffering from, or at risk of, cytotoxicity caused
 CC by superoxide radicals (claimed). As such, they can be used as
 CC antioxidants in the treatment of a variety of disorders, including
 CC inflammation (claimed), reperfusion injury following ischemia
 CC (claimed), and cellular damage caused by chemotherapeutic agents.
 CC Note. The present sequence is not shown in the specification but
 CC is derived from the hmnSOD sequence given on page 53-54.
 XX
 SQ Sequence 222 AA;
 Query Match 51.0%; Score 74; DB 20; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.00069;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 KYSLPELDYFSATPEYISGQINEXYT 28
 Db 25 KHSLPDLPYDYGALPEPHNAQIMQIHHS 52
 RESULT 25
 AAW98173
 ID AAW98173 standard; Protein; 222 AA.
 XX
 AC AAW98173;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human manganese superoxide dismutase Q143H mutant.
 XX
 KW Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
 KW inflammation; reperfusion injury; therapy; mutant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT Peptide
 FT Protein
 FT Location/Qualifiers
 FT 1..24
 FT /note= "signal peptide"
 FT 25..222
 FT /note= "mature protein"

FT Active-site 50
 FT /note= "His-26"
 FT Active-site 54
 FT /note= "His-30"
 FT Active-site 58
 FT /note= "Tyr-58"
 FT Active-site 98
 FT /note= "Tyr-74"
 FT Active-site 167
 FT /note= "Gln-143"
 FT Active-site 183
 FT /note= "Asp-159"
 FT Active-site 185
 FT /note= "Trp-161"
 FT Active-site 187
 FT /note= "His-163"
 FT Misc-difference 155
 FT /label= Gln, Glu
 FT Misc-difference 167
 FT /note= "Gln replaces His in wild-type hmnSOD"
 XX
 PN W0991088-A1.
 XX
 PD 18-MAR-1999.
 XX
 XX 10-SEP-1998; 98WO-US18842.
 PF 10-SEP-1997; 97US-0927230.
 XX
 XX (UYFL) UNIV FLORIDA.
 XX Nick HS, Silverman DN;
 XX WPI; 1999-229242/19.
 XX
 DR New recombinant human manganese superoxide dismutase proteins
 XX
 PS Claim 14; Page -: 61pp; English.
 CC This protein is a Q143H mutant of human manganese superoxide
 CC dismutase (hmnSOD, see also AAW98170). Novel modified hmnSOD
 CC proteins having catalytic activity which differs from natural
 CC hmnSOD are claimed. The modified proteins (see also AAW98171-77)
 CC exhibit reduced or no product inhibition, or have greater
 CC activity, or both, compared to natural hmnSOD. The modifications
 CC involve one or amino acid substitutions within the active site of
 CC the enzyme, especially at residues His-26, His-30, Tyr-34, His-74,
 CC Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-34 and His-30
 CC are located near the active site metal, are highly conserved, and
 CC are involved in a hydrogen bond relay which links the active site
 CC metal-bound hydroxyl group to ordered solvent, and are thus all
 CC potentially involved in catalytic activity, product inhibition
 CC and/or enzyme stability. Modified hmnSODs, or expression vectors
 CC in which a modified hmnSOD nucleic acid is linked to a promoter
 CC (preferably mammalian), are used to protect a cell line from damage
 CC caused by superoxide radicals (claimed). They can also be used to
 CC treat subjects suffering from, or at risk of, cytotoxicity caused
 CC by superoxide radicals (claimed). As such, they can be used as
 CC antioxidants in the treatment of a variety of disorders, including
 CC inflammation (claimed), reperfusion injury following ischemia
 CC (claimed), and cellular damage caused by chemotherapeutic agents.
 CC Note. The present sequence is not shown in the specification but
 CC is derived from the hmnSOD sequence given on page 53-54.
 XX
 SQ Sequence 222 AA;
 Query Match 51.0%; Score 74; DB 20; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.00069;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 KYSLPELDYFSATPEYISGQINEXYT 28
 Db 25 KHSLPDLPYDYGALPEPHNAQIMQIHHS 52

RESULT 26
AAW98174
ID AAW98174 standard; Protein: 222 AA.
XX
AC AAW98174;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human manganese superoxide dismutase Q143D mutant.
XX
KM Superoxide dismutase; MnSOD; SOD; human; protein engineering;
KM enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
KM inflammation; reperfusion injury; therapy; mutant.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key
FH Peptide
FT Location/Qualifiers
FT 1..24
FT /note= "signal peptide"
FT Protein
FT 25..222
FT /note= "mature protein"
FT 50
FT /note= "His-26"
FT 54
FT /note= "His-30"
FT 58
FT /note= "Tyr-58"
FT 98
FT /note= "Tyr-74"
FT 167
FT /note= "Gln-143"
FT 183
FT /note= "Asp-159"
FT 185
FT /note= "Tyr-161"
FT Active-site
FT 187
FT /note= "His-163"
FT Misc-difference
FT 155
FT /label= Gln, Glu
FT 167
FT Misc-difference
FT 167
FT /note= "Gln replaces Asp in wild-type hMnSOD"
XX
PN W09913088-A1.
XX
XX 18-MAR-1999.
XX
PF 10-SEP-1998; 98MO-US18842.
XX
PR 10-SEP-1997; 97US-0927230.
XX
PA (UYFL) UNIV FLORIDA.
XX
PI Nick HS, Silverman DN;
XX
DR WPI; 1999-229242/19.
XX
PS New recombinant human manganese superoxide dismutase proteins
PS Claim 14; Page -; 61pp; English.
XX
CC This protein is a Q143D mutant of human manganese superoxide
CC dismutase (hMnSOD, see also AAW98170). Novel modified hMnSOD
CC proteins having catalytic activity which differs from natural
CC hMnSOD are claimed. The modified proteins (see also AAW98171-77)
CC exhibit reduced or no product inhibition, or have greater
CC activity, or both, compared to natural hMnSOD. The modifications
CC involve one or amino acid substitutions within the active site of
CC the enzyme, especially at residues His-26, His-30, Tyr-34, His-74,
CC Gln-143, Asp-159, Tyr-161 and His-163. Gln-143, Tyr-34 and His-30
CC are located near the active site metal, are highly conserved, and

CC are involved in a hydrogen bond relay which links the active site
CC metal-bound hydroxyl group to ordered solvent, and are thus all
CC potentially involved in catalytic activity, product inhibition
CC and/or enzyme stability. Modified hMnSODs, or expression vectors
CC in which a modified hMnSOD nucleic acid is linked to a promoter
CC (preferably mammalian), are used to protect a cell line from damage
CC caused by superoxide radicals (claimed). They can also be used to
CC treat subjects suffering from, or at risk of, cytotoxicity caused
CC by superoxide radicals (claimed). As such, they can be used as
CC antioxidants in the treatment of a variety of disorders, including
CC inflammation (claimed), reperfusion injury following ischemia
CC (claimed), and cellular damage caused by chemotherapeutic agents.
CC Note. The present sequence is not shown in the specification but
CC is derived from the hMnSOD sequence given on page 53-54.
XX
SQ Sequence 222 AA;
XX
Query Match 51.0%; Score 74; DB 20; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00069;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY 1 KYSLPELDYERFATEPYISQGINEIXYT 28
Db 25 KHSLPDLPYDYGALDPHINQIMQIHHS 52
XX
RESULT 27
AAW98175
ID AAW98175 standard; Protein: 222 AA.
XX
AC AAW98175;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human manganese superoxide dismutase Q143E mutant.
XX
XX
KM Superoxide dismutase; MnSOD; SOD; human; protein engineering;
KM enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
KM inflammation; reperfusion injury; therapy; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FH Peptide
FT Location/Qualifiers
FT 1..24
FT /note= "signal peptide"
FT Protein
FT 25..222
FT /note= "mature protein"
FT 50
FT /note= "His-26"
FT 54
FT /note= "His-30"
FT 58
FT /note= "Tyr-58"
FT 98
FT /note= "Tyr-74"
FT 167
FT /note= "Gln-143"
FT 183
FT /note= "Asp-159"
FT 185
FT /note= "Tyr-161"
FT Active-site
FT 187
FT /note= "His-163"
FT Misc-difference
FT 155
FT /label= Gln, Glu
FT 167
FT /note= "Gln replaces Glu in wild-type hMnSOD"
XX
PN W09913088-A1.
XX
PD 18-MAR-1999.
XX

PF 10-SEP-1998; 98WO-US18842.
 XX
 PR 10-SEP-1997; 97US-0927230.
 XX
 PA (UYFL) UNIV FLORIDA.
 XX
 PI Nick HS, Silverman DN;
 XX
 DR WPI; 1999-229242/19.
 XX
 FT New recombinant human manganese superoxide dismutase proteins
 XX
 PS Claim 14; Page -; 61pp; English.
 XX
 CC This protein is a Q143E mutant of human manganese superoxide
 CC dismutase (hmnSOD, see also AAW98170). Novel modified hmnSOD
 CC proteins having catalytic activity which differs from natural
 CC hmnSOD are claimed. The modified proteins (see also AAW98171-77)
 CC exhibit reduced or no product inhibition, or have greater
 CC activity, or both, compared to natural hmnSOD. The modifications
 CC involve one or amino acid substitutions within the active site of
 CC the enzyme, especially at residues His-26, His-30, Tyr-34, His-74,
 CC Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-34 and His-30
 CC are located near the active site metal, are highly conserved, and
 CC are involved in a hydrogen bond relay which links the active site
 CC metal-bound hydroxyl group to ordered solvent, and are thus all
 CC potentially involved in catalytic activity, product inhibition
 CC and/or enzyme stability. Modified hmnSODs, or expression vectors
 CC in which a modified hmnSOD nucleic acid is linked to a promoter
 CC (preferably mammalian), are used to protect a cell line from damage
 CC caused by superoxide radicals (claimed). They can also be used to
 CC treat subjects suffering from, or at risk of, cytotoxicity caused
 CC by superoxide radicals (claimed). As such, they can be used as
 CC antioxidants in the treatment of a variety of disorders, including
 CC inflammation (claimed), reperfusion injury following ischemia
 CC (claimed), and cellular damage caused by chemotherapeutic agents.
 CC Note. The present sequence is not shown in the specification but
 CC is derived from the hmnSOD sequence given on page 53-54.
 XX
 SQ Sequence 222 AA;
 Query Match 51.0%; Score 74; DB 20; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.00069;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KYSLPELDYFSATEPYISGOINEXYT 28
 DB 25 KHSLPDLPEYDYGALPHINAQIMQLHHS 52
 ID AAW98176 standard; Protein; 222 AA.
 XX
 AC AAW98176;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human manganese superoxide dismutase H30N mutant.
 XX
 KM Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KM enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
 KM inflammation; reperfusion injury; therapy; mutant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein /note= "signal peptide"
 FT 25..222
 FT /note= "mature protein"
 FT Active-site 50

FT /note= "His-26"
 FT Active-site 54
 FT /note= "His-30"
 FT Active-site 58
 FT /note= "Tyr-58"
 FT Active-site 98
 FT /note= "Tyr-74"
 FT Active-site 167
 FT /note= "Gln-143"
 FT Active-site 183
 FT /note= "Asp-159"
 FT Active-site 185
 FT /note= "Trp-161"
 FT Active-site 187
 FT /note= "His-163"
 FT Misc-difference 155
 FT /label= Gln, Glu
 FT Misc-difference 54
 FT /note= "His replaces Asn in wild-type hmnSOD"
 PN W09913086-A1.
 PD 18-MAR-1999.
 XX
 PF 10-SEP-1998; 98WO-US18842.
 XX
 PR 10-SEP-1997; 97US-0927230.
 XX
 PA (UYFL) UNIV FLORIDA.
 XX
 PI Nick HS, Silverman DN;
 XX
 DR WPI; 1999-229242/19.
 XX
 FT New recombinant human manganese superoxide dismutase proteins
 XX
 PS Claim 33; Page -; 61pp; English.
 XX
 CC This protein is a H30N mutant of human manganese superoxide
 CC dismutase (hmnSOD, see also AAW98170). Novel modified hmnSOD
 CC proteins having catalytic activity which differs from natural
 CC hmnSOD are claimed. The modified proteins (see also AAW98172-77)
 CC exhibit reduced or no product inhibition, or have greater
 CC activity, or both, compared to natural hmnSOD. The modifications
 CC involve one or amino acid substitutions within the active site of
 CC the enzyme, especially at residues His-26, His-30, Tyr-34, His-74,
 CC Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-34 and His-30
 CC are located near the active site metal, are highly conserved, and
 CC are involved in a hydrogen bond relay which links the active site
 CC metal-bound hydroxyl group to ordered solvent, and are thus all
 CC potentially involved in catalytic activity, product inhibition
 CC and/or enzyme stability. Modified hmnSODs, or expression
 CC vectors in which a modified hmnSOD nucleic acid is linked to a
 CC promoter (preferably mammalian), are used to protect a cell line
 CC from damage caused by superoxide radicals (claimed). They can also
 CC be used to treat subjects suffering from, or at risk of,
 CC cytotoxicity caused by superoxide radicals (claimed). As such,
 CC they can be used as antioxidants in the treatment of a variety of
 CC disorders, including inflammation (claimed), reperfusion injury
 CC following ischemia (claimed), and cellular damage caused by
 CC chemotherapeutic agents.
 CC Note. The present sequence is not shown in the specification but
 CC is derived from the hmnSOD sequence given on page 53-54.
 XX
 SQ Sequence 222 AA;
 Query Match 51.0%; Score 74; DB 20; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.00069;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KYSLPELDYFSATEPYISGOINEXYT 28
 DB 25 KHSLPDLPEYDYGALPHINAQIMQLHHS 52

RESULT 29
 AAW98177
 ID AAW98177 standard; Protein; 222 AA.
 AC AAW98177;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human manganese superoxide dismutase H30S mutant.
 XX
 KM Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KM enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
 KM inflammation; reperfusion injury; therapy; mutant.
 XX
 OS Homo sapiens.
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..24
 FT /note= "signal peptide"
 FT Protein 25..222
 FT /note= "mature protein"
 FT 50
 FT /note= "His-26"
 FT 54
 FT /note= "His-30"
 FT 58
 FT /note= "Tyr-58"
 FT 98
 FT /note= "Tyr-74"
 FT 167
 FT /note= "Gln-143"
 FT 183
 FT /note= "Asp-159"
 FT 185
 FT /note= "Trp-161"
 FT 187
 FT /note= "His-163"
 FT 155
 FT /label= Gln, Glu
 FT Misc-difference 54
 FT /note= "His replaces Ser in wild-type hMnSOD"
 FT
 XX
 XX W09913088-A1.
 XX
 XX 18-MAR-1999.
 XX
 XX 10-SEP-1998; 98MO-US18842.
 XX PF
 XX 10-SEP-1997; 97US-0927230.
 XX PR
 XX (UYFL) UNIV FLORIDA.
 XX PA
 XX Nick HS, Silverman DN;
 XX PI
 XX WPI; 1999-229242/19.
 XX DR
 XX
 XX New recombinant human manganese superoxide dismutase proteins
 XX
 XX Claim 33; Page -; 61pp; English.
 XX
 CC This protein is a H30S mutant of human manganese superoxide
 CC dismutase (hMnSOD, see also AAW98170). Novel modified hMnSOD
 CC proteins having catalytic activity which differs from natural
 CC hMnSOD are claimed. The modified proteins (see also AAW98172-77)
 CC exhibit reduced or no product inhibition, or have greater
 CC activity, or both, compared to natural hMnSOD. The modifications
 CC involve one or amino acid substitutions within the active site of
 CC the enzyme, especially at residues His-26, His-30, Tyr-34, His-74,
 CC Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-34 and His-30
 CC are located near the active site metal, are highly conserved, and

CC are involved in a hydrogen bond relay which links the active site
 CC metal-bound hydroxyl group to ordered solvent, and are thus all
 CC potentially involved in catalytic activity, product inhibition
 CC and/or enzyme stability. Modified hMnSODs, or expression
 CC vectors in which a modified hMnSOD nucleic acid is linked to a
 CC promoter (preferably mammalian), are used to protect a cell line
 CC from damage caused by superoxide radicals (claimed). They can also
 CC be used to treat subjects suffering from, or at risk of,
 CC cytotoxicity caused by superoxide radicals (claimed). As such,
 CC they can be used as antioxidants in the treatment of a variety of
 CC disorders, including inflammation (claimed), reperfusion injury
 CC following ischemia (claimed), and cellular damage caused by
 CC chemotherapeutic agents.
 CC Note. The present sequence is not shown in the specification but
 CC is derived from the hMnSOD sequence given on page 53-54.
 XX
 SQ Sequence 222 AA;
 Query Match 51.0%; Score 74; DB 20; Length 222;
 Best Local Similarity 42.3%; Pred. No. 0.00069;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KYSLPELDYERSATEPYISQINEIXYT 28
 DB 25 KHSLPDLPYDYGALPHEINQIQLHRS 52
 RESULT 30
 AAW98169
 ID AAW98169 standard; Protein; 222 AA.
 AC AAW98169;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human native manganese superoxide dismutase.
 XX
 KM Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KM enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
 KM inflammation; reperfusion injury; therapy.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..24
 FT /note= "signal peptide"
 FT Protein 25..222
 FT /note= "mature protein"
 FT 50
 FT /note= "His-26"
 FT 54
 FT /note= "His-30"
 FT 58
 FT /note= "Tyr-58"
 FT 98
 FT /note= "Tyr-74"
 FT 167
 FT /note= "Gln-143"
 FT 183
 FT /note= "Asp-159"
 FT 185
 FT /note= "Trp-161"
 FT 187
 FT /note= "His-163"
 FT Active-site
 W09913088-A1.
 18-MAR-1999.
 10-SEP-1998; 98MO-US18842.
 10-SEP-1997; 97US-0927230.


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FT /note= "mature protein"
XX
PN US6326003-B1.
XX
PD 04-DEC-2001.
XX
PF 14-OCT-1986; 86US-0918534.
XX
PR 14-OCT-1986; 86US-0918534.
XX
PA (CHIR ) CHIRON CORP.
XX
PI Halliwell RA, Bell GI, Mullenbach GT;
XX
DR WPI; 2002-129495/17.
DR N-PSDB; ABA94453.
XX
PT Treating inflammatory joint disease such as osteoarthritis, rheumatoid
PT arthritis and post ischemic tissue injury, comprises injecting human
PT manganese superoxide dismutase -
XX
PS Example 2; Fig 4; 14pp; English.
XX
CC The invention relates to a method of treating a patient with inflammatory
CC joint disease. The method involves intra-articularly injecting into the
CC afflicted joint a solution of human manganese superoxide dismutase
CC (hSODm). The treatment is used to treat an inflammatory joint disease,
CC particularly osteoarthritis or rheumatoid arthritis. The method can also
CC be used to treat post ischemic tissue injury. The present sequence
CC represents the hSODm polypeptide.
XX
SQ Sequence 222 AA;
XX
Query Match 51.0%; Score 74; DB 23; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00069;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
OY 1 KYSLPELDYFSGATEPYISQGINEIXYT 28
Db 25 KHSLPDLPEYDYGALPHEPHINQIMQLHHS 52
XX
RESULT 39
AAP80551
ID AAP80551 standard; protein; 223 AA.
XX
AC AAP80551;
XX
DT 22-OCT-1990 (first entry)
XX
DE Human manganese superoxide dismutase.
XX
KW Human manganese superoxide dismutase; oxygen free radicals.
XX
OS Homo sapiens.
XX
PN EP284105-A.
XX
PD 28-SEP-1988.
XX
PF 25-MAR-1988; 88EP-0104880.
XX
PR 26-FEB-1988; 88US-0161117.
PR 27-MAR-1987; 87US-0032734.
XX
PA (BIOT-) BIO-TECHNOLOGY GENERAL CORPORATION.
XX
PI Hartman JR, Beck Y, Nimrod A;
XX
DR WPI; 1988-272584/39.
DR N-PSDB; AAN81158.
XX
PT Recombinant human manganese superoxidedismutase -

```

```

PT used for treating, e.g. reperfusion injury, inflammation,
PT arthritis, bronchial pulmonary dysplasia or lung fibrosis.
XX
PS Disclosure; ; pp; English.
XX
CC Human manganese superoxide dismutase or its analogues or mutants is
CC used to treat subjects suffering from a disorder associated with the
CC generation of oxygen free radicals, eg reperfusion injury following
CC ischaemia or organ transplant, inflammation caused by Crohn's disease
CC or colitis, synovial inflammation induced by bacterial lipopolysaccharide
CC endotoxin, arthritis, bronchial pulmonary dysplasia or lung fibrosis
CC by radiation or an anti-neoplastic agent, eg bleomycin. It can also be
CC used to prolong the life of excised organs. As it remains in the serum
CC for long periods, it may be used as a long-acting therapeutic agent.
CC Dosage is 1-200 mg/joint or 1-100, esp. 3-50, mg/kg body wt. daily.
CC It is given intra-articularly, intratracheally, sc or iv.
XX
SQ Sequence 223 AA;
XX
Query Match 51.0%; Score 74; DB 9; Length 223;
Best Local Similarity 42.9%; Pred. No. 0.0007;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
OY 1 KYSLPELDYFSGATEPYISQGINEIXYT 28
Db 26 KHSLPDLPEYDYGALPHEPHINQIMQLHHS 53
XX
RESULT 40
AAV55849
ID AAV55849 standard; Protein; 226 AA.
XX
AC AAV55849;
XX
DT 06-MAR-2000 (first entry)
XX
DE Human manganese superoxide dismutase (MnSOD) mutant protein.
XX
KW Manganese superoxide dismutase; MnSOD; ECSOD; proteoglycan; human;
KW endothelial; oxidative damage; pulmonary inflammatory injury; cancer;
KW lung disease; hypoxia; ischemia; reperfusion injury; arthritis;
KW hyperoxia; atherosclerosis; lupus erythematosus; hypertension;
KW neutrophil-mediated inflammation; mutant.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN W09958547-A1.
XX
PD 18-NOV-1999.
XX
PF 06-MAY-1999; 99WO-US09921.
XX
PR 08-MAY-1998; 98US-0075019.
XX
PA (WEBB-) WEBB-WARING INST BIOMEDICAL RES.
XX
PI McCord JM, Gao B, Flores SC;
XX
DR WPI; 2000-062283/05.
DR N-PSDB; AA239781, AA239782.
XX
PT Modified manganese superoxide dismutase, methods of production and
PT antibodies -
XX
PS Claim 29; Page 74-75; 83pp; English.
XX
CC The invention provides a nucleic acid molecule encoding a genetically
CC modified manganese superoxide dismutase (MnSOD). The nucleic acid
CC comprises a first nucleic acid sequence encoding an enzymatically active
CC portion of MnSOD; and a second nucleic acid sequence encoding a peptide
CC (ECSOD) that binds to polyanionic polysaccharides or proteoglycans on
CC endothelial cell surfaces. The protein protects a mammal, especially

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OM protein - protein search, using sw model

Run on: April 9, 2003, 14:00:55 ; Search time 14.3119 Seconds

(without alignments)
279.314 Million cell updates/sec

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Perfect score: 30

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	10	23.3	23	ABW05612	S. cerevisiae mang
3	7	23.3	407	AAW61416	Arabidopsis thalia
4	7	23.3	512	AAW614175	Arabidopsis thalia
5	7	23.3	521	AAW614175	Arabidopsis thalia
6	6	20.0	7	ABW08465	Mouse tumour speci
7	6	20.0	7	ABW08476	Peptide related to
8	6	20.0	9	ABW08466	Mouse tumour speci
9	6	20.0	10	ABW08467	Mouse tumour speci
10	6	20.0	19	ABW66263	IGE fcepsion RI b

11	6	20.0	20	23	ABW08468	Mouse tumour speci
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13	6	20.0	50	22	ABW36416	Peptide #3922 enco
14	6	20.0	50	22	AAW57176	Human brain expres
15	6	20.0	50	22	AAW69579	Human bone marrow
16	6	20.0	50	22	AAW17397	Peptide #3831 enco
17	6	20.0	50	22	AAW29917	Human peptide enco
18	6	20.0	52	22	ABW39201	Human peptide enco
19	6	20.0	52	22	AAW58434	Propionibacterium
20	6	20.0	52	22	AAW5746	Propionibacterium
21	6	20.0	60	22	ABW14809	Human nervous syst
22	6	20.0	62	23	ABW08458	Mouse tumour speci
23	6	20.0	81	19	AAW75089	Human secreted pro
24	6	20.0	136	22	AAW01578	Human polypeptide
25	6	20.0	146	21	AAW6397	Human prostate can
26	6	20.0	163	23	ABW6232	Streptococcus poly
27	6	20.0	188	19	AAW53253	Candida albicans f
28	6	20.0	200	22	AAW32973	C. glutamicum prote
29	6	20.0	207	22	AAW00514	C. melanoscola sup
30	6	20.0	207	23	ABW47790	Listeria monocytog
31	6	20.0	214	20	AAW34657	C. pneumoniae prot
32	6	20.0	221	22	AAW94056	Human protein sequ
33	6	20.0	226	22	AAW78026	Piscirickettsia sa
34	6	20.0	294	21	AAW49754	Arabidopsis thalia
35	6	20.0	294	21	AAW50274	Arabidopsis thalia
36	6	20.0	311	21	AAW29351	Arabidopsis thalia
37	6	20.0	312	21	AAW49753	Arabidopsis thalia
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54	6	20.0	901	22	AAW97741	H. annus LOX prote
55	6	20.0	934	23	ABW34123	Human protein from
56	6	20.0	1023	22	AAW11436	D. discoideum ster
57	6	20.0	1596	23	AAW20271	Human lung, specifi
58	5	16.7	5	23	ABW66201	Phage display g3 1
59	5	16.7	9	17	AAW49494	Human leucocyte an
60	6	16.7	9	22	AAW23850	Human MHC class I
61	5	16.7	9	22	AAW24148	Human MHC class I
62	5	16.7	9	22	AAW24221	Human MHC class I
63	5	16.7	9	22	AAW12507	Human HIV-1 Th-CTL
64	5	16.7	9	22	AAW49390	Simian immunodef
65	5	16.7	9	23	ABW34938	Human bone marrow
66	5	16.7	10	22	AAW23867	Human MHC class I
67	5	16.7	10	22	AAW23986	Human MHC class I
68	5	16.7	10	22	AAW24059	Human MHC class I
69	5	16.7	10	22	AAW24179	Human MHC class I
70	5	16.7	11	12	AAW10552	Human MHC class I
71	5	16.7	12	17	AAW07947	Residues 429-444 o
72	5	16.7	13	21	AAW65886	gpi20 peptide 1029
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74	5	16.7	14	22	AAW98508	Human peptide #178
75	5	16.7	15	19	AAW76955	Human peptide #178
76	5	16.7	15	19	AAW76952	Fusion immunoglob
77	5	16.7	15	23	AAW10681	Human immunoglob
78	5	16.7	16	17	AAW12610	Peptide A155 conta
79	5	16.7	17	10	AAW91153	Artificial peptide
80	5	16.7	18	21	AAW79501	Eimeria tenella SO
81	5	16.7	18	23	ABW66234	IGE fcepsion RI b
82	5	16.7	19	17	AAW07951	gpi20 peptide DW-3
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87	5	16.7	20	23	ABG66642	Phage displayed g3	160	5	16.7	21	23	ABG66629	Phage displayed g3
88	5	16.7	21	22	ABG66475	Synthetic HAV p3d	161	5	16.7	21	23	ABG66637	Phage displayed g3
89	5	16.7	21	22	ABG66200	Phage displayed g3	162	5	16.7	21	23	ABG66638	Phage displayed g3
90	5	16.7	21	23	ABG66202	IGE Fcepillon Ri b	163	5	16.7	21	23	ABG66639	Phage displayed g3
91	5	16.7	21	23	ABG66218	IGE Fcepillon Ri b	164	5	16.7	21	23	ABG66640	Phage displayed g3
92	5	16.7	21	23	ABG66221	IGE Fcepillon Ri b	165	5	16.7	21	23	ABG66641	Phage displayed g3
93	5	16.7	21	23	ABG66252	IGE Fcepillon Ri b	166	5	16.7	23	12	AAH11644	Peptide 1017/88 ba
94	5	16.7	21	23	ABG66253	IGE Fcepillon Ri b	167	5	16.7	23	21	AAV70282	Plasmidum falcipt
95	5	16.7	21	23	ABG66254	IGE Fcepillon Ri b	168	5	16.7	23	23	ABG66625	IGE Fcepillon Ri b
96	5	16.7	21	23	ABG66264	IGE Fcepillon Ri b	169	5	16.7	23	12	AAH11630	Peptide 1029/16 ba
97	5	16.7	21	23	ABG66273	IGE Fcepillon Ri b	170	5	16.7	24	14	AAH33837	Cluster peptide PC
98	5	16.7	21	23	ABG66359	IGE Fcepillon Ri b	171	5	16.7	24	15	AAH33845	HIV-1 gp120-35 epi
99	5	16.7	21	23	ABG66460	IGE Fcepillon Ri b	172	5	16.7	24	16	AAH66431	PC1US 3-18 (421-44
100	5	16.7	21	23	ABG66461	IGE Fcepillon Ri b	173	5	16.7	24	20	AAH05353	HIV-1 C1UVAAC pep1
101	5	16.7	21	23	ABG66462	IGE Fcepillon Ri b	174	5	16.7	24	23	ABG66271	IGE Fcepillon Ri b
102	5	16.7	21	23	ABG66463	IGE Fcepillon Ri b	175	5	16.7	24	23	ABG66588	IGE Fcepillon Ri b
103	5	16.7	21	23	ABG66464	IGE Fcepillon Ri b	176	5	16.7	24	23	ABG66589	IGE Fcepillon Ri b
104	5	16.7	21	23	ABG66465	IGE Fcepillon Ri b	177	5	16.7	24	23	ABG66590	IGE Fcepillon Ri b
105	5	16.7	21	23	ABG66480	IGE Fcepillon Ri b	178	5	16.7	24	23	ABG66591	IGE Fcepillon Ri b
106	5	16.7	21	23	ABG66510	IGE Fcepillon Ri b	179	5	16.7	24	23	ABG66592	IGE Fcepillon Ri b
107	5	16.7	21	23	ABG66511	IGE Fcepillon Ri b	180	5	16.7	24	23	ABG66593	IGE Fcepillon Ri b
108	5	16.7	21	23	ABG66512	IGE Fcepillon Ri b	181	5	16.7	24	23	ABG66594	IGE Fcepillon Ri b
109	5	16.7	21	23	ABG66513	IGE Fcepillon Ri b	182	5	16.7	24	23	ABG66595	IGE Fcepillon Ri b
110	5	16.7	21	23	ABG66514	IGE Fcepillon Ri b	183	5	16.7	24	23	ABG66596	IGE Fcepillon Ri b
111	5	16.7	21	23	ABG66515	IGE Fcepillon Ri b	184	5	16.7	24	23	ABG66597	IGE Fcepillon Ri b
112	5	16.7	21	23	ABG66516	IGE Fcepillon Ri b	185	5	16.7	25	8	AAH71144	Anti-HIV peptide 5
113	5	16.7	21	23	ABG66517	IGE Fcepillon Ri b	186	5	16.7	25	9	AAH80749	Sequence of peptid
114	5	16.7	21	23	ABG66518	IGE Fcepillon Ri b	187	5	16.7	25	13	AAH27331	Peptide corresp. c
115	5	16.7	21	23	ABG66519	IGE Fcepillon Ri b	188	5	16.7	26	20	AAH25833	Human secreted pro
116	5	16.7	21	23	ABG66520	IGE Fcepillon Ri b	189	5	16.7	26	23	ABG66272	IGE Fcepillon Ri b
117	5	16.7	21	23	ABG66521	IGE Fcepillon Ri b	190	5	16.7	26	23	ABG66598	IGE Fcepillon Ri b
118	5	16.7	21	23	ABG66522	IGE Fcepillon Ri b	191	5	16.7	26	23	ABG66599	IGE Fcepillon Ri b
119	5	16.7	21	23	ABG66523	IGE Fcepillon Ri b	192	5	16.7	26	23	ABG66600	IGE Fcepillon Ri b
120	5	16.7	21	23	ABG66524	IGE Fcepillon Ri b	193	5	16.7	26	23	ABG66601	IGE Fcepillon Ri b
121	5	16.7	21	23	ABG66525	IGE Fcepillon Ri b	194	5	16.7	26	23	ABG66602	IGE Fcepillon Ri b
122	5	16.7	21	23	ABG66526	IGE Fcepillon Ri b	195	5	16.7	27	15	AAH63844	HIV-1 gp120-34 epi
123	5	16.7	21	23	ABG66527	IGE Fcepillon Ri b	196	5	16.7	28	11	AAH03100	Human immunodefict
124	5	16.7	21	23	ABG66528	IGE Fcepillon Ri b	197	5	16.7	28	11	AAH09346	Sequence of centra
125	5	16.7	21	23	ABG66529	IGE Fcepillon Ri b	198	5	16.7	28	12	AAH11631	Peptide 1005/45 ba
126	5	16.7	21	23	ABG66530	IGE Fcepillon Ri b	199	5	16.7	28	13	AAH23032	Cyclic 1005-45 pep
127	5	16.7	21	23	ABG66531	IGE Fcepillon Ri b	200	5	16.7	28	16	AAH67718	HIV isolate LAI-II
128	5	16.7	21	23	ABG66564	IGE Fcepillon Ri b	201	5	16.7	28	19	AAH54910	HIV gp120 envelope
129	5	16.7	21	23	ABG66565	IGE Fcepillon Ri b	202	5	16.7	28	19	AAH54911	HIV gp120 envelope
130	5	16.7	21	23	ABG66566	IGE Fcepillon Ri b	203	5	16.7	28	19	AAH54914	HIV gp120 envelope
131	5	16.7	21	23	ABG66567	IGE Fcepillon Ri b	204	5	16.7	28	19	AAH54915	HIV gp120 envelope
132	5	16.7	21	23	ABG66568	IGE Fcepillon Ri b	205	5	16.7	28	19	AAH54909	HIV gp120 envelope
133	5	16.7	21	23	ABG66569	IGE Fcepillon Ri b	206	5	16.7	29	13	AAH27330	Peptide corresp. c
134	5	16.7	21	23	ABG66570	IGE Fcepillon Ri b	207	5	16.7	29	15	AAH58550	HIV env CD4 bindin
135	5	16.7	21	23	ABG66571	IGE Fcepillon Ri b	208	5	16.7	29	22	AAH12470	HIV Th-CTL peptide
136	5	16.7	21	23	ABG66572	IGE Fcepillon Ri b	209	5	16.7	29	22	AAH49394	Simian immunodefict
137	5	16.7	21	23	ABG66573	IGE Fcepillon Ri b	210	5	16.7	29	23	AAH70233	HIV/SIV TH-CTL epi
138	5	16.7	21	23	ABG66574	IGE Fcepillon Ri b	211	5	16.7	32	19	AAH76910	Fusion immunoglobi
139	5	16.7	21	23	ABG66575	IGE Fcepillon Ri b	212	5	16.7	33	23	ABG40641	Human peptide enco
140	5	16.7	21	23	ABG66576	IGE Fcepillon Ri b	213	5	16.7	34	22	AAH48734	Mouise liver growth
141	5	16.7	21	23	ABG66577	IGE Fcepillon Ri b	214	5	16.7	34	23	AAH10677	Peptide T35S conta
142	5	16.7	21	23	ABG66578	IGE Fcepillon Ri b	215	5	16.7	35	12	AAH13121	Binding site of G3
143	5	16.7	21	23	ABG66579	IGE Fcepillon Ri b	216	5	16.7	36	12	AAH14592	HIV gp120-derived
144	5	16.7	21	23	ABG66580	IGE Fcepillon Ri b	217	5	16.7	36	22	AAH64773	Human secreted pro
145	5	16.7	21	23	ABG66581	IGE Fcepillon Ri b	218	5	16.7	37	22	AAH63980	Amino acid sequenc
146	5	16.7	21	23	ABG66582	IGE Fcepillon Ri b	219	5	16.7	39	16	AAH66445	PC1US 3-18 (421-44
147	5	16.7	21	23	ABG66583	IGE Fcepillon Ri b	220	5	16.7	39	16	AAH66408	PC1US 3-18 (421-44
148	5	16.7	21	23	ABG66584	IGE Fcepillon Ri b	221	5	16.7	39	19	AAH66088	S. pneumoniae deri
149	5	16.7	21	23	ABG66585	IGE Fcepillon Ri b	222	5	16.7	39	20	AAH05346	HIV-1 C1UVAAC pep1
150	5	16.7	21	23	ABG66586	IGE Fcepillon Ri b	223	5	16.7	39	20	AAH05339	HIV-1 C1UVAAC pep1
151	5	16.7	21	23	ABG66587	IGE Fcepillon Ri b	224	5	16.7	39	22	AAH28435	Peptide #1086 enco
152	5	16.7	21	23	ABG66617	Phage displayed g3	225	5	16.7	39	22	AAH33617	Peptide #1123 enco
153	5	16.7	21	23	ABG66619	Phage displayed g3	226	5	16.7	39	22	AAH19072	Protein #1071 enco
154	5	16.7	21	23	ABG66620	Phage displayed g3	227	5	16.7	39	22	AAH07857	Synthetic peptide
155	5	16.7	21	23	ABG66621	Phage displayed g3	228	5	16.7	39	22	AAH54350	Human brain expres
156	5	16.7	21	23	ABG66624	Phage displayed g3	229	5	16.7	39	22	AAH66791	Human Bone marrow

230	5	16.7	39	22	AA014657	Peptide #1091 enco
231	5	16.7	39	22	AA027076	Peptide #1113 enco
232	5	16.7	39	22	AA02380	Peptide #1062 enco
233	5	16.7	39	23	ABG68641	HIV-1 gp160 V3 loc
234	5	16.7	39	23	ABG68648	HIV-1 gp160 V3 loc
235	5	16.7	39	23	ABG36446	Human peptide enco
236	5	16.7	40	20	AAW93231	Human cytochrome p
237	5	16.7	40	20	AAW93232	Human cytochrome p
238	5	16.7	41	22	ABG22627	Novel human diagno
239	5	16.7	44	14	AA041470	HIV-1 gp160/120 fr
240	5	16.7	45	15	AA060792	HIV virus-1 gp120
241	5	16.7	46	22	AB095935	Human testicular a
242	5	16.7	46	22	AAW95238	Human reproductiv
243	5	16.7	49	7	AA061106	Protein encoded by
244	5	16.7	49	22	AA040487	Human SGP014 phosp
245	5	16.7	51	22	ABG29596	Novel human diagno
246	5	16.7	52	21	AA058752	Arabidopsis thalia
247	5	16.7	52	22	AAU18951	Novel lung cancer
248	5	16.7	52	22	AAU17963	Novel human respir
249	5	16.7	54	16	AA071644	Circumsporozolite R
250	5	16.7	54	22	AAU14653	Novel bone marrow
251	5	16.7	55	23	ABP07553	Human ORFX protein
252	5	16.7	56	7	AA061109	Protein encoded by
253	5	16.7	56	7	AA061107	Protein encoded by
254	5	16.7	56	23	ABP33744	Human ORF2717 prot
255	5	16.7	57	22	AAU039400	Protonibacterium
256	5	16.7	57	23	ABP08560	Human ORFX protein
257	5	16.7	58	12	AA014591	HIV gp120-derived
258	5	16.7	58	19	AA040522	Chicken p75 neurot
259	5	16.7	58	19	AA040520	Human p75 neurotro
260	5	16.7	58	19	AA040521	Rat p75 neurotrophin
261	5	16.7	60	22	AB014861	Human nervous syst
262	5	16.7	61	20	AA039194	M. tuberculosis an
263	5	16.7	61	20	AA039051	M. tuberculosis re
264	5	16.7	61	23	ABP34409	Human ORF3382 prot
265	5	16.7	62	21	AA015941	Arabidopsis thalia
266	5	16.7	62	22	AAU04069	Protonibacterium
267	5	16.7	63	22	AAU21392	Human novel foetal
268	5	16.7	63	22	AA085133	Human immune/haema
269	5	16.7	64	22	AA095535	Human reproductiv
270	5	16.7	65	22	AB028619	Peptide #1270 enco
271	5	16.7	65	22	AB033802	Peptide #1308 enco
272	5	16.7	65	22	AB019245	Protein #1244 enco
273	5	16.7	65	22	AA054568	Human brain expres
274	5	16.7	65	22	AA066975	Human bone marrow
275	5	16.7	65	22	AA014835	Peptide #1269 enco
276	5	16.7	65	22	AA027262	Peptide #1299 enco
277	5	16.7	65	22	AA025560	Peptide #1242 enco
278	5	16.7	66	23	ABG36632	Human peptide enco
279	5	16.7	66	16	AA066442	Plasmodium falcipa
280	5	16.7	66	20	AA000258	Human secreted pro
281	5	16.7	66	22	AAU44897	Protonibacterium
282	5	16.7	66	22	AA01076	Human immune/haema
283	5	16.7	68	15	AA047845	HIV gp120 coat pro
284	5	16.7	69	22	AA075957	Human colon cancer
285	5	16.7	70	22	ABG27298	Novel human diagno
286	5	16.7	71	22	ABG12595	Novel human diagno
287	5	16.7	73	23	ABP1128	Human ORFX protein
288	5	16.7	74	23	ABP32966	Human ORF139 prot
289	5	16.7	75	22	AA083306	Human immune/haema
290	5	16.7	76	20	AA094643	TNF-R extracellula
291	5	16.7	76	22	AA069195	Human TNF-R extrac
292	5	16.7	77	22	AB041024	Peptide #8530 enco
293	5	16.7	78	20	AA059900	Human normal pancr
294	5	16.7	78	20	AA059919	Human normal pancr
295	5	16.7	78	22	AAU64977	Protonibacterium
296	5	16.7	79	23	AAU075600	Human type IV coll
297	5	16.7	80	22	AAU07528	Protonibacterium
298	5	16.7	80	22	ABG1296	Novel human diagno
299	5	16.7	81	22	AA089740	Human immune/haema
300	5	16.7	81	23	AAU081025	Human alpha2 macro
301	5	16.7	83	11	AA030106	CD4 receptor prote
302	5	16.7	83	11	AA09349	Sequence corresep.

303	5	16.7	83	22	AAU23141	Novel human enzyme
304	5	16.7	84	21	AA015357	Arabidopsis thalia
305	5	16.7	84	22	ABG26358	Novel human diagno
306	5	16.7	85	22	AAU14747	Novel bone marrow
307	5	16.7	85	23	AAU10479	HIV/Siv TH-CTL epi
308	5	16.7	87	21	AA036837	Arabidopsis thalia
309	5	16.7	88	22	AA092974	Human digestive sy
310	5	16.7	88	22	AAU20070	Human liver associ
311	5	16.7	88	23	ABP40931	Human liver antigen
312	5	16.7	88	23	AAU75607	Human type IV coll
313	5	16.7	88	23	AAU75608	Human type IV coll
314	5	16.7	90	8	AA081887	Sequence of human
315	5	16.7	90	21	AA036836	Arabidopsis thalia
316	5	16.7	90	21	AA020990	Human secreted pro
317	5	16.7	91	22	AB040418	Peptide #7924 enco
318	5	16.7	91	22	AB024781	Protein #6780 enco
319	5	16.7	91	22	AA061225	Human brain expres
320	5	16.7	91	22	AA073945	Human bone marrow
321	5	16.7	91	22	AA034123	Human ovarian and/
322	5	16.7	92	22	AB010771	Human peptide enco
323	5	16.7	92	22	AA020771	Human reproductiv
324	5	16.7	92	22	AA094434	Human reproductiv
325	5	16.7	92	22	AA089608	Human immune/haema
326	5	16.7	93	22	AA000268	Human polypeptide
327	5	16.7	94	20	AA029670	Human src-family k
328	5	16.7	94	22	AAU08732	Src-family kinase
329	5	16.7	94	22	AA042147	Human polypeptide
330	5	16.7	94	23	ABP34090	Human ORF3063 prot
331	5	16.7	95	22	AA089809	Human immune/haema
332	5	16.7	95	23	ABP02403	Human ORFX protein
333	5	16.7	96	21	AA062138	Protonibacterium
334	5	16.7	97	21	AA025332	Eucalyptus grandis
335	5	16.7	99	21	AA057752	Arabidopsis thalia
336	5	16.7	99	21	AA059853	Arabidopsis thalia
337	5	16.7	99	21	AA060252	Arabidopsis thalia
338	5	16.7	99	22	AA041923	Protonibacterium
339	5	16.7	99	23	ABP28999	Streptococcus poly
340	5	16.7	100	23	AB089123	Human polypeptide
341	5	16.7	101	23	ABP06470	Human ORFX protein
342	5	16.7	102	21	AA04069	Human secreted pro
343	5	16.7	102	21	AA04086	Human secreted pro
344	5	16.7	102	23	ABP34257	Human structural p
345	5	16.7	102	23	ABP04321	Human ORFX protein
346	5	16.7	104	23	ABP06168	Human ORFX protein
347	5	16.7	105	22	AB03916	Human musculoskele
348	5	16.7	105	23	AB080297	Human polypeptide
349	5	16.7	106	22	AAU1827	Protonibacterium
350	5	16.7	108	21	AA064613	Nonclassical cadhe
351	5	16.7	109	23	ABP05073	Human Abeta bindin
352	5	16.7	111	21	AA097159	Micromonospora eve
353	5	16.7	111	22	AAU04889	Human alpha2 macro
354	5	16.7	111	23	AAU081024	Human alpha2 macro
355	5	16.7	115	13	AA029911	Type C natriuretic
356	5	16.7	116	19	AA080401	A secreted protein
357	5	16.7	116	21	AA032655	Eucalyptus grandis
358	5	16.7	117	23	ABP32154	Human ORF1127 prot
359	5	16.7	120	18	AAU27855	Staphylococcus aur
360	5	16.7	120	22	AA063953	Protonibacterium
361	5	16.7	120	22	AAU23179	Novel human enzyme
362	5	16.7	120	22	AAU21843	Novel human neopla
363	5	16.7	121	21	AA036835	Arabidopsis thalia
364	5	16.7	123	21	AA027109	Zea mays protein f
365	5	16.7	123	23	AAU75554	Human type IV coll
366	5	16.7	125	22	AAU27552	Human G-protein co
367	5	16.7	126	21	AA057751	Arabidopsis thalia
368	5	16.7	126	21	AA060251	Arabidopsis thalia
369	5	16.7	126	23	AAU81023	Human alpha2 macro
370	5	16.7	127	20	AA013140	Human secreted pro
371	5	16.7	127	22	AA050235	Catalpa lysine dec
372	5	16.7	127	23	AAU76417	AbMy-W1 transcript
373	5	16.7	129	21	AA058374	AbMy-W1 transcript
374	5	16.7	129	21	AA058375	BDMV transcription
375	5	16.7	129	21	AA058376	BDMV transcription

376	5	16.7	129	21	AAVS6384	TMV transcription	449	5	16.7	173	22	AAAB64410	Amino acid sequenc
377	5	16.7	132	23	AAU75597	Human type IV coll	450	5	16.7	174	21	AAAG47393	Arabinidopsis thalia
378	5	16.7	133	21	AAAB25166	Eucalyptus grandis	451	5	16.7	178	13	AAAR22564	Antibody specific
379	5	16.7	133	21	AAAG19951	Arabinidopsis thalia	452	5	16.7	178	21	AAAG16324	Arabinidopsis thalia
380	5	16.7	134	21	AAAG47394	Arabinidopsis thalia	453	5	16.7	178	21	AAAG44500	Arabinidopsis thalia
381	5	16.7	134	22	ABG28264	Novel human diegno	454	5	16.7	178	21	AAAG53228	Arabinidopsis thalia
382	5	16.7	135	20	AAVS9796	Human normal ovari	455	5	16.7	179	10	AAAP92014	HIV portion of HTL
383	5	16.7	135	22	ABG07756	Novel human diegno	456	5	16.7	179	10	AAAP93537	HIV portion of fus
384	5	16.7	135	22	ABAB48396	Listeria monocytog	457	5	16.7	179	23	ABBB1829	Hericidially activ
385	5	16.7	137	18	AAAB23387	Goat cytotoxic 14	458	5	16.7	180	11	AAAR07280	Circumsporozite a
386	5	16.7	137	19	AAW71473	Amino acid sequenc	459	5	16.7	180	22	AAAG78506	Recombinant HIV en
387	5	16.7	137	19	AAW50927	Protein p14 useful	460	5	16.7	181	15	AAAR9610	HIV-1 gp120 conser
388	5	16.7	137	19	AAW56483	14 kDa protein com	461	5	16.7	181	21	AAAG06198	Arabinidopsis thalia
389	5	16.7	137	20	AAV32859	Human heat shock p	462	5	16.7	181	21	AAAG47704	Arabinidopsis thalia
390	5	16.7	137	21	AAAB36233	Goat recombinant U	463	5	16.7	181	22	ABG16191	Novel human diegno
391	5	16.7	138	22	AAAG31625	Arabinidopsis thalia	464	5	16.7	181	22	ABG329332	Novel human diegno
392	5	16.7	138	22	AAU030541	Novel human secret	465	5	16.7	182	21	ABG44356	Arabinidopsis thalia
393	5	16.7	138	22	AAAB92929	Human protein sequ	466	5	16.7	182	22	ABG16763	Novel human diegno
394	5	16.7	139	21	AAAB36234	Goat natural UK114	467	5	16.7	182	22	AAAB93656	Human protein sequ
395	5	16.7	140	21	AAAG14313	Arabinidopsis thalia	468	5	16.7	183	22	ABBS8960	Drosophila melanog
396	5	16.7	140	21	AAAG27696	Arabinidopsis thalia	469	5	16.7	185	5	AAAP40154	Sequence of human
397	5	16.7	140	21	AAAG28604	Arabinidopsis thalia	470	5	16.7	185	5	AAAP40155	Sequence of human
398	5	16.7	140	21	AAAG53204	Arabinidopsis thalia	471	5	16.7	185	10	AAAP94632	Amino acid sequenc
399	5	16.7	140	21	AAAG53209	Arabinidopsis thalia	472	5	16.7	185	23	ABG61819	Prostate cancer-as
400	5	16.7	140	21	AAAG53232	Arabinidopsis thalia	473	5	16.7	186	22	ABG15763	Novel human diegno
401	5	16.7	140	22	AAU54719	Proionlactacertium	474	5	16.7	187	22	AAU87327	Novel central nerv
402	5	16.7	140	22	AAAG89765	C glutamicum prote	475	5	16.7	189	19	AAAN29746	TNF related endoth
403	5	16.7	141	21	AAV82474	Mouse Apg12 protei	476	5	16.7	189	21	AAAG46008	Arabinidopsis thalia
404	5	16.7	141	22	ABG25718	Novel human diegno	477	5	16.7	189	22	ABBS92936	Human testicular a
405	5	16.7	142	21	AAAG44357	Arabinidopsis thalia	478	5	16.7	189	22	AAU87615	Novel central nerv
406	5	16.7	142	22	ABBI12182	Human neutral prot	479	5	16.7	189	22	AAW52239	Human reproductive
407	5	16.7	146	21	AAAG06199	Arabinidopsis thalia	480	5	16.7	189	22	AAAG3564	Human polypeptide
408	5	16.7	146	22	AAAG47705	Arabinidopsis thalia	481	5	16.7	189	22	AAAG3639	Human polypeptide
409	5	16.7	146	22	AAE00895	Human TREPA (TNP r	482	5	16.7	189	22	AAE00892	Human URAfiag TRP
410	5	16.7	147	22	AAAB96299	Ptactive helix-tur	483	5	16.7	189	22	AAU19951	Novel human calcit
411	5	16.7	147	23	ABP41536	Human ovarian ancl	484	5	16.7	191	19	AAAG4139	Human interferon r
412	5	16.7	148	21	AAAG51579	Arabinidopsis thalia	485	5	16.7	191	19	AAAG62287	Human protein phos
413	5	16.7	148	22	AAU39237	Proionlactacertium	486	5	16.7	191	19	AAAG51215	Amino acid sequenc
414	5	16.7	149	21	AAAG24388	Arabinidopsis thalia	487	5	16.7	191	21	AAAG14312	Arabinidopsis thalia
415	5	16.7	149	21	AAAG51576	Arabinidopsis thalia	488	5	16.7	191	21	AAAG27695	Arabinidopsis thalia
416	5	16.7	149	23	AAAG51582	Arabinidopsis thalia	489	5	16.7	191	21	AAAG32321	Arabinidopsis thalia
417	5	16.7	149	23	ABP28394	Streptococcus poly	490	5	16.7	191	23	AAU75596	Human type IV coll
418	5	16.7	149	23	ABBA48303	Listeria monocytog	491	5	16.7	193	21	AAAG28603	Arabinidopsis thalia
419	5	16.7	150	15	AAAS8552	MEAV vaccine. Syn	492	5	16.7	193	21	AAAG53208	Arabinidopsis thalia
420	5	16.7	151	22	ABG21145	Novel human diegno	493	5	16.7	193	22	ABBE2640	Drosophila melanog
421	5	16.7	153	23	AAU81020	Human alpha2 macro	494	5	16.7	194	14	AAAR39483	Human apoaIV mutel
422	5	16.7	157	22	AAU25566	Human G Protein-Co	495	5	16.7	195	22	ABG00698	Novel human diegno
423	5	16.7	159	21	AAAB25331	Eucalyptus grandis	496	5	16.7	196	22	AAAG1796	C glutanicum prote
424	5	16.7	160	22	AAAM51676	Human ATP depend	497	5	16.7	196	22	AAAB74038	Staphylococcus aur
425	5	16.7	160	23	AAOL6936	Human ATP-depend	498	5	16.7	196	22	AAAB49627	GTP-binding protei
426	5	16.7	161	21	AAAG19950	Arabinidopsis thalia	499	5	16.7	197	22	AAAB60072	Human protein SEQ
427	5	16.7	161	21	AAAG46009	Arabinidopsis thalia	500	5	16.7	197	22	AAAB79505	Hericidially activ
428	5	16.7	161	22	ABG02697	Novel human diegno	501	5	16.7	200	23	ABBB92146	Arabinidopsis thalia
429	5	16.7	162	13	AAAR21140	Polypeptide encode	502	5	16.7	205	21	AAAG53203	Arabinidopsis thalia
430	5	16.7	162	21	AAAB54164	Human pancreatic c	503	5	16.7	206	21	AAAB42001	Human OREF ORF1765
431	5	16.7	162	22	ABBS5554	Lactococcus lactis	504	5	16.7	209	22	AAW35590	Human TNRL3 protei
432	5	16.7	162	23	ABBS3404	E. chaffeensis OMP-	505	5	16.7	209	22	ABG29051	Novel human diegno
433	5	16.7	164	20	AAV06951	Drosophila melanog	506	5	16.7	209	22	AAU23499	Novel human diegno
434	5	16.7	164	22	ABBB61833	Arabinidopsis thalia	507	5	16.7	210	23	ABP25506	Streptococcus poly
435	5	16.7	165	21	AAAG23658	Arabinidopsis thalia	508	5	16.7	211	20	AAW35591	Mouse TNRL3 protei
436	5	16.7	166	21	AAAG51578	Novel human enzyme	509	5	16.7	211	20	AAV95918	Human Goodpasture
437	5	16.7	166	22	AAU23140	Novel human enzyme	510	5	16.7	212	22	AAU45973	Proionlactacertium
438	5	16.7	166	22	AAU23688	Novel human enzyme	511	5	16.7	212	22	ABG17051	Novel human diegno
439	5	16.7	167	20	AAV38569	Nisseeria meningit	512	5	16.7	214	21	AAV79494	Elmeira tenella 25
440	5	16.7	167	22	ABBB97760	Human secretory po	513	5	16.7	215	21	AAAG06187	Arabinidopsis thalia
441	5	16.7	169	22	AAE06783	Human dual-specific	514	5	16.7	215	21	AAAG12970	Arabinidopsis thalia
442	5	16.7	169	22	AAAB64339	Human MAP-kinase p	515	5	16.7	215	21	AAAG47703	Staphylococcus aur
443	5	16.7	170	19	AAAB64200	Human calcineurin.	516	5	16.7	215	22	AAU37468	Staphylococcus aur
444	5	16.7	170	21	AAAB09977	Human CNRII protei	517	5	16.7	215	23	ABP42892	Human ovarian anti
445	5	16.7	170	21	AAAB09978	Human HCNB protein	518	5	16.7	215	23	AAV13950	Hericidially activ
446	5	16.7	170	22	AAO14411	Calcineurin B subu	519	5	16.7	217	20	AAV13950	HIV gp120 v3 loop.
447	5	16.7	170	22	ABBB60493	Drosophila melanog	520	5	16.7	218	16	AAAR79164	Partial sequence o
448	5	16.7	171	22	AAU17530	Novel signal trans	521	5	16.7	218	20	AAAY44172	Human type IV coll

522	5	16.7	218	21	AAV56784	Human alpha3 type	595	5	16.7	261	20	AAV38934	Neisseria gonorrhoe
523	5	16.7	218	22	AAE09484	Human alpha-3 chain	596	5	16.7	261	21	AAAB42113	Human ORFX ORF1877
524	5	16.7	219	21	AAAG29766	Arabidopsis thaliana	597	5	16.7	261	21	AAAG24387	Arabidopsis thaliana
525	5	16.7	219	21	AAAG45793	Arabidopsis thaliana	598	5	16.7	262	21	AAAB25330	Eucalyptus grandis
526	5	16.7	220	22	AAU02911	Angiotensin convert	599	5	16.7	263	22	AAU51961	Propionibacterium
528	5	16.7	220	23	AAU10477	Mouse pancreatic p	600	5	16.7	264	22	AAAM0361	Human polypeptide
529	5	16.7	221	21	AAAG17322	Arabidopsis thaliana	601	5	16.7	264	22	AAAB94175	Human protein sequ
530	5	16.7	223	22	AAAB97131	Corynebacterium di	602	5	16.7	265	22	ABAG16595	Novel human diagno
531	5	16.7	224	22	AAAB6984	Ngfr protein. Uni	603	5	16.7	265	23	ABAP29956	Streptococcus epi
532	5	16.7	225	19	AAAM47524	Mus musculus. Unou	604	5	16.7	265	23	ABAP29951	Streptococcus poly
533	5	16.7	225	21	AAAB07527	Amino acid sequenc	605	5	16.7	268	20	AAAY1993	Type IV collagen N
534	5	16.7	225	21	AAAG34261	Arabidopsis thaliana	606	5	16.7	268	20	AAAY7555	Human alpha3(IV)N
535	5	16.7	225	22	ABAG16600	Novel human diagno	607	5	16.7	268	22	ABAG15429	Novel human diagno
536	5	16.7	226	12	AAAR13901	Nitrite hydratase	608	5	16.7	269	22	ABAG10707	Novel human diagno
537	5	16.7	226	11	AAAG14311	Arabidopsis thaliana	609	5	16.7	270	18	AAAM29816	Mammalian AMPK bet
538	5	16.7	226	21	AAAG53230	Arabidopsis thaliana	610	5	16.7	270	23	ABAP28995	Streptococcus poly
539	5	16.7	226	22	AAAG80788	C diphtheriae DtxR	611	5	16.7	271	22	ABBE6816	Drosophila melanog
540	5	16.7	228	21	AAAG15809	Arabidopsis thaliana	612	5	16.7	271	23	AAAM51458	Human microglobulin
541	5	16.7	229	10	AAAP94802	Pb1r HIV fusion p	613	5	16.7	273	21	AAAG46007	Arabidopsis thaliana
542	5	16.7	229	11	AAAR04494	HIV fusion protein	614	5	16.7	273	22	AAAG10707	TWEAK extracellular
543	5	16.7	229	21	AAAG44499	Arabidopsis thaliana	615	5	16.7	274	21	AAAG51580	Arabidopsis thaliana
544	5	16.7	230	23	ABBS54940	Arabidopsis thaliana	616	5	16.7	274	23	ABAP25484	Streptococcus poly
545	5	16.7	231	22	ABAG24191	Lactococcus lactis	617	5	16.7	275	20	AAAY06956	E. chafeensis OMP-
546	5	16.7	231	9	AAAP81143	Novel human diagno	618	5	16.7	275	21	AAAG05586	Arabidopsis thaliana
547	5	16.7	234	10	AAAP92010	Sequence of fusion	619	5	16.7	275	23	AAAG24386	Ehrlichia chaffe
548	5	16.7	234	14	AAAR1943	HTLV-III fusion pr	620	5	16.7	276	21	AAAG24386	Arabidopsis thaliana
549	5	16.7	234	22	AAAG81970	Recombinant PBI fu	621	5	16.7	276	21	AAAY96466	Partial soybean 4-
550	5	16.7	235	21	AAAG15808	S. epidermidis ope	622	5	16.7	276	22	AAU62637	Propionibacterium
551	5	16.7	236	21	AAAG29765	Arabidopsis thaliana	623	5	16.7	276	22	ABAG05655	Novel human diagno
552	5	16.7	236	23	ABAP26002	Streptococcus poly	624	5	16.7	278	22	AAE04866	Corynebacterium g1
553	5	16.7	236	23	ABAP26003	Streptococcus poly	625	5	16.7	279	23	ABAG21482	Novel human diagno
554	5	16.7	238	22	ABBS61493	Drosophila melanog	626	5	16.7	279	23	ABBB4768	DNA polymerase III
555	5	16.7	239	22	AAAG98390	Escherichia coli p	627	5	16.7	280	20	AAAM60949	E. chafeensis OMP-
556	5	16.7	240	21	AAAG53202	Arabidopsis thaliana	628	5	16.7	282	19	AAAM60150	M. vaccae truncate
557	5	16.7	243	21	AAAG29764	Arabidopsis thaliana	629	5	16.7	282	20	AAAY14897	M. vaccae truncate
558	5	16.7	244	23	AAU075595	Human type IV coll	630	5	16.7	282	23	ABBR73503	M vaccae GV-38A tr
559	5	16.7	245	21	AAAG19949	Arabidopsis thaliana	631	5	16.7	284	19	AAAM47525	Homo sapiens tumo
560	5	16.7	245	21	AAAG46024	Arabidopsis thaliana	632	5	16.7	284	22	ABG15436	Novel human diagno
561	5	16.7	245	21	AAAG67942	Human type IV coll	633	5	16.7	284	23	ABBR76193	Human kidney injur
562	5	16.7	245	23	AAU075589	Human type IV coll	634	5	16.7	284	23	AAAT17831	Herpes simplex vir
563	5	16.7	246	20	AAV60028	Human endometrium	635	5	16.7	285	20	AAAY06957	E. chafeensis OMP-
564	5	16.7	246	22	AAAB47009	Wild type E. coli	636	5	16.7	285	21	AAAB25373	Pinus radiata cell
565	5	16.7	248	21	AAV68779	Amino acid sequenc	637	5	16.7	285	21	AAAY76141	Human secreted pro
566	5	16.7	249	19	AAAM29745	TNF related endothe	638	5	16.7	285	23	ABBB9378	Human polypeptide
567	5	16.7	249	20	AAV093659	Human tumour necro	639	5	16.7	285	23	AAU73408	Ehrlichia chaffe
568	5	16.7	249	21	AAAB07526	Human acid sequenc	640	5	16.7	286	21	AAAG51575	Arabidopsis thaliana
569	5	16.7	249	22	AAAB05338	Human TREPA (TNF r	641	5	16.7	286	22	AAU023781	Novel human enzyme
570	5	16.7	249	23	AAAB00891	Human BLVS binding	642	5	16.7	288	21	AAAB41910	Human ORFX ORF1674
571	5	16.7	249	23	AAAP45149	Human PRO207 poly	643	5	16.7	288	21	AAAG46023	Arabidopsis thaliana
572	5	16.7	250	21	AAU061129	Human alpha-2-macr	644	5	16.7	289	20	AAAY06966	E. canis p30-6 pro
573	5	16.7	250	10	AAAP97158	Peptide expressed	645	5	16.7	289	21	AAAB4452	Virulence gene pro
574	5	16.7	251	15	AAAR1885	BioC gene prod. in	646	5	16.7	289	21	AAAY95553	Chlamydia pneumoni
575	5	16.7	251	23	ABAP45677	p75-NTR (neurotrop	647	5	16.7	289	22	ABBE64137	Drosophila melanog
576	5	16.7	251	23	ABAP45677	Human BLVS binding	648	5	16.7	291	23	ABAP29525	Streptococcus poly
577	5	16.7	251	23	ABAP45677	Human kidney injur	649	5	16.7	291	23	AAU73409	Ehrlichia chaffe
578	5	16.7	251	23	AAAB76194	Human type IV coll	650	5	16.7	292	20	AAAY06967	E. canis p30-7 pro
579	5	16.7	252	21	AAAG77392	Arabidopsis thaliana	651	5	16.7	292	22	ABG29598	Novel human diagno
580	5	16.7	252	22	AAAG33024	C glutamicum prote	652	5	16.7	293	20	AAAY06965	E. canis p30-5 pro
581	5	16.7	254	20	AAU075598	Human type IV coll	653	5	16.7	293	21	AAAG50529	Arabidopsis thaliana
582	5	16.7	255	20	AAU075729	Rupescrta stem pit	654	5	16.7	293	23	AAU096115	Ehrlichia chaffe
583	5	16.7	256	21	AAAG31623	Arabidopsis thaliana	655	5	16.7	293	23	AAU73412	Ehrlichia chaffe
584	5	16.7	257	21	AAAG50530	Arabidopsis thaliana	656	5	16.7	294	22	ABBS2678	Escherichia coli p
585	5	16.7	257	21	AAAG51577	Arabidopsis thaliana	657	5	16.7	294	22	ABBS2898	Escherichia coli p
586	5	16.7	257	23	ABBA9570	Listeria monocytog	658	5	16.7	294	22	ABBS3033	Escherichia coli p
587	5	16.7	258	21	AAAG15807	Arabidopsis thaliana	659	5	16.7	295	20	AAAY06953	E. chateensis OMP-
588	5	16.7	258	23	ABAP30605	Streptococcus poly	660	5	16.7	295	23	AAU73404	Ehrlichia chaffe
589	5	16.7	258	23	ABBS2143	Herbicidially activ	661	5	16.7	297	8	AAAP71198	Sequence of HTLV-I
590	5	16.7	259	20	AAAY38931	Neisseria meningit	662	5	16.7	297	20	AAAY14916	Extended amino aci
591	5	16.7	259	23	ABAP2476	Herbicidially activ	663	5	16.7	297	21	AAAG44498	Arabidopsis thaliana
592	5	16.7	260	21	AAAG44355	Arabidopsis thaliana	664	5	16.7	297	21	AAAG53226	Arabidopsis thaliana
593	5	16.7	260	21	AAAG51581	Arabidopsis thaliana	665	5	16.7	297	22	ABBE88339	Drosophila melanog
594	5	16.7	260	23	ABBS2475	Herbicidially activ	666	5	16.7	297	23	ABBR73522	M vaccae GV-38A tr
							667	5	16.7	298	23	AAU73410	Ehrlichia chaffe

668	5	16.7	300	19	AAV6084	5	16.7	337	20	AAV30158	Rat dorsal root re
669	5	16.7	300	22	AAAG38272	5	16.7	337	21	AAAG46830	Arabidopsis thalia
670	5	16.7	300	22	AAAG82163	5	16.7	337	21	AAAG46870	Arabidopsis thalia
671	5	16.7	301	21	AAAG24811	5	16.7	338	21	AAAG07164	Arabidopsis thalia
672	5	16.7	301	21	AAAG57945	5	16.7	338	22	AAU37864	Streptococcus pneu
673	5	16.7	301	22	AAAG39049	5	16.7	338	22	AAU38052	Streptococcus pneu
674	5	16.7	301	22	AAU12254	5	16.7	339	21	AAAG05228	Arabidopsis thalia
675	5	16.7	301	22	AAAB51638	5	16.7	339	21	AAAG05228	Arabidopsis thalia
676	5	16.7	302	22	AAAB76876	5	16.7	339	22	AAU09964	Human cytidine dea
677	5	16.7	302	22	AAU95531	5	16.7	340	21	AAU10263	Novel human secret
678	5	16.7	304	20	AAV35465	5	16.7	341	22	AAAG14354	Arabidopsis thalia
679	5	16.7	304	22	AAAG46022	5	16.7	341	22	ABG21567	Novel human diagno
680	5	16.7	305	23	AAU75568	5	16.7	341	23	AAAG0726	Haemophilus paraga
681	5	16.7	306	20	AAV30814	5	16.7	342	23	AAAG0726	Haemophilus paraga
682	5	16.7	307	22	ABBA4255	5	16.7	342	14	AAAR39489	Human apoAIV mutel
683	5	16.7	309	12	AAAR13175	5	16.7	342	14	AAAR39491	Human apoAIV mutel
684	5	16.7	310	23	ABBA54948	5	16.7	342	14	AAAR39496	Human apoAIV mutel
685	5	16.7	310	23	AAO17807	5	16.7	342	14	AAAR39498	Human apoAIV mutel
686	5	16.7	313	21	AAAG38271	5	16.7	344	21	AAAG12969	Arabidopsis thalia
687	5	16.7	313	22	AAAG82332	5	16.7	344	21	AAAG14353	Arabidopsis thalia
688	5	16.7	314	22	AAAB41627	5	16.7	344	21	AAV75045	Neisseria meningit
689	5	16.7	314	22	AAAB63384	5	16.7	344	23	AAAG0716	Haemophilus paraga
690	5	16.7	314	22	AAAG40835	5	16.7	344	23	AAAG0717	Haemophilus paraga
691	5	16.7	315	22	AAAB70792	5	16.7	344	23	AAAG0718	Haemophilus paraga
692	5	16.7	316	21	AAAB25566	5	16.7	344	23	AAAG0719	Haemophilus paraga
693	5	16.7	316	21	AAAG50528	5	16.7	344	23	AAAG0721	Haemophilus paraga
694	5	16.7	317	19	AAW72043	5	16.7	344	23	AAAG0722	Haemophilus paraga
695	5	16.7	317	23	ABG10146	5	16.7	344	23	AAAG0724	Haemophilus paraga
696	5	16.7	317	23	ABP39692	5	16.7	344	23	AAAG0725	Haemophilus paraga
697	5	16.7	319	8	AAV71199	5	16.7	344	23	AAAG0727	Haemophilus paraga
698	5	16.7	319	11	AAAR07945	5	16.7	346	14	AAAR39493	Human apoAIV mutel
699	5	16.7	319	12	AAAR13176	5	16.7	346	14	AAAR39493	Human apoAIV mutel
700	5	16.7	319	22	ABBA67007	5	16.7	347	22	AAAB89101	Chenopodium album
701	5	16.7	320	22	ABBA70584	5	16.7	347	23	AAAB89101	Chenopodium album
702	5	16.7	321	20	AAV14209	5	16.7	347	23	AAAB89101	Chenopodium album
703	5	16.7	321	20	AAV14205	5	16.7	347	23	AAAB89101	Chenopodium album
704	5	16.7	322	20	AAV14205	5	16.7	347	23	AAAB89101	Chenopodium album
705	5	16.7	323	22	ABG18805	5	16.7	349	22	AAAB88376	Recombinant vaccin
706	5	16.7	323	22	ABG18805	5	16.7	349	22	AAAB88376	Recombinant vaccin
707	5	16.7	324	21	AAAG34260	5	16.7	350	22	AAAG01198	Novel human diagno
708	5	16.7	325	21	AAAG13668	5	16.7	351	21	AAAB44591	Virulence gene pro
709	5	16.7	325	21	AAAG38270	5	16.7	352	22	AAAB82753	Human protein sequ
710	5	16.7	326	21	AAAG07166	5	16.7	353	10	AAAP92015	HIV portion of Htl
711	5	16.7	326	21	AAAG46832	5	16.7	353	10	AAAP93538	HIV portion of fus
712	5	16.7	327	12	AAAR13177	5	16.7	353	21	AAAG14352	Arabidopsis thalia
713	5	16.7	327	12	AAAG09096	5	16.7	353	21	AAAG14352	Arabidopsis thalia
714	5	16.7	328	14	AAAR39484	5	16.7	357	22	AAAB92759	Human protein sequ
715	5	16.7	328	21	AAAG34259	5	16.7	357	22	AAAB92759	Human protein sequ
716	5	16.7	328	23	ABP38384	5	16.7	363	14	AAAR39478	Human apoAIV mutel
717	5	16.7	329	22	ABG16057	5	16.7	363	14	AAAR39479	Human apoAIV mutel
718	5	16.7	329	22	ABG16224	5	16.7	363	22	ABG28654	Novel human diagno
719	5	16.7	330	21	AAAG07165	5	16.7	365	21	AAAG05565	Arabidopsis thalia
720	5	16.7	330	21	AAAG46831	5	16.7	365	22	AAAB94163	Human protein sequ
721	5	16.7	330	21	AAAG46871	5	16.7	366	22	ABBA57854	Novel human diagno
722	5	16.7	330	22	ABG13035	5	16.7	366	22	ABG05895	Novel human diagno
723	5	16.7	330	22	AAAB78995	5	16.7	366	22	AAAB6277	Putative P. abysal
724	5	16.7	330	23	ABBA93378	5	16.7	367	21	AAAG24566	Arabidopsis thalia
725	5	16.7	330	23	ABBA93379	5	16.7	369	22	AAAG1904	C glutamicum prote
726	5	16.7	331	22	AAAG91206	5	16.7	371	21	AAAG05585	Arabidopsis thalia
727	5	16.7	332	21	AAAG05229	5	16.7	371	22	ABG13741	Novel human diagno
728	5	16.7	332	22	ABG24501	5	16.7	371	22	ABG14939	Novel human diagno
729	5	16.7	333	14	AAAR39488	5	16.7	372	22	ABG04187	Novel human diagno
730	5	16.7	333	14	AAAR39490	5	16.7	373	14	AAAR39486	Human apoAIV mutel
731	5	16.7	333	14	AAAR39495	5	16.7	374	22	AAAB61161	Streptomyces livid
732	5	16.7	333	14	AAAR39497	5	16.7	375	23	ABP6286	Streptococcus poly
733	5	16.7	333	14	AAAR39497	5	16.7	377	14	AAAR39483	Human apoAIV mutel
734	5	16.7	334	12	ABG08757	5	16.7	377	14	AAAR39480	Human apoAIV mutel
735	5	16.7	335	12	AAAR13178	5	16.7	377	14	AAAR39499	Human apoAIV mutel
736	5	16.7	335	12	AAAR13179	5	16.7	377	14	AAAR39500	Human apoAIV mutel
737	5	16.7	335	22	AAAG90576	5	16.7	377	14	AAAR39502	Human apoAIV mutel
738	5	16.7	336	22	ABBA52466	5	16.7	377	14	AAAR39501	Human apoAIV mutel
739	5	16.7	337	14	AAAR39485	5	16.7	377	14	AAAR45242	Human apoAIV mutel
740	5	16.7	337	14	AAAR39492	5	16.7	377	14	AAAR45243	Human apoAIV mutel
	5	16.7	337	14	AAAR39494	5	16.7	377	14	AAAR45244	Human apoAIV mutel

814	5	16.7	377	22	AAB93692	Human protein sequ	887	5	16.7	411	17	AAW00276	Cyanobacterial lyc
815	5	16.7	377	23	AAO14939	Human UFD2-associa	888	5	16.7	412	7	AAPE0416	CS protein of mala
816	5	16.7	378	21	AAG13816	Arabidopsis thalia	889	5	16.7	412	9	AAPE0835	Sequence encoded b
817	5	16.7	378	21	AAG31676	Arabidopsis thalia	890	5	16.7	413	23	ABR93471	Hericidially activ
818	5	16.7	378	22	ABR65454	Drosophila melanog	891	5	16.7	414	23	ABR49456	Listeria monocytog
819	5	16.7	379	23	AAO17802	H influenzae B/H-N	892	5	16.7	416	14	AAK44434	Subtilisin-like se
820	5	16.7	381	20	AAV38570	Neisseria meningit	893	5	16.7	416	22	ABR58589	Drosophila melano
821	5	16.7	381	21	AAV75046	Neisseria meningit	894	5	16.7	417	16	AAK70649	Mouise azospermia
822	5	16.7	382	20	AAV38571	Neisseria gonorrhoe	895	5	16.7	419	22	AAU40408	Propionibacterium
823	5	16.7	382	21	AAV75044	Neisseria gonorrhoe	896	5	16.7	419	22	AAU98367	Escherichia coli p
824	5	16.7	383	22	AAW41928	Human polypeptide	897	5	16.7	420	23	ABR54041	Lactococcus lactis
825	5	16.7	383	22	AAW41928	Human polypeptide	898	5	16.7	421	22	AAK70801	S cerevisiae apopt
826	5	16.7	384	21	AAAG1781	Arabidopsis thalia	899	5	16.7	421	22	AAK68332	Amino acid sequenc
827	5	16.7	384	21	AAAG48096	Arabidopsis thalia	900	5	16.7	423	10	AAPE92013	HIV portion of HTL
828	5	16.7	384	21	AAAB71205	Drosophila melanog	901	5	16.7	423	10	AAPE93536	Sequence of HIV po
829	5	16.7	386	21	AAAB25527	Pinus radiata cell	902	5	16.7	423	21	AAAG5563	Arabidopsis thalia
830	5	16.7	386	22	AAAG31815	Arabidopsis thalia	903	5	16.7	423	21	AAAG5563	Arabidopsis thalia
831	5	16.7	386	22	AAAG4290	Human gene 11 enco	904	5	16.7	423	21	AAAG14141	Arabidopsis thalia
832	5	16.7	386	23	ABR93375	Herbicidially activ	905	5	16.7	423	21	AAAG32447	Arabidopsis thalia
833	5	16.7	388	22	AAAB51345	Mouse HS-glycoprot	906	5	16.7	424	14	AAK37796	RTS protein. Synt
834	5	16.7	389	21	AAAG5564	Arabidopsis thalia	907	5	16.7	424	16	AAK66202	Complete human bon
835	5	16.7	389	22	ABR85000	Drosophila melanog	908	5	16.7	425	21	AAAY92029	Human bone morphog
836	5	16.7	389	23	ABR89418	Human polypeptide	909	5	16.7	425	21	AAAY92370	p75-NTR (neurotrop
837	5	16.7	393	21	AAAG5584	Arabidopsis thalia	910	5	16.7	425	22	ABG29201	Novel human diagno
838	5	16.7	394	15	AAAG33814	Arabidopsis thalia	911	5	16.7	425	23	AAE21671	Rat neurotrophic r
839	5	16.7	394	16	AAK63601	MAP-kinase-phospha	912	5	16.7	426	21	AAAG20523	Arabidopsis thalia
840	5	16.7	394	15	AAK78635	Partial MAP kinase	913	5	16.7	427	20	AAAY33483	Human neutrophil r
841	5	16.7	394	22	AAAB76875	Human lung tumour	914	5	16.7	427	22	ABG19522	Novel human diagno
842	5	16.7	394	22	AAAB76878	Human lung tumour	915	5	16.7	427	22	ABR36699	Human tumour necro
843	5	16.7	394	22	AAAG7448	Amino acid sequenc	916	5	16.7	427	22	AAAB50894	Human neurotrophic
844	5	16.7	394	22	AAAG7627	Amino acid sequenc	917	5	16.7	427	23	AAE21670	Human neurotrophic
845	5	16.7	394	23	AAU85530	SV40 lung tumour p	918	5	16.7	427	23	ABR92637	Hericidially activ
846	5	16.7	396	18	AAW34218	L515 lung tumour	919	5	16.7	428	23	ABR33860	Lactococcus lactis
847	5	16.7	396	19	AAW5819	Streptomyces hydro	920	5	16.7	429	21	AAU92983	Arabidopsis transc
848	5	16.7	396	22	AAAB5819	Streptomyces roseo	921	5	16.7	429	21	AAE26811	Beta-primeverosid
849	5	16.7	396	22	AAAB90664	Human secreted pro	922	5	16.7	429	23	ABR48863	Listeria monocytog
850	5	16.7	396	23	AAU10860	Human apolipoprote	923	5	16.7	431	22	ABG06289	Novel human diagno
851	5	16.7	396	23	AAU10861	Human apolipoprote	924	5	16.7	431	22	AAAB95196	Human protein sequ
852	5	16.7	396	23	AAU10862	Human apolipoprote	925	5	16.7	432	22	AAAG90924	C glutamicum prote
853	5	16.7	396	23	AAU10863	Human apolipoprote	926	5	16.7	434	22	AAE09453	Human sbg6804SPAR
854	5	16.7	396	23	AAU10864	Human apolipoprote	927	5	16.7	434	23	AAE17534	Human protein modi
855	5	16.7	396	23	AAU10865	Human apolipoprote	928	5	16.7	435	21	AAAB19384	Amino acid sequenc
856	5	16.7	396	23	AAU10866	Human apolipoprote	929	5	16.7	435	22	AAAG50500	Arabidopsis thalia
857	5	16.7	396	23	AAU10867	Human apolipoprote	930	5	16.7	435	22	AAAB39070	Human polypeptide
858	5	16.7	396	23	AAU10868	Human apolipoprote	931	5	16.7	436	21	ABR48846	Listeria monocytog
859	5	16.7	398	21	AAAB29612	Human apolipoprote	932	5	16.7	436	22	AAAG31674	Arabidopsis thalia
860	5	16.7	398	22	ABR59946	Cat flea HMT ANON/	933	5	16.7	437	23	ABG18343	Novel human diagno
861	5	16.7	398	23	ABR59946	Drosophila melanog	934	5	16.7	437	23	ABR78795	Human NOV1 protein
862	5	16.7	399	21	AAAB53914	Lactococcus lactis	935	5	16.7	440	23	AAE23386	Human intracellular
863	5	16.7	399	22	ABG15380	Novel acid sequenc	936	5	16.7	440	23	ABP47784	Protein #30 relate
864	5	16.7	399	22	AAW93874	Novel human diagno	937	5	16.7	441	23	ABP26921	Streptococcus poly
865	5	16.7	399	22	AAAB04208	Human polypeptide	938	5	16.7	441	23	AAU09884	Novel human secret
866	5	16.7	399	22	AAAB04230	Human gene 11 enco	939	5	16.7	443	22	AAE05813	Human small cell 1
867	5	16.7	399	23	AAAB04230	Human gene 11 enco	940	5	16.7	445	16	AAK72451	Brevibacterium fla
868	5	16.7	399	23	ABG64487	Human albumin fusi	941	5	16.7	445	18	AAW23285	Brevibacterium lac
869	5	16.7	401	22	ABG03895	Novel human diagno	942	5	16.7	445	19	AAW06588	B. lactofermentum
870	5	16.7	401	22	ABG10083	Novel human diagno	943	5	16.7	445	19	AAW68150	Diaminopimelate de
871	5	16.7	401	22	ABG13038	Novel human diagno	944	5	16.7	445	19	AAW69552	Brevibacterium lac
872	5	16.7	401	23	ABR33038	Recombinant protei	945	5	16.7	445	19	AAW47399	B. lactofermentum
873	5	16.7	402	21	AAU85617	Arabidopsis thalia	946	5	16.7	445	22	AAAG6811	Human zinc finger
874	5	16.7	403	21	AAAG31675	Arabidopsis thalia	947	5	16.7	445	22	AAW78643	Human protein SEQ
875	5	16.7	403	21	AAAG20623	Arabidopsis thalia	948	5	16.7	447	20	AAAG3197	C glutamicum prote
876	5	16.7	405	23	ABP40414	Staphylococcus epi	949	5	16.7	445	22	AAE04862	Corynebacterium gl
877	5	16.7	406	20	AAW82680	Streptococcus sp. t	950	5	16.7	445	22	AAE04862	Corynebacterium gl
878	5	16.7	406	22	AAW39645	Human polypeptide	951	5	16.7	445	22	AAK94631	Human protein sequ
879	5	16.7	407	23	ABG61840	Prostate cancer-as	952	5	16.7	445	23	ABR89471	Human polypeptide
880	5	16.7	407	23	ABR70666	Drosophila melanog	953	5	16.7	447	20	AAAG54714	Arabidopsis thalia
881	5	16.7	408	22	ABG19521	Novel human diagno	954	5	16.7	448	23	AAAY35554	C. pneumoniae prot
882	5	16.7	408	22	AAE09452	Human sbg6804SPAR	955	5	16.7	449	21	ABR54422	Lactococcus lactis
883	5	16.7	408	23	AAW41431	Human polypeptide	956	5	16.7	449	21	AAAY96476	Soybean 4-hydroxyp
884	5	16.7	409	22	ABR08246	Human SPARC-homolo	957	5	16.7	449	22	AAAG22396	C glutamicum prote
885	5	16.7	411	9	AAPE83144	Propionibacterium	958	5	16.7	450	22	AAK78891	C. glutamicum SRT
886	5	16.7	411	16	AAK76980	Sequence encoded b	959	5	16.7	451	16	AAW50772	Rice ubiquitin lig
						Lycopene cyclase.						AAK63088	Breast tumor kinas

960	5	16.7	451	22	ABG02799	Novel human diagno
961	5	16.7	452	22	ABB68662	Drosophila melanog
962	5	16.7	452	22	AAW59808	TuTC protein. Tha
963	5	16.7	453	21	AAW42565	Arabidopsis thalia
964	5	16.7	455	19	AAW60147	M. vaccae antigen
965	5	16.7	455	20	AAV14894	Amino acid sequenc
966	5	16.7	455	21	AAW26983	Human NGFR p75. H
967	5	16.7	455	23	ABB73500	M vaccae GV-38A pa
968	5	16.7	458	20	AAV38932	Neisseria meningit
969	5	16.7	458	20	AAV38933	Neisseria meningit
970	5	16.7	458	20	AAV38935	Neisseria gonorrhoe
971	5	16.7	458	23	ABP30342	Streptococcus poly
972	5	16.7	458	23	AAU72978	Neisseria meningit
973	5	16.7	459	21	AAW14140	Arabidopsis thalia
974	5	16.7	459	21	AAW32446	Arabidopsis thalia
975	5	16.7	459	22	AAW79656	Corynebacterium gl
976	5	16.7	460	22	AAU46872	Propionibacterium
977	5	16.7	465	21	AAW31991	Arabidopsis thalia
978	5	16.7	465	22	AAW95369	Human protein sequ
979	5	16.7	465	23	ABG65646	Human breast speci
980	5	16.7	466	21	AAW33073	Arabidopsis thalia
981	5	16.7	466	23	ABP28095	Streptococcus poly
982	5	16.7	466	23	ABW54231	Lactococcus lactis
983	5	16.7	467	23	ABP28094	Streptococcus poly
984	5	16.7	469	19	AAW50248	Sequence of bovine
985	5	16.7	469	19	AAW37061	HIV-1 breakthrough
986	5	16.7	469	20	AAW88483	Bovine papillomavi
987	5	16.7	470	22	ABW55574	Drosophila melanog
988	5	16.7	470	22	ABG16644	Novel human diagno
989	5	16.7	471	16	AAW79163	Partial sequence o
990	5	16.7	471	20	AAV44171	Bovine type IV col
991	5	16.7	471	20	AAV14914	Extended amino aci
992	5	16.7	471	21	AAW50499	Arabidopsis thalia
993	5	16.7	471	21	AAW56783	Arabidopsis thalia
994	5	16.7	471	22	AAW09483	Bovine alpha-3 cha
995	5	16.7	471	22	ABW73520	M vaccae GV-38A pr
996	5	16.7	473	6	AAW50288	Sequence encoded b
997	5	16.7	473	23	AAE23641	White mustard myr3
998	5	16.7	474	22	ABW63130	Drosophila melanog
999	5	16.7	475	22	ABW58603	Drosophila melanog
1000	5	16.7	475	23	ABP30445	Streptococcus poly

ALIGNMENTS

RESULT 1
ID AAW53252 standard; Protein; 30 AA.

AAW53252;
30-JUN-1998 (first entry)

Candida albicans allergen - antigenic protein SEQ ID NO:2.

Candida albicans; vaccine; allergen; antigenic protein; fungal antigen;
immune response; infection; insoluble.

Candida albicans.

Key Location/Qualifiers

Misc-difference 26 /note= "any amino acid"

Misc-difference 29 /note= "any amino acid"

Misc-difference 30 /note= "any amino acid"

W09809990-A1.

12-MAR-1998.

XX

PF 29-AUG-1997; 97WO-JP03041.
XX 31-MAR-1997; 97JP-0099775.
PR 04-SEP-1996; 96JP-0255400.
XX (TAKI) TAKARA SHUZO CO LTD.
XX Endo M, Kato I, Mizutani S, Takesako K;
PI WPI, 1998-193553/17.
XX Fungal antigens comprising insoluble fraction of fungal cells -
PT useful for, e.g. stimulating immune response and treatment and
PT diagnosis of fungal infection(s)
PS Claim 26; Page 75; 108pp; Japanese.
XX The present sequence represents an active vaccine component or allergen
CC derived from Candida albicans, which is an antigenic protein. The
CC present invention describes fungal antigens, comprising the insoluble
CC fraction of fungal cells having completely/partially removed cell walls.
CC Also described are nucleic acids encoding the antigens and a method for
CC producing the antigens. The antigens can be used for preparing
CC therapeutic compositions for stimulating immune response, e.g. as a
CC vaccine. They can be used for treatment of fungal infections, treatment
CC and prevention of allergies and diagnosis of fungal infections in
CC vertebrates. The vaccines are not live, and have low toxicity.
XX Sequence 30 AA;
SQ
Query Match 90.0%; Score 27; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 KYSLPELDYSPATRPYISQINELIXYT 28
DB 1 KYSLPELDYSPATRPYISQINELIXYT 28
RESULT 2
ID ABB05612 standard; Protein; 233 AA.
XX ABB05612;
XX 24-APR-2002 (first entry)
XX S. cerevisiae manganese superoxide dismutase protein SEQ ID NO:31.
XX Aspergillus oryzae; mutant; modified; reduced transcription; hormone;
XX reduced translation; reduced secretion; receptor; antibody; reporter;
XX enzyme; lipase; manganese superoxide dismutase.
XX Saccharomyces cerevisiae.
XX Synthetic.
XX US6323002-B1.
XX 27-NOV-2001.
XX 25-JUN-1999; 99US-0339972.
XX 12-SEP-1997; 97US-0928692.
XX 13-SEP-1996; 96US-0713312.
XX (NOVO) NOVOZYMES BIOTECH INC.
XX Brody H, Yaver DS, Lamsa M, Hansen K;
PI WPI, 2002-16301/72.
XX Producing a polypeptide using a cell for reducing the production of the
PT polypeptide, comprises inserting DNA into the genome of the cell at a

PT position not within the polypeptide coding sequence or a regulatory
 XX sequence -
 PS Example 17; Column 125-128; 129pp; English.
 CC The present invention describes a method for producing a polypeptide (PI)
 CC comprising cultivating a mutant cell whose parent cell comprises a DNA
 CC sequence encoding PI, by introducing a nucleic acid construct into the
 CC genome of the parent cell at a locus not within the PI sequence, so
 CC that PI transcription, translation or secretion is reduced, and
 CC recovering PI. The method is used to produce a polypeptide, such as a
 CC recombinant or heterologous hormone, hormone variant, receptor, antibody,
 CC reporter or enzyme, particularly an oxidoreductase, transferase,
 CC hydrolase, lyase, isomerase or ligase. The present sequence represents
 CC a Saccharomyces cerevisiae manganese superoxide dismutase protein which
 CC shares significant identity with the mutant Aspergillus oryzae DB571058
 CC protein, which is used in an example from the present invention.
 XX
 CC Sequence 233 AA;
 Query Match 33.3%; Score 10; DB 23; Length 233;
 Best Local Similarity 100.0%; Pred. No. 0.0053;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CY 15 EPIYSGQINE 24
 |||||
 DB 41 EPIYSGQINE 50
 RESULT 3
 AAG14176
 ID AAG14176 standard; Protein; 407 AA.
 XX
 AC AAG14176;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 13938.
 XX
 KM Protein identification; signal transduction pathway; metabolic pathway;
 KM hybridisation assay; genetic mapping; gene expression control; promoter;
 KM termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN BP1033405-A2.
 XX
 ID 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
 XX
 XX 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 23-APR-1999; 99US-0130891.
 PR 28-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 04-MAY-1999; 99US-0132407.
 PR 05-MAY-1999; 99US-0132484.
 PR 06-MAY-1999; 99US-0132485.
 PR 06-MAY-1999; 99US-0132486.
 PR 06-MAY-1999; 99US-0132487.
 PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134218.
 PR 14-MAY-1999; 99US-0134219.
 PR 14-MAY-1999; 99US-0134221.
 PR 14-MAY-1999; 99US-0134370.
 PR 18-MAY-1999; 99US-0134768.
 PR 19-MAY-1999; 99US-0134941.
 PR 20-MAY-1999; 99US-0135124.
 PR 21-MAY-1999; 99US-0135353.
 PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136382.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139451.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139452.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
 PR 18-JUN-1999; 99US-0139763.
 PR 21-JUN-1999; 99US-0139817.
 PR 22-JUN-1999; 99US-0139899.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 24-JUN-1999; 99US-0140635.
 PR 28-JUN-1999; 99US-0140823.
 PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 20-JUL-1999; 99US-0144352.
 PR 20-JUL-1999; 99US-0144632.
 PR 20-JUL-1999; 99US-0144884.
 PR 21-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145088.
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 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145226.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
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PR 29-OCT-1999; 99US-0162142.

Query Match 23.3%; Score 7; DB 21; Length 407;
Best Local Similarity 100.0%; Pred. No. 16;
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OY 12 SATEPYI 18
Db 131 SATEPYI 137

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AC AAG14175;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 13937.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Query Match 23.3%; Score 7; DB 21; Length 512;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 226 SATPEYI 242

RESULT 5
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AC AAG14174;
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 13936.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13936.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
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XX 25-FEB-2000; 2000EP-0301439.
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Query Match 23.3%; Score 7; DB 21; Length 521;

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Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 12 SATEPYI 18
Db 245 SATEPYI 251

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RESULT 6
ABB08465
ID ABB08465 standard; Peptide; 7 AA.

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AC ABB08465;

DT 29-JUL-2002 (first entry)

DE Mouse tumour specific antigenic related protein #1.

KW Proton pump inhibitor; tumour-specific antigenic peptide;

KW cyostatic; tumour; mouse.

OS Mus sp.

PN JP2001286284-A.

PD 16-OCT-2001.

PF 05-APR-2000; 2000JP-0103966.

PR 05-APR-2000; 2000JP-0103966.

PA (SATO/) SATO N.

PA (SUZU/) SUZUKI N.

PA (YAMA/) YAMAGUCHI M.

DR WPI; 2002-134186/18.

PT Gene diagnostic agent and gene treating agent for tumours comprises

PT using tumour-specific antigen and proton pump inhibitor as antitumour

PT agent

XX Example 2; Page 30; 80pp; Japanese.

PS This invention relates to a diagnostic agent or treating agent for

CC tumours by using a tumour specific antigen and a proton pump

CC inhibitor. The method is cyostatic in its action and the

CC tumour-specific antigen peptide is useful for treating and preventing

CC cancers. This amino acid sequence is related to the tumour specific

XX antigen and proton pump of the invention.

SO Sequence 7 AA;

Query Match

Best Local Similarity 100.0%; Score 6; DB 23; Length 7;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 FSATBP 16

Db 1 FSATBP 6

RESULT 7

ABB08476

ID ABB08476 standard; Peptide; 7 AA.

XX ABB08476;

DT 29-JUL-2002 (first entry)

DE Peptide related to tumour specific antigen.

KW Proton pump inhibitor; tumour-specific antigenic peptide;

KW cyostatic; tumour.

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XX OS Unidentified.
XX XX
XX PN JP2001286284-A.
XX XX
XX PD 16-OCT-2001.
XX XX
XX PF 05-APR-2000; 2000JP-0103966.
XX XX
XX PR 05-APR-2000; 2000JP-0103966.
XX XX
XX PA (SATO/) SATO N.
XX PA (SUZU/) SUZUKI N.
XX PA (YAMA/) YAMAGUCHI M.
XX XX
XX DR WPI; 2002-134186/18.
XX XX
XX PT Gene diagnostic agent and gene creating agent for tumours comprises
XX PT using tumour-specific antigen and proton pump inhibitor as antitumour
XX PT agent -
XX XX
XX SS Claim 23; Page 4; 80pp; Japanese.
XX XX
XX CC This invention relates to a diagnostic agent or treating agent for
XX CC tumours by using a tumour specific antigen and a proton pump
XX CC inhibitor. The method is cytostatic in its action and the
XX CC tumour-specific antigen peptide is useful for treating and preventing
XX CC cancers. This amino acid sequence is related to the tumour specific
XX CC antigen and proton pump of the invention.
XX XX
XX SQ Sequence 7 AA;
XX XX
XX Query Match 20.0%; Score 6; DB 23; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 FSATEP 16
Db 1 FSATEP 6
XX XX
XX RESULT 8
XX ABB08466
XX ID ABB08466 standard; Peptide; 9 AA.
XX XX
XX AC ABB08466;
XX XX
XX DT 29-JUL-2002 (first entry)
XX XX
XX BB Mouse tumour specific antigenic related protein #2.
XX XX
XX KW Proton pump inhibitor; tumour-specific antigenic peptide;
XX KW cytostatic; tumour; mouse.
XX XX
XX OS Mus sp.
XX XX
XX PN JP2001286284-A.
XX XX
XX PD 16-OCT-2001.
XX XX
XX PF 05-APR-2000; 2000JP-0103966.
XX XX
XX PR 05-APR-2000; 2000JP-0103966.
XX XX
XX PA (SATO/) SATO N.
XX PA (SUZU/) SUZUKI N.
XX PA (YAMA/) YAMAGUCHI M.
XX XX
XX DR WPI; 2002-134186/18.
XX XX
XX PT Gene diagnostic agent and gene creating agent for tumours comprises
XX PT using tumour-specific antigen and proton pump inhibitor as antitumour
XX PT agent -

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XX PS Claim 25; Page 30; 80pp; Japanese.
XX XX
XX CC This invention relates to a diagnostic agent or treating agent for
XX CC tumours by using a tumour specific antigen and a proton pump
XX CC inhibitor. The method is cytostatic in its action and the
XX CC tumour-specific antigen peptide is useful for treating and preventing
XX CC cancers. This amino acid sequence is related to the tumour specific
XX CC antigen and proton pump of the invention.
XX XX
XX SQ Sequence 9 AA;
XX XX
XX Query Match 20.0%; Score 6; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 FSATEP 16
Db 2 FSATEP 7
XX XX
XX RESULT 9
XX ABB08467
XX ID ABB08467 standard; Peptide; 10 AA.
XX XX
XX AC ABB08467;
XX XX
XX DT 29-JUL-2002 (first entry)
XX XX
XX DE Mouse tumour specific antigenic related protein #3.
XX XX
XX KW Proton pump inhibitor; tumour-specific antigenic peptide;
XX KW cytostatic; tumour; mouse.
XX XX
XX OS Mus sp.
XX XX
XX PN JP2001286284-A.
XX XX
XX PD 16-OCT-2001.
XX XX
XX PF 05-APR-2000; 2000JP-0103966.
XX XX
XX PR 05-APR-2000; 2000JP-0103966.
XX XX
XX PA (SATO/) SATO N.
XX PA (SUZU/) SUZUKI N.
XX PA (YAMA/) YAMAGUCHI M.
XX XX
XX DR WPI; 2002-134186/18.
XX XX
XX PT Gene diagnostic agent and gene creating agent for tumours comprises
XX PT using tumour-specific antigen and proton pump inhibitor as antitumour
XX PT agent -
XX XX
XX PS Claim 25; Page 30; 80pp; Japanese.
XX XX
XX CC This invention relates to a diagnostic agent or treating agent for
XX CC tumours by using a tumour specific antigen and a proton pump
XX CC inhibitor. The method is cytostatic in its action and the
XX CC tumour-specific antigen peptide is useful for treating and preventing
XX CC cancers. This amino acid sequence is related to the tumour specific
XX CC antigen and proton pump of the invention.
XX XX
XX SQ Sequence 10 AA;
XX XX
XX Query Match 20.0%; Score 6; DB 23; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 5.5;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 FSATEP 16
Db 3 FSATEP 8

```

RESULT 10
 ABG6263
 ID ABG6263 standard; Peptide; 19 AA.
 XX
 AC ABG6263;
 XX
 DT 29-AUG-2002 (first entry)
 XX
 DE IGE Fcepsilon RI binding peptide from phage displayed g3 library IGE154.
 XX
 KM IGE receptor; immunoglobulin; FcepsilonRI; antagonist; phage display;
 KM protein co-ordinate data; IGE-mediated disease; allergic rhinitis;
 KM asthma; allergic asthma; atopic dermatitis; urticaria-angioedema;
 KM parasitic infection; IGE myeloma; immune-related disorder;
 KM inflammatory disorder; diabetes mellitus; reperfusion injury; stroke;
 KM IGE-mediated gastrointestinal inflammatory disease; burn;
 KM immune rejection of graft; myocardial infarction; atherosclerosis;
 KM acute lung injury; haemorrhagic shock; septic shock;
 KM acute tubular necrosis; endometriosis; degenerative joint disease;
 KM pancreatitis.
 KM
 XX
 OS Synthetic.
 XX
 PN WO200226781-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 26-SEP-2001; 2001WO-US30289.
 XX
 PR 26-SEP-2000; 2000US-235353P.
 PR 23-MAR-2001; 2001US-278540P.
 XX
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lowman HB, Reynolds ME, Nakamura GR, Starovassnik MA;
 XX
 DR WPI; 2002-444016/47.
 XX
 XX
 PT A peptide useful for treating a IGE-mediated disease or disorder in a
 PT host e.g. allergic rhinitis, asthma, which competes with immunoglobulin
 PT E for binding to high affinity IGE receptor in an in vitro assay -
 XX
 XX
 PS Example 12; Page 120; 328pp; English.
 XX
 CC The invention relates to a peptide which competes with immunoglobulin
 CC (Ig) E 134 comprising a sequence (S1), for binding the high affinity IGE
 CC receptor (FcepsilonRI) in an in vitro assay and having a formula given in
 CC the specification. Also included are a fusion protein comprising the
 CC peptide, a pharmaceutical composition (C) comprising the peptide,
 CC designing a compound that mimics the three-dimensional surface
 CC structure of the peptide, a compound with a solvent accessible surface
 CC that mimics the solvent accessible surface defined by the side chains of
 CC residues (R) Pro4, Phe6, Pro16, Cys3, Cys7, Cys15 and Cys19 of IGE134,
 CC a peptide with structural coordinates as given in the specification,
 CC selecting a peptide mimetic which binds to FcepsilonRI and blocks
 CC binding of IGE and a peptide mimetic which mimics the coordinates of
 CC IGE134 residues (R). (C) is useful for inhibiting the binding of IGE to
 CC high affinity IGE receptor (FcepsilonRI). Peptides of the formula given
 CC in the specification are useful for inhibiting the binding of an IGE to
 CC molecule which blocks the interaction of IGE with high affinity IGE
 CC receptor. The peptide is also useful for inhibiting the activation of
 CC high affinity IGE receptor. The peptide is useful for treating an IGE-
 CC mediated disease or disorder in a host. (C) is useful in research,
 CC diagnostic, therapeutic and prophylactic methods. The peptide is also
 CC useful for inhibiting IGE-mediated or associated processes such as IGE-
 CC dependent activation and degranulation of mast cells and basophils, as
 CC well as consequent release of inflammatory mediators such as histamine.
 CC (C) is useful for treating allergic rhinitis, asthma (e.g. allergic
 CC asthma), atopic dermatitis, urticaria-angioedema, parasitic infection,
 CC IGE myeloma, immune-related disorders, inflammatory disorders, diabetes
 CC mellitus, IGE-mediated gastrointestinal inflammatory disease, immune

CC rejection of grafts, reperfusion injury, stroke, myocardial infarction,
 CC atherosclerosis, acute lung injury, haemorrhagic shock, burn, septic
 CC shock, acute tubular necrosis, endometriosis, degenerative joint disease
 CC and pancreatitis. The present sequence is a peptide of the invention
 CC expressed from a phage display library.
 XX
 SQ Sequence 19 AA;
 XX
 Query Match 20.0%; Score 6; DB 23; Length 19;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PELDYE 10
 DQ 7 PELDYE 12
 XX
 RESULT 11
 ABB08468
 ID ABB08468 standard; Protein; 20 AA.
 XX
 AC ABB08468;
 XX
 DT 29-JUL-2002 (first entry)
 XX
 DE Mouse tumour specific antigenic related protein #4.
 XX
 KM Proton pump inhibitor; tumour-specific antigenic peptide;
 KM cyrostatic; tumour; mouse.
 KM
 OS Mus sp.
 XX
 PN JP2001286284-A.
 XX
 PD 16-OCT-2001.
 XX
 PF 05-APR-2000; 2000JP-0103966.
 XX
 PR 05-APR-2000; 2000JP-0103966.
 XX
 PA (SATO/) SATO N.
 PA (SUZU/) SUZUKI N.
 PA (YAMA/) YAMAGUCHI M.
 XX
 DR WPI; 2002-134186/18.
 XX
 XX
 PT Gene diagnostic agent and gene treating agent for tumours comprises
 PT using tumour-specific antigen and proton pump inhibitor as antitumour
 PT agent -
 XX
 PS Claim 25; Page 30; 80pp; Japanese.
 XX
 CC This invention relates to a diagnostic agent or treating agent for
 CC tumours by using a tumour specific antigen and a proton pump
 CC inhibitor. The method is cyostatic in its action and the
 CC tumour-specific antigen peptide is useful for treating and preventing
 CC cancers. This amino acid sequence is related to the tumour specific
 CC antigen and proton pump of the invention.
 CC
 XX
 SQ Sequence 20 AA;
 XX
 Query Match 20.0%; Score 6; DB 23; Length 20;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 FSATEP 16
 DQ 4 FSATEP 9
 XX
 RESULT 12
 AAB78878
 ID AAB78878 standard; Protein; 44 AA.

XX AAB78878;
 AC
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE C. glutamicum SRT protein sequence SEQ ID NO:16.
 XX
 KW Corynebacterium glutamicum; stress; resistance; tolerance; SRT;
 KW fine chemical production; organic acid; proteiogenic amino acid;
 KW nonproteogenic amino acid; purine base; pyrimidine base; nucleoside;
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
 KW carboxylate; aromatic compound; vitamin; cofactor; polypeptide; enzyme;
 KW evolutionary study; environmental hazard; fermentation.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN WO200100804-A2.
 XX
 PD 04-JAN-2001.
 XX
 PF 23-JUN-2000; 2000WO-1B00922.
 XX
 PR 25-JUN-1999; 99US-0141031.
 PR 01-JUL-1999; 99DE-1030429.
 PR 01-JUL-1999; 99US-0142692.
 PR 08-JUL-1999; 99DE-1031413.
 PR 08-JUL-1999; 99DE-1031457.
 PR 08-JUL-1999; 99DE-1031541.
 PR 09-JUL-1999; 99DE-1032209.
 PR 09-JUL-1999; 99DE-1032230.
 PR 14-JUL-1999; 99DE-1032914.
 PR 27-AUG-1999; 99DE-1040764.
 PR 27-AUG-1999; 99US-0151214.
 PR 31-AUG-1999; 99DE-1041382.
 XX
 PA (BADI) BASF AG.
 XX
 PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberman G, Lee H,
 PI Kim H;
 XX
 DR WPI: 2001-061972/07.
 DR N-PSDB; AAF70991.
 XX
 PT New isolated Corynebacterium glutamicum nucleic acid encoding a stress,
 PT tolerance or resistance protein, for production or modulation of
 PT production of fine chemicals, such as, e.g. amino acids, lipide,
 PT carbohydrates, or enzymes -
 PT
 XX
 PS Claim 20; Page 138; 526pp; English.
 XX
 CC AAF70984 to AAF71133 encode the Corynebacterium glutamicum stress,
 CC resistance, and tolerance (SRT) proteins given in AAB78871 to AAB79020.
 CC The C. glutamicum SRT genes (I) can be used in vectors (II) for
 CC expression in host cells and production of fine chemicals, such as, an
 CC organic acid, a proteiogenic or nonproteogenic amino acid (preferred),
 CC a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a
 CC saturated or unsaturated fatty acid, a diol, a carboxylate, an aromatic
 CC compound, a vitamin, a cofactor, a polypeptide, or an enzyme. The fine
 CC chemical production can be modulated. The presence of (I) or the SRT
 CC or proteins (III) encoded by them are used for diagnosing the presence
 CC or activity of Corynebacterium diptheriae. (I), (II), (III) and host
 CC cells containing them can be used to map the genomes of organisms related
 CC to C. glutamicum, to identify and localise C. glutamicum sequences of
 CC interest, in evolutionary studies, in determination of SRT protein
 CC regions required for function, in modulating the SRT protein activity,
 CC and in modulating the activity of an SRT pathway. (II) are used to permit
 CC C. glutamicum to survive in an environment that is normally
 CC environmentally or chemically hazardous to it. (I) and protein molecules
 CC encoded by it increase the survival of C. glutamicum to chemical and
 CC environmental hazards and provide a means for continued growth and
 CC multiplication in large scale fermentative growth conditions. By
 CC increasing the growth rate or maintaining a normal growth rate in poor or
 CC toxic conditions, the yield, production and/or efficiency or production

CC of fine chemicals from a culture may be increased.
 XX
 XX
 SQ Sequence 44 AA;

Query Match 20.0%; Score 6; DB 22; Length 44;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LPELDY 9
 |||||
 Db 6 LPELDY 11

RESULT 13

ABB36416
 ID ABB36416 standard; Peptide; 50 AA.

AC ABB36416;

DT 04-FEB-2002 (first entry)

DE Peptide #3922 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

PN WO200157277-A2.

XX 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00669.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI: 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human fetal liver -

XX Claim 27; SEQ ID NO 29051; 639pp + sequence listing; English.

CC The invention relates to a single exon nucleic acid probe for

CC measuring human gene expression in a sample derived from human foetal

CC liver. The single exon nucleic acid probes may be used for predicting,

CC measuring and displaying gene expression in samples derived from human

CC foetal liver. The present sequence is a peptide encoded by a single exon

CC nucleic acid probe of the invention.

CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 50 AA;

XX Query Match 20.0%; Score 6; DB 22; Length 50;

XX Best Local Similarity 100.0%; Pred. No. 26;

XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 SATPEY 17
 |||||
 Db 10 SATPEY 15


```

RESULT 14
AAM57176
ID AAM57176 standard; Protein; 50 AA.
XX
XX
AC AAM57176;
XX
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29281.
XX
XX Human; brain expressed exon; gene expression analysis; probe;
KM microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00667.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX
XX Example 4; SEQ ID NO: 29281; 650bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system,
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX CC the probes of the invention.
XX
XX
SQ Sequence 50 AA;
XX
XX Query Match 20.0%; Score 6; DB 22; Length 50;
XX Best Local Similarity 100.0%; Pred. No. 26;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 12 SATPEY 17
XX |||||
XX Db 10 SATPEY 15
XX
XX
XX RESULT 15
XX AAM69579
XX ID AAM69579 standard; Protein; 50 AA.
XX
XX
XX AAM69579;
XX
XX
XX 06-NOV-2001 (first entry)
XX
XX
XX Human bone marrow expressed probe encoded protein SEQ ID NO: 29885.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma.
XX
XX

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OS Homo sapiens.
XX
XX PN WO200157276-A2.
XX
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US00668.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow -
XX
XX Example 4; SEQ ID NO: 29885; 658bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukemia and myeloma. The present sequence is a
XX CC protein encoded by one of the probes of the invention.
XX
XX
SQ Sequence 50 AA;
XX
XX Query Match 20.0%; Score 6; DB 22; Length 50;
XX Best Local Similarity 100.0%; Pred. No. 26;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 12 SATPEY 17
XX |||||
XX Db 10 SATPEY 15
XX
XX
XX RESULT 16
XX AAM17397
XX ID AAM17397 standard; Protein; 50 AA.
XX
XX
XX AAM17397;
XX
XX
XX 12-OCT-2001 (first entry)
XX
XX DE Peptide #3831 encoded by probe for measuring cervical gene expression.
XX
XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX KW cervical cancer.
XX
XX
XX OS Homo sapiens.
XX
XX PN WO200157278-A2.
XX
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US00670.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX

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XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
XX Claim 27; SEQ ID No 22223; 487bp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
CC (SENIP: see A110068-A128459). The present sequence is a peptide encoded
CC by one such probe. The SENIPs are derived from human HeLa cells. The SENIPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 50 AA;
XX
XX Query Match 20.0%; Score 6; DB 22; Length 50;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 12 SATPEY 17
DB 10 SATPEY 15
XX
XX RESULT 17
XX AAM29917
XX ID AAM29917 standard; Protein; 50 AA.
XX
XX AAM29917;
XX
XX 17-OCT-2001 (first entry)
XX
XX Peptide #3954 encoded by probe for measuring placental gene expression.
XX
XX Probe: microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00663.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX

PS Claim 27; SEQ ID No 30186; 654bp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENIP:
CC see A11315-A157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX
XX Sequence 50 AA;
XX
XX Query Match 20.0%; Score 6; DB 22; Length 50;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 12 SATPEY 17
DB 10 SATPEY 15
XX
XX RESULT 18
XX ABG39201
XX ID ABG39201 standard; Peptide; 50 AA.
XX
XX ABG39201;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human peptide encoded by genome-derived single exon probe SEQ ID 28866.
XX
XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karsagen syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease.
XX
XX Homo sapiens.
XX
XX WO200186003-A2.
XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US00665.
XX
XX 04-FEB-2000; 2000US-180312P.
XX 26-MAY-2000; 2000US-207456P.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-234687P.
XX 27-SEP-2000; 2000US-236359P.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX
XX Claim 27; SEQ ID No 28866; 634bp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 1287 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of

CC probes; the novel set of probes which hybridise at high stringency to a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung, comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemorrhoidosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
CC pulmonary alveolar proteinosis, Karsenger syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a peptide/protein
CC encoded by a single exon probe of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 50 AA;

Query Match 20.0%; Score 6; DB 23; Length 50;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SATPEY 17
| | | | |
Db 10 SATPEY 15

RESULT 19

AAU58434
ID AAU58434 standard; Protein; 52 AA.

XX AAU58434;

XX 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #19330.

XX SAPHO syndrome; synovitis; acne; pustulosis; hyperteosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

PD 01-NOV-2001.

PF 20-APR-2001; 2001WO-US12865.

PR 21-APR-2000; 2000US-199047P.

PR 02-JUN-2000; 2000US-208841P.

PR 07-JUL-2000; 2000US-216747P.

PA (CORI-) CORIXA CORP.

XX Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI, 2001-616774/71.

DR N-PSDB; AAS59591.

PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -

XX Example 1; SEQ ID No 19629; 1069bp; English.

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 52 AA;

Query Match 20.0%; Score 6; DB 22; Length 52;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SATPEY 17
| | | | |
Db 9 SATPEY 14

RESULT 20

AAU65746
ID AAU65746 standard; Protein; 52 AA.

XX AAU65746;

XX 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #26642.

XX SAPHO syndrome; synovitis; acne; pustulosis; hyperteosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

PD 01-NOV-2001.

PF 20-APR-2001; 2001WO-US12865.

PR 21-APR-2000; 2000US-199047P.

PR 02-JUN-2000; 2000US-208841P.

PR 07-JUL-2000; 2000US-216747P.

PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249287.
PR 17-NOV-2000; 2000US-0249289.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM,
XX
XX WPI; 2001-541565/60.
XX
XX N-PSDB; ABA11135.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
XX
XX PT useful for preventing, diagnosing and/or treating nervous system
XX
XX PT cancers and metastases -

XX
PS Claim 11; SEQ ID NO 3466; 1701pp + Sequence listing; English.
XX
XX The invention relates to novel genes (AB11004-ABA21534) and proteins
CC (AB14678-AB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 AA;
Query Match 20.0%; Score 6; DB 22; Length 60;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 8 DYERSA 13
Db 50 DYERSA 55
RESULT 22
ABB08458
ID ABB08458 standard; Protein; 62 AA.
XX
XX ABB08458;
XX
XX 29-JUL-2002 (first entry)
XX
XX Mouse tumour specific antigenic peptide #2.
XX
XX Proton pump inhibitor; tumour-specific antigenic peptide;
XX
XX cytosolic; tumour; murine.
XX
XX Mus musculus.
XX
XX JP2001286284-A.
XX
XX 16-OCT-2001.
XX
XX 05-APR-2000; 2000JP-0103966.
XX
XX 05-APR-2000; 2000JP-0103966.
XX
XX (SATO/) SATO N.
XX
XX (SUZUKI) SUZUKI N.
XX
XX (YAMA/) YAMAGUCHI M.
XX
XX WPI; 2002-134186/18.
XX
XX N-PSDB; ABA99214.
XX
XX Gene diagnostic agent and gene treating agent for tumours comprises
XX
XX PT using tumour-specific antigen and proton pump inhibitor as antitumour
XX
XX PT agent -
XX
XX Claim 24; Page 49; 80pp; Japanese.
XX
XX This invention relates to a diagnostic agent or treating agent for
XX
XX CC tumours by using a tumour specific antigen and a proton pump
XX
XX CC inhibitor. The method is cytosolic in its action and the
XX
XX CC tumour-specific antigen peptide is useful for treating and preventing

CC cancers. This sequence is a mouse tumour-specific
CC antigenic peptide.
XX
SQ Sequence 62 AA;
Query Match 20.0%; Score 6; DB 23; Length 62;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 11 PSATEP 16
Db 49 PSATEP 54
RESULT 23
AAW75089
ID AAW75089 standard; Protein; 81 AA.
XX
AC AAW75089;
XX
DT 28-JAN-1999 (first entry)
XX
DE Human secreted protein encoded by gene 33 clone HEMD84.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; osteoarthritis; thyroid; digestion;
KW osteoporosis; arthritis; testis; lung; chylodiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
FN MO9839446-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98MO-US04492.
XX
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
PR 11-APR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.
PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043315.
PR 11-APR-1997; 97US-0043568.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.
PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
PR 23-MAY-1997; 97US-0047584.

PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056632.
PR 22-AUG-1997; 97US-0056636.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
PR 22-AUG-1997; 97US-0056864.
PR 22-AUG-1997; 97US-0056872.
PR 22-AUG-1997; 97US-0056874.
PR 22-AUG-1997; 97US-0056875.
PR 22-AUG-1997; 97US-0056876.
PR 22-AUG-1997; 97US-0056877.
PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056921.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057761.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
XX Feng P, Ferris AM, Fischer CL, Graves KA, Greene JM, Hu JS, CA;
PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen K;
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX WPI: 1998-609887/51.
DR N-PSDB; AAV34186.
DR
XX
PT New isolated human genes and the secreted polypeptides they encode

PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1; Page 298; 447pp; English.
XX
CC This sequence represents a secreted human protein encoded by the gene
CC clone detailed in the descriptor line.
CC The gene can be used to generate fusion proteins by linking to the gene
CC to a human immunoglobulin Fc portion (e.g. AAV34145) for increasing the
CC stability of the fused protein as compared to the human protein only.
CC The invention relates to 70 novel genes and their fragments (nucleic
CC acid sequences: AAV34154-V34276; amino acid sequences AAW75057-W75179)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 70
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV34154 for described uses).
SQ
Sequence 81 AA;
Query Match 20.0%; Score 6; DB 19; Length 81;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 ATEPYI 18
|||
Db 71 ATEPYI 76
RESULT 24
AAO01578
ID AAO01578 standard; Protein; 136 AA.
XX
AC AAO01578;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 15470.
XX
KM Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KM vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
KM tissue growth factor; immunomodulatory; cancer; leukaemia;
KM nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
EN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI81509.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 15470; 1399pp + Sequence Listing; English.
CC
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce

CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, hematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ
Sequence 136 AA;
Query Match 20.0%; Score 6; DB 22; Length 136;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 PYISQ 21
|||
Db 6 PYISQ 11
RESULT 25
AAB56397
ID AAB56397 standard; Protein; 146 AA.
XX
AC AAB56397;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen protein sequence SEQ ID NO:975.
XX
KM Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KM neuroprotective; cytoskeletal; cardioactive; immunomodulatory; muscular;
KM vulnery; gastrointestinal; nephrotoxic; antineoplastic; gynaecological;
KM antibacterial; gene therapy; neural; immune; reproductive; renal;
KM gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KM wound; infectious disease.
XX
OS Homo sapiens.
XX
EN WO200055174-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05988.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587513/55.
DR N-PSDB; AAF15600.
XX
PT Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer -
XX
PS Claim 11; Page 1415-1416; 2338pp; English.
XX
CC AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytoskeletal,
CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
CC nephrotoxic, antineoplastic, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat

CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention.

XX Sequence 146 AA;

Query Match 20.0%; Score 6; DB 21; Length 146;

Best Local Similarity 100.0%; Pred. No. 71; Mismatches 0; Indels 0; Gaps 0;

Qy 17 YISGQI 22
 |||||
 Db 41 YISGQI 46

RESULT 26

ABP26232 ID ABP26232 standard; Protein; 163 AA.

XX ABP26232;

DT 02-JUL-2002 (first entry)

DE Streptococcus polypeptide SEQ ID NO 1640.

XX Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;

KM group A streptococcus; Streptococcus pyogenes; antibacterial;
 KM antinflammatory; infection; vaccine; meningitis; gene therapy.

XX Streptococcus pyogenes.

PN WO200234771-A2.

XX 02-MAY-2002.

PF 29-OCT-2001; 2001WO-GB04789.

PR 27-OCT-2000; 2000GB-0026333.

PR 24-NOV-2000; 2000GB-0028727.

PR 07-MAR-2001; 2001GB-0005640.

PA (CHIR-) CHIRON SPA.

PI (GENO-) INST GENOMIC RES.

PI Telford J, Maignani V, Margalit Ros YI, Grandi G, Fraser C;

PI Tectelin H;

XX WPI; 2002-352536/38.

XX N-PSDB; AAB66863.

PT New Streptococcus protein for the treatment or prevention of infection

PT or disease caused by Streptococcus bacteria, such as meningitis, and

PT for detecting a compound that binds to the protein -

XX Claim 1; Page 3315; 4525pp; English.

CC The invention relates to a protein (ABP25413-ABP30895) from group B

CC streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS

CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in

CC the specification. The proteins have antibacterial and antiinflammatory

CC activity. (i), nucleic acids encoding (i), AAB66044-ABN71526 and

CC antibodies that bind (i) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by

CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

CC Nucleic acids encoding (i) are used to detect Streptococcus in a

CC biological sample. (i) is used to determine whether a compound binds to

CC (i). A composition comprising (i) or a nucleic acid encoding (i), may be

CC used as a vaccine or diagnostic composition. The disease caused by

CC Streptococcus that is prevented or treated may be meningitis. Nucleic

CC acid encoding (i) may be used to recombinantly produce (i) and may be

CC used in gene therapy. Antibodies to (i) are used for affinity

CC chromatography, immunoassays, and distinguishing/identifying

CC Streptococcus proteins.

XX Streptococcus proteins.

XX Sequence 163 AA;

Query Match 20.0%; Score 6; DB 23; Length 163;

Best Local Similarity 100.0%; Pred. No. 79;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SLPELD 8
 |||||
 Db 139 SLPELD 144

RESULT 27
 AAM53253 ID AAM53253 standard; Protein; 188 AA.

XX AAM53253;

DT 30-JUL-1998 (first entry)

DE Candida albicans fungal antigen - allergen SEQ ID NO:6.

XX Candida albicans; vaccine; allergen; antigenic protein; fungal antigen;

KM immune response; infection; insoluble.

XX Candida albicans.

XX WO9809990-A1.

XX 12-MAR-1998.

XX 29-AUG-1997; 97WO-JP03041.

XX 31-MAR-1997; 97JP-0099775.

XX 04-SEP-1996; 96JP-0255400.

XX (TAKI) TAKARA SHUZO CO LTD.

XX Endo M, Kato I, Mizutani S, Takesako K;

XX WPI; 1998-193553/17.

XX N-PSDB; AAV20822.

XX Fungal antigens comprising insoluble fraction of fungal cells -

XX useful for, e.g. stimulating immune response and treatment and

XX diagnosis of fungal infection(s)

XX Claim 28; Page 79-80; 108pp; Japanese.

CC The present sequence represents an active vaccine component or allergen

CC derived from Candida albicans, which is an antigenic protein. The

CC present invention describes fungal antigens, comprising the insoluble

CC fraction of fungal cells having completely/partially removed cell walls.

CC Also described are nucleic acids encoding the antigens and a method for

CC producing the antigens. The antigens can be used for preparing

CC therapeutic compositions for stimulating immune response, e.g. as a

CC vaccine. They can be used for treatment of fungal infections, treatment

CC and prevention of allergies and diagnosis of fungal infections in

CC vertebrates. The vaccines are not live, and have low toxicity.

XX Sequence 188 AA;

Query Match 20.0%; Score 6; DB 19; Length 188;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 ATEPYI 18
 |||||
 Db 1 ATEPYI 6

RESULT 28
 AAG92973 standard; Protein; 200 AA.
 ID AAG92973 standard; Protein; 200 AA.
 XX
 AC AAG92973;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE C glutamicum protein fragment SEQ ID NO: 6727.
 XX
 KM Corynebacterium; amino acid synthesis; vitamin; saccharide;
 KM organic acid synthesis.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN EP1108790-A2.
 XX
 PD 20-JUN-2001.
 XX
 PR 18-DEC-2000; 2000EP-0127688.
 XX
 PR 16-DEC-1999; 99JP-0377484.
 PR 07-APR-2000; 2000JP-0159162.
 PR 03-AUG-2000; 2000JP-0280988.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tetsushi N, Senoh A, Ikeda M, Ozaki A;
 XX
 DR WPI; 2001-376931/40.
 XX
 DR N-PSDB; AAH68192.
 PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analysing
 PT expression profile or pattern of a gene and identifying homologous gene
 PT
 XX
 PS Claim 17; SEQ ID NO: 6727; 246bp + Sequence Listing; English.
 XX
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of corynebacterium bacterium, measuring expression amount and
 CC analysing the expression profile or expression pattern of a gene derived
 CC from Corynebacterium bacterium, and identifying a homologue of a gene derived
 CC from corynebacterium bacterium. Corynebacterium bacteria are useful for producing
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a protein described
 CC in the exemplification of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC European Patent Office.
 XX
 SQ Sequence 200 AA;
 XX
 Query Match 20.0%; Score 6; DB 22; Length 200;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LPELDY 9
 Db 6 LPELDY 11
 XX
 RESULT 29
 AAU00514 standard; Protein; 200 AA.
 ID AAU00514 standard; Protein; 200 AA.
 XX
 AC AAU00514;
 XX
 DT 09-MAY-2001 (first entry)
 XX

DE C. melassecola superoxide dismutase.
 XX
 KM Superoxide dismutase; sod; corynebacterium microorganism; metabolite;
 KM vitamin; D-pantothenic acid; L-lysine; amplification; animal nutrition.
 XX
 OS Corynebacterium melassecola.
 XX
 PN EP1077261-A2.
 XX
 PD 21-FEB-2001.
 XX
 PR 02-AUG-2000; 2000EP-0116669.
 XX
 PR 13-AUG-1999; 99US-0373731.
 XX
 PA (DEGS) DEGUSSA-HUELS AG.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Merkmann M, Guyonvarch A, Marx A;
 XX
 DR WPI; 2001-212718/22.
 DR N-PSDB; AAS00520.
 XX
 PT New DNA encoding superoxide dismutase of Corynebacterium, useful for
 PT producing transformants with increased production of metabolites,
 PT particularly lysine -
 XX
 PS Claim 3; Page 14-15; 19pp; English.
 XX
 CC The sequence represents Corynebacterium melassecola superoxide dismutase
 CC (sod) polypeptide. Corynebacterium microorganisms may be transformed with a
 CC sod DNA sequence and the sod gene can be amplified. Sod is then often
 CC overexpressed in corynebacterium bacteria. Corynebacterium that overexpress sod
 CC are used for production of metabolites, particularly nucleotides,
 CC vitamins and amino acids, especially D-pantothenic acid or, specifically,
 CC L-lysine. These metabolites are useful in human or animal nutrition and
 CC as pharmaceuticals. Overexpression of sod in corynebacterium increases the
 CC yield of particular metabolites.
 XX
 SQ Sequence 200 AA;
 XX
 Query Match 20.0%; Score 6; DB 22; Length 200;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LPELDY 9
 Db 6 LPELDY 11
 XX
 RESULT 30
 ABB47790 standard; Protein; 207 AA.
 ID ABB47790 standard; Protein; 207 AA.
 XX
 AC ABB47790;
 XX
 DT 05-FEB-2002 (first entry)
 XX
 DE Listeria monocytogenes protein #494.
 XX
 KM Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KM vitamin B12; bacterial infection; disease.
 XX
 OS Listeria monocytogenes.
 XX
 PN WO200177335-A2.
 XX
 PD 18-OCT-2001.
 XX
 PR 11-APR-2001; 2001WO-FR01118.
 XX
 PR 11-APR-2000; 2000FR-0004629.
 XX

PA (INSP) INST PASTEUR.
XX
XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Feihl H, Dehoux P,
PI Duesuguet O, Chetoui F, Nedjari H, Glaeser P, Kunst F, Cossart P,
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA,
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A,
PI Chakraborty T, Domann E, Hahn T, Berche P, Charbit A, Durant L,
PI Perez-Diaz J, Baguero F, Garcia Del Portillo F, Gomez-Lopez N,
PI Madueno E, De Pablos B, Wehlant J, Kaerst U, Entian K, Hauf J,
PI Rose M, Voss H;
XX WPI; 2002-010914/01.
XX
XX Genomic sequence for *Listeria monocytogenes*, useful e.g. for treatment
PT and prevention of *Listeria* and related bacterial infections, and
PT related polypeptides -
XX
XX Claim 6; SEQ ID No 495; 192pp; French.
XX
XX The present invention relates to the genome sequence of *Listeria*
CC *monocytogenes* EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in *L.*
CC *monocytogenes* and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of *L. monocytogenes* and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate *L. monocytogenes*-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by *L.*
CC *monocytogenes* and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPD
CC at ftp.wipd.int/pub/published_pct_sequences.
XX
XX Sequence 207 AA;
SQ
Query Match 20.0%; Score 6; DB 23; Length 207;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 16 PYISGO 21
|||
|||
Db 191 PYISGO 196
RESULT 31
AY34657
ID AAY34657 standard; Protein; 214 AA.
XX
XX AAY34657;
AC
XX
XX 13-SEP-1999 (first entry)
DT
XX
XX C. pneumoniae protein involved in intermediate metabolism.
DE
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope.
XX
XX Chlamydia pneumoniae.
OS
XX
XX W09927105-A2.
FN
XX
XX 03-JUN-1999.
PD
XX
XX 20-NOV-1998; 98WO-1B01890.
PF
XX
XX 04-NOV-1998; 98US-0107078.
PR
XX
XX 21-NOV-1997; 97FR-0014673.
PR

XX
XX (GEST) GENSET.
PA
XX
XX Griffiths R;
PI
XX
XX WPI; 1999-357842/30.
DR
XX
XX Genome sequence of *Chlamydia pneumoniae*
PT
XX
XX Page 665; Disclosure; 1912pp; English.
PS
XX
XX AAY34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAX91990) of *Chlamydia pneumoniae*.
CC C. pneumoniae causes respiratory diseases such as pneumonia and
CC bronchitis and is thought to be a contributing factor in heart
CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in
CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae.
XX
XX Sequence 214 AA;
SQ
Query Match 20.0%; Score 6; DB 20; Length 214;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 YSLPEL 7
|||
|||
Db 13 YSLPEL 18
RESULT 32
AAB94056
ID AAB94056 standard; Protein; 221 AA.
XX
XX AAB94056;
AC
XX
XX 26-JUN-2001 (first entry)
DT
XX
XX Human protein sequence SEQ ID NO:14228.
DE
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
KW
XX
XX Homo sapiens.
OS
XX
XX EP1074617-A2.
FN
XX
XX 07-FEB-2001.
PD
XX
XX 28-JUL-2000; 2000EP-0116126.
PE
XX
XX 29-JUL-1999; 99JP-0248036.
PR
XX
XX 27-AUG-1999; 99JP-0300253.
PR
XX
XX 11-JAN-2000; 2000JP-0118776.
PR
XX
XX 02-MAY-2000; 2000JP-0183767.
PR
XX
XX 09-JUN-2000; 2000JP-0241899.
XX
XX (HELI-) HELIX RES INST.
PA
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Negai K, Otsuki T;
PI WPI; 2001-318749/34.
DR
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
XX Claim 8; SEQ ID 14228; 2537pp + CD ROM; English.
PS

XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH1628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
CC
SQ Sequence 221 AA;
Query Match 20.0%; Score 6; DB 22; Length 221;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 ATEPYI 18
Db 211 ATEPYI 216
RESULT 33
AAG78026
ID AAG78026 standard; Protein; 226 AA.
XX
AC AAG78026;
XX
DT 15-JAN-2002 (first entry)
XX
DE Piscirickettsia salmonis ICME.
XX
KW Piscirickettsia salmonis; piscirickettsiosis; salmonid rickettsial;
KW septicæmia; SRS; surface antigen; vaccine; antibacterial; fish;
XX type strain LF-89.
XX
OS Piscirickettsia salmonis.
XX
PN WO200168865-A2.
XX
PD 20-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-GB01055.
XX
PR 11-MAR-2000; 2000GB-0005838.
PR 01-JUL-2000; 2000GB-0016080.
PR 01-JUL-2000; 2000GB-0016082.
PR 29-JUL-2000; 2000GB-0018599.
XX
PA (AQUA-) AQUA HEALTH EURO LTD.
XX
PI Simard N, Brouwers H, Jones S, Griffiths S, Valenzuela P,
PI Burzio L;
XX
XX WPI; 2001-639050/73.
DR N-PSDB; AAH79041.
XX
XX New nucleic acids encoding an amino acid sequence homologous to the
PT surface antigen present on Piscirickettsia salmonis are useful to
PT protect fish against piscirickettsiosis -

XX Claim 6; Fig 6; 25pp; English.
PS
XX
XX The invention relates to nucleic acid sequences and the encoded protein
CC of a least part of the surface antigen present on Piscirickettsia
CC salmonis for production of a vaccine with antibacterial activity to
CC protect fish against P. salmonis which causes piscirickettsiosis, also
CC known as salmonid rickettsial septicæmia.
XX
SQ Sequence 226 AA;
Query Match 20.0%; Score 6; DB 22; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 SLPELD 8
Db 98 SLPELD 103
RESULT 34
AAG49754
ID AAG49754 standard; Protein; 294 AA.
XX
AC AAG49754;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 62974.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0138119.
PR 16-JUN-1999; 99US-0138452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160757.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161920.

PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 20.0%; Score 6; DB 21; Length 294;
Best Local Similarity 100.0%; Pred. No.1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ATEPYI 18
|||
Db 20 ATEPYI 25

RESULT 35
AAG50274
ID AAG50274 standard; Protein; 294 AA.

XX AAG50274;

AC 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 63691.

XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

XX Arabidopsis thaliana.

XX EPI033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123160.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hydridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
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Query Match 20.0%; Score 6; DB 21; Length 311;
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 Db 38 ATEPYI 43

RESULT 37

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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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Db 38 ATEPYI 43

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DT 18-OCT-2000 (first entry)
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;

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Qy 13 ATEPYI 18

Db 38 ATEPYI 43

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ABBS4867;

16-MAY-2002 (first entry)

Lactococcus lactis protein purm.

Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.

Lactococcus lactis IL1403.

FR2807446-A1.

XX 12-OCT-2001.
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 PF 11-APR-2000; 2000FR-0004630.
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 PA Bolotine A, Sorokine A, Renault P, Ehrlich SD;
 PI WPI; 2002-043418/06.
 DR New nucleotide sequence useful in the identification or Lactococcus
 XX lactic acid and related species -
 PT
 PS Claim 6; SEQ ID No 1569; 2504bp; French.
 XX The present invention is related to a Lactococcus lactis nucleotide
 CC sequence (AB90521) and related proteins (AB853300-AB855621). The
 CC nucleic acid sequence is useful in the detection and/or amplification of
 CC nucleic acid sequence, particularly to identify Lactococcus lactis or
 CC related species. The proteins of the invention are useful for the
 CC biosynthesis or biodegradation of a composition of interest. The
 CC invention helps research in lactic bacteria, particularly useful in the
 CC production of yogurt and cheese.
 CC Note: The sequence data for this patent is based on equivalent patent
 CC WO00017734 (published 18-OCT-2001) which is available in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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 XX Protein identification; signal transduction pathway; metabolic pathway;
 KM hybridisation assay; genetic mapping; gene expression control; promoter;
 KM termination sequence.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX EPI033405-A2.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 20.0%; Score 6; DB 21; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 ATEPYI 18
|||||
Db 82 ATEPYI 87

Search completed: April 9, 2003, 14:14:13
Job time : 35.3119 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 8, 2003, 01:31:08 ; Search time 443.807 Seconds
(without alignments)
1967.259 Million cell updates/sec

Title: US-09-987-190-2
Perfect score: 145
Sequence: 1 KYSLEPDIYFSAPEYISQINEIXYXX 30

Scoring table: BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Rgapop 6.0 , Rgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-O=/cgm2.1/USPTO.spool/US09987190/runat.02042003.092632.19221/app.query.fasta_1.526
-DB=GenEmbl -OPMT=fastap -SUFFIX=rge -MIMATCH=0.1 -LOFCL=0 -LOFEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09987190 @CGN 1.1 1758 @runat.02042003.092632.19221 -NCPU=6 -ICPU=3
-NO_XLPEXY -NO_WAMP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -RGAPOP=6 -RGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sbs:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*
15: em_ba:*
16: em_fun:*
17: em_in:*
18: em_mu:*
19: em_mu:*
20: em_mu:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sbs:*
28: em_un:*

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_man:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htg_hum:*
40: em_htg_mus:*
41: em_htg_oher:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	97.2	1859	8 AF031478	AF031478 Candida a
2	107	73.8	2332	8 CSMSOD	Y11598 Candida sp.
3	103	71.0	735	1 NAU02341	U02341 Nocardia as
4	101	69.7	666	1 AF333434	AF333434 Mycobacte
5	101	69.7	960	1 MAU11550	U11550 Mycobacteri
6	101	69.7	1741	1 AF180816	AF180816 Mycobacte
7	100	69.0	815	1 D13288	D13288 Mycobacteri
8	100	69.0	908	11 CNS06105	AL400539 T3 end of
9	100	69.0	2045	8 SCSDOMNG	X02156 Yeast gene
10	100	69.0	18715	8 YSCHL2825	U10400 Saccharomyc
11	100	69.0	24431	8 YSCH9780	U0555 Saccharomyc
12	99	68.3	1071	1 AP061031	AF061031 Mycobacte
13	99	68.3	1478	1 MFSODA	X70914 M. fortulum
14	98	67.6	649	1 MLEPSOD	X16453 Mycobacteri
15	98	67.6	344050	1 MLEPRTN1	AL583917 Mycobacte
16	94	64.8	790	1 MTSD	X52861 M. tuberculo
17	94	64.8	943	1 AF077406	AF077406 Mycobacte
18	94	64.8	1321	1 AF061030	AF061030 Mycobacte
19	94	64.8	14282	1 AB007188	AB007188 Mycobacte
20	94	64.8	37751	1 MTCY1A6	X91650 P. freudente
21	91	62.8	567	1 PFSOD	Y09012 P. freudente
22	91	62.8	567	1 PFSOD	AB079877 Marsupena
23	80	55.2	655	3 AB079877	AB079877 Equus cab
24	80	55.2	954	4 AB001693	AF312188 Gordonia
25	80	55.2	4439	1 GSP312188	E15569 cDNA encodi
26	79	54.5	812	6 E15569	AX123311 Sequence
27	77	53.1	600	6 AX123311	I28808 Oryctolagus
28	77	53.1	606	4 RABMSD	AB055218 Corynebac
29	77	53.1	960	1 AB055218	AX136077 Sequence
30	77	53.1	1143	6 AX136077	BD011434 DNA, amin
31	77	53.1	1143	6 BD011434	AF236111 Corynebac
32	77	53.1	2207	1 AF236111	AX127153 Sequence
33	77	53.1	309400	6 AX127153	AF005283 Corynebac
34	77	53.1	325651	1 AP005283	AF521909 Trichinel
35	75	52.4	663	3 AF521909	AF278864 Digitalis
36	76	52.4	761	8 DLA278864	AX465763 Sequence
37	74	51.0	325	6 AX465763	S78832 Sod-2-manga
38	74	51.0	535	10 S7883281	ARI30379 Sequence
39	74	51.0	594	6 ARI30379	A12180 Artificial
40	74	51.0	600	6 A12180	A12191 Artificial
41	74	51.0	600	6 A12191	A12200 Nucleotide
42	74	51.0	600	6 A12200	B03557 Synthetic D
43	74	51.0	609	6 E03557	AF236110 Acidianus
44	74	51.0	636	1 AF236110	
45	74	51.0	636	1 AF236110	

ALIGNMENTS

RESULT 1

AF031478 1859 bp DNA linear PLN 13-JAN-2000
LOCUS AF031478
DEFINITION Candida albicans manganese-superoxide dismutase precursor (SOD2)
gene, complete cds.
AF031478
VERSION AF031478.1 GI:2623884
KEYWORDS
SOURCE
ORGANISM
Candida albicans.
Candida albicans.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitospotic Saccharomycetales; Candida.
REFERENCE
1 (bases 1 to 1859)
Rhee,G.E., Hwang,C.S., Brady,M.J., Kim,S.T., Kim,Y.R., Huh,W.K.,
Baek,Y.U., Lee,B.H., Lee,J.S. and Kang,S.O.
Manganese-containing superoxide dismutase and its gene from Candida
albicans
JOURNAL Biochim. Biophys. Acta 1426 (3), 409-419 (1999)
MEDLINE 99177423
PUBMED 10076057
REFERENCE 2 (bases 1 to 1859)
Kang,S.O. and Rhee,G.
Direct Submission
Submitted (26-OCT-1997) Microbiology, Seoul National University,
Shinlim-dong, Kwanak-gu, Seoul 151-742, Republic of Korea
JOURNAL
TITLE
AUTHORS
FEATURES
Location/Qualifiers
1. 1859
/organism="Candida albicans"
/db_xref="taxon:5476"
gene 848. 1552
/gene="SOD2"
848. 1552
/gene="SOD2"
/note="Mn-SOD"
/codon_start=1
/transl_table=12
/product="manganese-superoxide dismutase precursor"
/protein_id="AAB86583.1"
/translation="MFSSIRSSRYLTKASATRTATLNAASKFTTRKYSPLDELYE
FSATRPYSGINRIHYTKHQTYYNNINAEQAVEKSGEYKVALAEKAINPFG
GGYINLCLMKNLAPVSGQPSSESKLGRQIVKQFSLDKLEITNGCLAIGQS
GWAIVNKKANGDITDVTITANODTVDPLPLAIDAWEHAYLYQYONKADYFN
LMHYINMKAEARREFP"
sig_peptide 848. 949
/gene="SOD2"
950. 1549
/gene="SOD2"
mat_peptide /product="manganese-superoxide dismutase"
BASE COUNT 601 a 310 c 312 g 636 t
ORIGIN
Alignment Scores:
Pred. No.: 1.44e-15 Length: 1859
Score: 141.00 Matches: 27
Percent Similarity: 96.43% Conservative: 0
Best Local Similarity: 96.43% Mismatches: 1
Query Match: 97.24% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x AF031478 (1-1859)
Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 950 AAATATGATTTCACGAATTCGACTATTCGCTACTGACCATCACTTCTTGGT 1009
Qy 21 GlnIleAsnGluIle**TyrThr 28
Db 1010 CAAATPAAACGAATTCACACT 1033
RESULT 2
CSMN50D 2332 bp DNA linear PLN 11-MAY-2001
LOCUS CSMN50D
DEFINITION Candida sp. HN95 MnSOD gene.

Y11598
VERSION Y11598.1 GI:1877052
KEYWORDS manganese superoxide dismutase; MnSOD gene.
SOURCE
ORGANISM
Candida sp. HN95.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitospotic Saccharomycetales; Candida.
REFERENCE
1 (bases 1 to 2332)
Hong,Y.M., Nam,Y.S. and Choi,S.Y.
TITLE
AUTHORS
JOURNAL Molecular Cloning and Characterization of Mn-Superoxide Dismutase
Gene from Candida sp
J. Microbiol. 35, 309-314 (1997)
REFERENCE 2 (bases 1 to 2332)
Choi,S.
AUTHORS
TITLE
JOURNAL Direct Submission
Submitted (04-MAR-1997) S. Choi, Hannam University, Microbiology,
133 Ojung-Dong, Taejeuk-ku, Taejeon, 300-791, SOUTH KOREA
JOURNAL
FEATURES
Location/Qualifiers
1. 2332
/organism="Candida sp. HN95"
/strain="HN95"
/db_xref="taxon:159257"
1435. 2332
/gene="MnSOD"
1435. 2332
/gene="MnSOD"
1500. 2183
/gene="MnSOD"
1500. 2183
/gene="MnSOD"
/codon_start=1
/protein_id="CAA72335.1"
/db_xref="GI:2398587"
/translation="MLSSAIKRSVAVGARSVSSVGAVRTKSLPDLMDFGALBP
HISGQINEIHYTKHQTYYNNINAEQAVEKSGEYKVALAEKAINPFGGYYTNC
LPMKNLAPKQGGGEPPEADSEPRAKRIVEYGSGLDNKATITNGKLAGIQQSGAFTYK
BAEKRYLYLN"
sig_peptide 1500. 1589
/gene="MnSOD"
1590. 2180
/gene="MnSOD"
mat_peptide /product="unnamed"
BASE COUNT 646 a 519 c 442 g 725 t
ORIGIN
Alignment Scores:
Pred. No.: 2.86e-09 Length: 2332
Score: 107.00 Matches: 20
Percent Similarity: 85.71% Conservative: 4
Best Local Similarity: 71.43% Mismatches: 4
Query Match: 73.79% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x CSMN50D (1-2332)
Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 1584 AAAGATGCTTACCGAATTCGATTGGGACTTCGAGGCTTGAGCCACATTTGGGA 1643
Qy 21 GlnIleAsnGluIle**TyrThr 28
Db 1644 CAGATCAACGAATTCACCTACACC 1667
RESULT 3
NAU02341 735 bp DNA linear BCT 12-MAR-1996
LOCUS NAU02341
DEFINITION Nocardia asteroides GUH2 superoxide dismutase gene, complete cds.
ACCESSION U02341
VERSION U02341.1 GI:484066
KEYWORDS
SOURCE
ORGANISM
Nocardia asteroides.
Nocardia asteroides
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

REFERENCE 1 Actinomycetales; Corynebacterineae; Nocardiaceae; Nocardia.
 AUTHORS 1 (bases 1 to 735)
 TITLE Alcedor, D.J., Chapman, G.D. and Beaman, B.L.
 JOURNAL Isolation, sequencing and expression of the superoxide
 MEDLINE dismutase-encoding gene (sod) of Nocardia asteroides strain GUN-2
 PUBMED Gene 164 (1), 143-147 (1995)
 7590304
 REFERENCE 2 (bases 1 to 735)
 AUTHORS Chapman, G.G.
 TITLE Direct Submission
 JOURNAL Submitted (01-OCT-1993) Gail D. Chapman, Medical Microbiology and
 Immunology, University of California at Davis, Medical Science
 Building 1A, Davis, CA 95616, USA
 location/Qualifiers

FEATURES
 source
 1..735
 /organism="Nocardia asteroides"
 /strain="GUN2"
 /db_xref="taxon:1824"
 /clone="clone PAC1500"
 /clone_11b="library EMBL-3"
 99..106
 /note="potential ribosome binding site"
 112..735
 /EC_number="1.15.1.1"
 /standard_name="SOD"
 /note="alternative start codon GTG"
 /codon_start=1
 /transl_table=11
 /product="superoxide dismutase"
 /protein_id="AA01964.1"
 /db_xref="GI:484067"
 /translation="MAEYTLPLDWDYALPEPHISQINELHSHKHAAYVAGANTL
 EKLEBARANEDHAIPLNEKNLAFHFGHVNHSIMWNLSPPGDKPVGELAAIDDA
 FGSFDRKRAQFSAANGLOSGGMAVGYDPLGKLTLPOLYDQANVPLGIIPLLQVD
 MMEHAFILQIKNVKADYVYKAFMNVNADYQKRYAATSKAGLIFG"

BASE COUNT 148 a 242 c 230 g 115 t

ORIGIN

Alignment Scores:
 Pred. No.: 3.64e-09 Length: 735
 Score: 103.00 Matches: 17
 Percent Similarity: 92.86% Conservative: 9
 Best Local Similarity: 60.71% Mismatches: 2
 Query Match: 71.03% Indels: 0
 Gaps: 0

DB: 1 Gaps: 0

9-987-190-2 (1-30) x NAU02341 (1-735)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 ::
 Db 118 GAGTACACCGCTCGGATTCGATTACGACTACACGCGCTCGAACCCACATCTCCGGG 177
 Qy 21 GlnTleAangluIle***TyrThr 28
 ::
 Db 178 CAGATCAACGAGCTGCACATTC 201

RESULT 4
 AF333434 666 bp DNA linear BCT 17-JAN-2001
 LOCUS Mycobacterium avium subsp. paratuberculosis superoxide dismutase
 DEFINITION gene, complete cds.
 ACCESSION AF333434
 VERSION AF333434
 KEYWORDS AF333434.1 GI:12247898

SOURCE
 ORGANISM Mycobacterium avium subsp. paratuberculosis.
 Mycobacterium avium subsp. paratuberculosis
 Bacteria; Firmicutes; Actinobacteriae; Actinobacteridae;
 Actinomycetales; Corynebacterineae; Mycobacteriaceae;
 Mycobacterium; Mycobacterium avium complex (MAC).
 1 (bases 1 to 666)
 Dheenadhayalan, V. and Chang, Y.F.
 Mycobacterium avium subsp. paratuberculosis superoxide dismutase

JOURNAL gene
 REFERENCE 2 Unpublished
 AUTHORS 2 (bases 1 to 666)
 TITLE Dheenadhayalan, V. and Chang, Y.F.
 JOURNAL Direct Submission
 Submitted (04-JAN-2001) Population Medicine and Diagnostic Science,
 College of Veterinary Medicine, Cornell University, P.O. Box 5786,
 Ithaca, NY 14853, USA
 location/Qualifiers

FEATURES
 source
 1..666
 /organism="Mycobacterium avium subsp. paratuberculosis"
 /sub_species="paratuberculosis"
 /db_xref="taxon:1770"
 34..666
 /codon_start=1
 /transl_table=11
 /product="superoxide dismutase"
 /protein_id="AA05084.1"
 /db_xref="GI:12247899"
 /translation="MAEYTLPLDWDYALPEPHISQINELHSHKHAAYVAGANTL
 AKLEBARANEDHAIPLNEKNLAFHFGHVNHSIMWNLSPPGDKPVGELAAIDDA
 FGSFDRKRAQFSAANGLOSGGMAVGYDPLGKLTLPOLYDQANVPLGIIPLL
 QVDMMEHAFILQIKNVKADYVYKAFMNVNADYQKRYAATSKAGLIFG"

BASE COUNT 142 a 221 c 196 g 107 t

ORIGIN

Alignment Scores:
 Pred. No.: 7.44e-09 Length: 666
 Score: 101.00 Matches: 17
 Percent Similarity: 92.86% Conservative: 9
 Best Local Similarity: 60.71% Mismatches: 2
 Query Match: 69.66% Indels: 0
 Gaps: 0

US-09-987-190-2 (1-30) x AF333434 (1-666)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 ::
 Db 40 GATACACCGCTCGGATTCGATTACGACTACACGCGCTCGAACCCACATCTCCGGG 99
 Qy 21 GlnTleAangluIle***TyrThr 28
 ::
 Db 100 CAGATCAACGAGCTGCACATTC 123

RESULT 5
 MAU11550 960 bp DNA linear BCT 25-SEP-1996
 LOCUS Mycobacterium avium TMC 724 superoxide dismutase (sod) gene,
 DEFINITION complete cds.
 ACCESSION U11550
 VERSION U11550.1 GI:555745

SOURCE
 ORGANISM Mycobacterium avium.
 Mycobacterium avium
 Bacteria; Firmicutes; Actinobacteriae; Actinobacteridae;
 Actinomycetales; Corynebacterineae; Mycobacteriaceae;
 Mycobacterium; Mycobacterium avium complex (MAC).
 1 (bases 1 to 960)
 Bescuyer, V., Haddad, N., Frehel, C. and Berche, P.
 Molecular characterization of a surface-exposed superoxide
 dismutase of Mycobacterium avium
 Microb. Pathog. 20 (1), 41-55 (1996)
 6692009

JOURNAL
 MEDLINE
 PUBMED 6692009
 REFERENCE 2 (bases 1 to 960)
 AUTHORS Bescuyer, V.E.
 TITLE Direct Submission
 JOURNAL Submitted (28-JUN-1994) Vincent E. Bescuyer, INSERM
 U411-Microbiologie, Faculte de Medecine Necker, 156 rue de
 Vaugirard, Paris 75015, France
 Location/Qualifiers

FEATURES
 source
 1..960
 /organism="Mycobacterium avium"

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/strain="TMC 724"
/db_xref="taxon:1764"
/clone="psOD1"
251..874
/gene="god"
251..874
/gene="god"
/function="molecular dismutation of oxygen free radicals"
/note="GTG start codon"
/codon_start=1
/evidence=experimental
/transl_table=1
/product="superoxide dismutase"
/protein_id="AAB08770.1"
/db_xref="GI:555746"
/translacion="MAEYTLDPDWDVAALPHISGQINIEIHTTKHATVYKVDNAL
AKLEARANEDHAAIPLNEKNIAPHLGCHVHNSIWMKLSDDGDKPGEIAAIDDA
FGSDPKFAQFSAANGSGGMVNLGDTLGSRLFTQLYDQGANVPLGIIPLLQVD
MWEHAFYLYQNVKADVYKAVMANVYNMADVQKRYAAATSKQGLIFG"
BASE COUNT      179 a      320 c      298 g      163 t
GIN
Assignment Scores:
Pred. No.:      1.17e-08      Length:      960
Score:      101.00      Matches:      17
Percent Similarity:      92.66%      Conservative:      9
Best Local Similarity:      60.71%      Mismatches:      2
Query Match:      69.66%      Indels:      0
DB:      1      Gaps:      0
US-09-987-190-2 (1-30) x MAU1550 (1-960)
Qy      1      LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      257      GAAATACACCTCCCGAGCTCGAGCTGGAGTACGAGCTTGGAACCGACATCTCGGG 316
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy      21      GlnIleAsnGlnIle**TyrThr 28
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      317      CAGATCAACGAGATCCACCAACC 340
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 6
AF180816      1741 bp      DNA      linear      BCT 30-NOV-2001
LOCUS      AF180816
DEFINITION      Mycobacterium avium subsp. paratuberculosis superoxide dismutase
                        (sod) gene, complete cds; and unknown gene.
ACCESSION      AF180816
VERSION
KEYWORDS
SOURCE
ORGANISM
.
Mycobacterium avium subsp. paratuberculosis.
Mycobacterium avium subsp. paratuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium avium complex (MAC).
1 (bases 1 to 1741)
Liu,X., Feng,Z., Harris,N.B., Cirillo,J.D., Bercovier,H. and
Barletta,R.G.
Identification of a secreted superoxide dismutase in Mycobacterium
avium ssp. paratuberculosis
FEMS Microbiol. Lett. 202 (2), 233-238 (2001)
21411748
PUBMED
21520620
2 (bases 1 to 1741)
Liu,X., Feng,Z., Cirillo,J. and Barletta,R.G.
Direct Submission
Submitted (25-AUG-1999) Veterinary and Biomedical Sciences,
University of Nebraska-Lincoln, Fair Street and East Campus Loop,
Lincoln, NE 68583-0905, USA
Location/Qualifiers
1..1741
/oranism="Mycobacterium avium subsp. paratuberculosis"
/strain="K-10"
/sub_species="paratuberculosis"
/db_xref="taxon:1770"
FEATURES
source

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CDS		260..883	/gene="rsod"
		1	/codon_start=1
		1	/transl_table=1
		1	/product="superoxide dismutase"
		1	/protein_id="AAG09425.1"
		1	/db_xref="GI:9957590"
		1	/translation="MAYTILPDLMDYALPEPHISQGINEIHTTKHATTVKGVNDLLAKLEEARAQEDDHAIFLNEKNLAFLHGHNHSIMWNKLSPDGDKPTGLAAIDDAFGSDKRRAQDSAAANGLOGSMAVLGYDVGSRLTFQLYDOANPLDIPLLOVDMMERAFPLYOKYNKYADVKAFFMVNMADVQKVYAATSXAQGLIFG"
		1041..1574	
CDS		1041..1574	/note="similar to Mycobacterium tuberculosis hypochetrical protein RV3847"
		1	/codon_start=1
		1	/transl_table=1
		1	/product="unknown"
		1	/protein_id="AAG09426.1"
		1	/db_xref="GI:9957591"
		1	/translation="METGSDRPYGVSFPFHSRGALKGFVISGRNPDSTKEKAQILMAVV RVALSPGLSLTTVFEGARELPDEPERGTGLVAETVGESAIIPGHFAHDQPAPL LMLHPSEITMPSLPECTGAASGCULLPGILPYLGHEBRAWVEAEADGTITSMSRVGV DPISHPTAILAMLIAA"
BASE COUNT	286 a	594 c	562 g
ORIGIN		299 t	
Alignment Scores:			
Pred. NO.:	2,45e-08	Length:	1741
Score:	101.00	Matches:	17
Percent Similarity:	92.86%	Conservative:	9
Best Local Similarity:	60.71%	Mismatches:	2
Query Match:	69.66%	Indels:	0
DB:	1	Gaps:	0
US-09-987-190-2 (1-30) x AF180816 (1-1741)			
Oy	1	LysTYSerLeuProGluLeuAspTYrCluPheSerAlaThrGluProtyrILEserely 20	
Db	266	GAATACACCCTGGCCCGACTGACATGCACTATGACGCGTGGAACCGCACATCTCGGGG 325	
Oy	21	GinLeaEngJulie***TyrrThr 28	
Db	326	CAGATCAAAGAGATCCACCAACC 349	
RESULT 7			
LOCUS	DJ3288	815 bp	DNA linear BCT 17-JUN-1998
DEFINITION	Mycobacterium lepraeurium DNA for Mn superoxide dismutase, complete cds.		
ACCESSION	DJ3288		
VERSION	DJ3288.1	GI:3228263	
KEYWORDS	Mn superoxide dismutase; Mycobacterium lepraemurium (strain:Hawaiian) DNA, clone_lib:lambda gt 11 and pUC118 clone:pMB67 and pMP49.		
SOURCE	MycoBacterium lepraemurium Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. 1 (bases 1 to 815) Nakamura,M. Unpublished 2 (bases 1 to 815) Nakamura,M. Direct Submission Submitted (21-SEP-1992) Masahiko Nakamura, Osaka University, Institute for Protein Research, 3-2 Yamadaoka, Suita, Osaka 565, Japan (E-mail:mshahiko@protein.osaka-u.ac.jp, Tel:06-879-8628, Fax:06-879-8629) Location/Qualifiers 1..815 /organism="Mycobacterium lepraemurium" /strain="Hawaiian"		
FEATURES			
source			

CDS

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AKLEERANEDHAAIFLNEKNLAFHGHVNHSLPMKRLSPDGDKPTGEIAAIDDA
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MMEHAFYIQYKADYKAFMNVNVMADVOKRYTAATSKTGGLFG"

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BASE COUNT 164 a 270 c 253 g 128 t

ORIGIN

Alignment Scores:

Pred. No.: 1.45e-08 Length: 815

Percent Similarity: 100.00 Matches: 17

Best Local Similarity: 89.29% Conservative: 8

Query Match: 60.71% Mismatches: 3

Indels: 0

Gaps: 0

US-09-987-190-2 (1-30) x D13288 (1-815)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 100 GAATACACCTCCCGACCTGAGCTAGACCTATGAAGCTTGGAACCGACATCTCGGGG 159

Qy 21 GlnIleAngIle***TyrThr 28

Db 160 CAGATTACAGATCCACACACC 183

RESULT 8

CNS06105

LOCUS T3 end of clone AS0AA022C08 of library AS0AA from strain CLIB 533

DEFINITION of Saccharomyces bayanus, sequence tagged site.

ACCESSION AL400539

VERSION AL400539.1 GI:12156708

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

Yeast species: Saccharomyces bayanus var. uv.

exiguus, Saccharomyces servazii, Zygosacchar.

Saccharomyces kluyveri, Kluyveromyces thermotol.

lactis var. lactis, Kluyveromyces marxianus var.

angusta, Debaryomyces hansenii var. hansenii, P.c.

Candida tropicalis and Yarrowia lipolytica. Genomic

5 kb were prepared and both extremities were sequence

keywords for description of this sequence and for the

the other extremity of this insert.

Location/Qualifiers

1..908

/organism="Saccharomyces bayanus"

/strain="CLIB 533"

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/db_xref="taxon:4931"

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similarity to S.pombe hypothetical protein]

1 putative frameshift (s)"

/evidence=not_experimental

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/note="similar to Saccharomyces cerevisiae ORF YHR008c [

SOD2 ; superoxide dismutase (Mn) precursor, mitochondrial

] "

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/note="similar to Saccharomyces cerevisiae ORF YHR009c [

similarity to S.pombe hypothetical protein]

Yeast species: Saccharomyces bayanus var. uv.

exiguus, Saccharomyces servazii, Zygosacchar.

Saccharomyces kluyveri, Kluyveromyces thermotol.

lactis var. lactis, Kluyveromyces marxianus var.

angusta, Debaryomyces hansenii var. hansenii, P.c.

Candida tropicalis and Yarrowia lipolytica. Genomic

5 kb were prepared and both extremities were sequence

keywords for description of this sequence and for the

the other extremity of this insert.

Location/Qualifiers

1..908

/organism="Saccharomyces bayanus"

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similarity to S.pombe hypothetical protein]

1 putative frameshift (s)"

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SOD2 ; superoxide dismutase (Mn) precursor, mitochondrial

] "

/evidence=not_experimental

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similarity to S.pombe hypothetical protein]

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misc_peptide		622 a 497 c 384 g 541 t 1 others
mat_peptide		
CDS		
BASE COUNT	622 a 497 c 384 g 541 t	1 others
ORIGIN		
Alignment Scores:		
Pred. No.:	4.54e-08	Length: 2045
Percent Similarity:	100.00	Matches: 18
Score:	82.14%	Conservative: 5
Local Similarity:	64.29%	Mismatches: 5
Match:	68.97%	Indels: 0
Gaps:	8	0
US-09-987-190-2 (1-30) x SCSODMNG (1-2045)		
Qy	1 LyeTySerLeuProGluIleuAapTyGluPheSerAlaThrGluProTyrlIesergly 20	
Db	637 AAAGCACCCTTCCGCACTTGAAGTGGACCTTCGGTGCACGTGAACCTATATCTCCGT 696	
Qy	21 GlnIleAsnGluIle**TyThr 28	
Db	697 CAAATCAACGAATGCATACAC 720	
RESULT 10		
LOCUS	YSCHL2825	18715 bp DNA linear PLN 04-SEP-1997
DEFINITION	Saccharomyces cerevisiae chromosome VIII cosmid L2825.	
ACCESSION	U10400.1	GI:500701
VERSION	U10400.1	GI:500701
KEYWORDS		
SOURCE	Saccharomyces cerevisiae.	
ORGANISM	Saccharomyces cerevisiae	
	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;	

REFERENCE	Saccharomycetales; Saccharomycetaceae; Saccharomyces.
AUTHORS	1 (bases 1 to 18715) Johnston, M., Andrews, S., Brinkman, R., Cooper, J., Ding, H., Dover, J., Du, Z., Favello, A., Fulton, L., Gattung, S., Gettsel, C., Kirsten, J., Kucaba, T., Hillier, L., Jier, M., Johnston, L., Keppeler, D., Langston, Y., Lettreille, P., Louis, E., Macri, C., Mardis, E., Mouset, L., Nhan, M., Rifken, L., Riles, L., St. Peter, H., Thornton, L., Trevaskis, E., Vaudin, M., Vaughan, K., Vignati, D., Wilcox, L., Willis, A., Wilson, R., Woldman, P. and Waterston, R.
TITLE	Complete nucleotide sequence of <i>Saccharomyces cerevisiae</i> chromosome VIII
JOURNAL	Science 265 (5181), 2077-2082 (1994)
MEDLINE	94378003
PUBMED	8091229
REFERENCE	2 (bases 1 to 18715) Du, Z. The sequence of <i>S. cerevisiae</i> cosmid L2825 Unpublished (1994)
JOURNAL	3 (bases 1 to 18715) Waterston, R. Direct Submission Submitted (06-JUN-1994)
REFERENCE	4 (bases 1 to 18715) Jia, Y. and Cherry, J.M. Direct Submission Submitted (04-SEP-1997)
AUTHORS	Department of Genetics, Stanford University, Saccharomyces Genome Database, Stanford, CA 94305-5120, USA
COMMENT	

Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA
e-mail: mj@sequencer.wustl.edu

NEIGHBORING COSMID INFORMATION:

This sequence includes nucleotides 1-17118 of lambda clone
YSC82825. It overlaps with the cosmid on the left (YSC89780) by
800 bp; with the cosmid on the right (YSC88082) by 1001 bp.

Location/Qualifiers

1. .18715

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Alignment Scores:
Pred. No.: 7,07e-07 Length: 18715
Score: 100.00 Matches: 18
Percent Similarity: 82.14% Conservative: 5
Best Local Similarity: 64.29% Mismatches: 5
Query Match: 68.97% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x YSCHL2825 (1-18715)
QY 1 LysTyrSerLeuPProGluLeuAspTyrGluubheseraIathrgluProtyrIleSercly 20
Db 751 AAAGTCACCTTGCCAGACTTGAAAGTGACCTTCGTGCATTGAACCTTATATCTCCGGT 692
QY 21 GlnIleAngIuile**TyrThr 28
Db 691 CAAATCAACGAATTCATTACACC 668

RESULT 11
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LOCUS YSCH9780
DEFINITION Saccharomyces cerevisiae chromosome VIII cosmid 9780.
ACCESSION U10555 U00093
VERSION U10555.1 GI:500813
KEYWORDS
SOURCE Saccharomyces cerevisiae.

ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetalei; Saccharomycetaceae; Saccharomycetes.
REFERENCE 1 (bases 1 to 24431)
AUTHORS Johnston, M., Andrews, S., Brinkman, R., Cooper, J., Ding, H., Dover, J.,
Du, Z., Favelli, A., Fulton, L., Gattung, S., Gelsel, C., Kisten, J.,
Kusaba, T., Hüller, L., Jier, M., Johnston, L., Keppler, D.,
Kugason, Y., Latreille, P., Louis, E., Macri, C., Mardis, E.,
Moussier, L., Nhan, M., Rifken, L., Riles, L., St. Peter, H., Thornton, L.,
Tverskakis, E., Vaudin, M., Vaughan, K., Vignati, D., Wilcox, L.,
Willis, A., Wilson, R., Wohlman, P. and Waterston, R.
TITLE Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
VIII
JOURNAL Science 265 (5181), 2077-2082 (1994)
MEDLINE 94378003
PUBMED 8091229
REFERENCE 2 (bases 1 to 24431)
AUTHORS Favelli, T.
TITLE The sequence of S. cerevisiae cosmid 9780
JOURNAL Unpublished (1994)
REFERENCE 3 (bases 1 to 24431)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1994)
REFERENCE 4 (bases 1 to 24431)
AUTHORS Jia, Y. and Cherry, J. M.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1997) Department of Genetics, Stanford
University, Saccharomyces Genome Database, Stanford, CA 94305-5120,
USA
COMMENT Curated by:
Saccharomyces Genome Database
URL: http://genome-www.stanford.edu/
e-mail: yeast-curator@genome.stanford.edu
Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA
e-mail: mj@sequencer.wustl.edu
NEIGHBORING COSMID INFORMATION:
This sequence includes nucleotides 10590-34824 of cosmid 9780. The
adjacent clone on the right is YSCHL2825. The adjacent clone on
the left is YSCHL5018.
location/Qualifiers
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PGTLNTEISIGIKORIDNSNDPTERALSPTNRSKQKPDLLVVLNPTNRALLL
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CDS
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/translation="MALNKLKNIPSLTNSHSSINGIASNANSPGADTDIDEND
ESGQSLINTISQKPGCDLSRITLPTPIIEKSMLEIRITQLOFPDVLAEHNSKDG
LQRFVKNVYATLACMHGPRAYKRPPLDIIQGHETAYWDLPNKQOAFYIAEGTSHHP
ESAFVMIPESNILRVGAVVPKSKFLNSSANAMEGLTVLOFLDIKANGKPEKTTIS
QPNVYARGILFGKRIELGDHMYTMGRKYVDLFEKFGTSGTYDAIEGTIKQYDGK
EYQISGKMDIMYIKDLREKSKKTVLFDTHQHFPLAPKVRPLEEGEYESRRLMKK

```

gene
CDS
      8696..8992
      /gene="QCR10"
      /join(8696..8701,8756..8992)
      /gene="QCR10"
      /note="YHR001W-A"
      /codon_start=1
      /product="Qcr10p: 8.5 kDa subunit of the quinol cytochrome
      oxidoreductase complex"
      /protein_id="BAB88434.1"
      /db_xref="GI:2351226"
      /translation="MAILQVYSHLSKTKGLHFGRLSLRLTAYPANLMLMGASMLGL
      FVPEFGMPKHODTLYKKIPLLGPTLEDDHTPEEDKN"
      9682..10755
      /gene="YHR002W"
      /gene="YHR002W"
      /note="YHR002W"
      /protein_id="BAB86424.1"
      /db_xref="GI:500815"
      /translation="MTRDSPDSNDSTYHINKNTQKTSFDRNSFDYIVRSLGAGISG
      SCATLIAPLDRIKILFQTSNPHYTKYGLIGLVEAKHIMINDGVRFQGSATL
      LEPFRAVKEVAYEQRITNLIPEKESHSRRLVSGSLGCVFTYPLDLYRVL
      AYEPHRAVKGRLIIKKIKYEPASATLIKNDYIINWGCWGNCFRGVVPYLGMI
      GVSPFADHLHDVLRKSPPAVSYVLEISDEDELRVOKORRPLRTWAEIISGLAGM
      ASQRAYPFEIRIRRLQVSAISPKTMIDHKQISIEIAHIIIFKRGVRFVGLSTGY
      IKTPVWACSFYVERKMNFGI"
      complement(10898..12187)
      /gene="YHR003C"
      /complement(10898..12187)
      /note="Weak similarity to thif (E. coli), moeb (E. coli),
      and ubiquitin activating enzyme (wheat)"
      /codon_start=1
      /evidence=not experimental
      /product="Yhr003cp"
      /protein_id="BAB86430.1"
      /db_xref="GI:500821"
      /translation="MANNTWQLIATLALISVFSQIQAQSVKWEYKLSAANKNTVSR
      PRQVDHLFREQLARNYAFLEEGEMRKIKEQYIYVAGEVGSVCTMLIRSGCKIM
      IIDENISIDSLNTHCCAVSIDGPKVQCKEHLSKIAPSEIKAKAKMTKENSND
      LIFADGSPPIYDCLNLESKYDLELYAHHNKIDVYSMWATKSPTRVSTINDISM
      TEPPISICVRKKLRKRGIALTGISIVFSNEMLDPRDDLIISPIDCEHRAIIVAVDEAL

```

VERSION	AF061031.2	GI:15724846
KEYWORDS	Mycobacterium smegmatis.	
SOURCE	Mycobacterium smegmatis	
ORGANISM	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae;	
REFERENCE	1 (bases 1 to 1071)	
AUTHORS	Hartsh,G. and Horwitz,M.A.	
TITLE	Export of recombinant Mycobacterium tuberculosis superoxide dismutase is dependent upon both information in the protein and mycobacterial export machinery. A model for studying export of leaderless proteins by pathogenic mycobacteria	
JOURNAL	J Biol. Chem. 274 (7), 4281-4292 (1999)	
MEDLINE	99134360	
PUBMED	9933629	
REFERENCE	2 (bases 1 to 1071)	
AUTHORS	Tullius,M.V., Hartsh,G. and Horwitz,M.A.	
TITLE	High extracellular levels of Mycobacterium tuberculosis glutamine synthetase and superoxide dismutase in actively growing cultures are due to high expression and extracellular stability rather than to a protein-specific export mechanism	
JOURNAL	Infect. Immun. 69 (10), 6348-6353 (2001)	
MEDLINE	21437642	
PUBMED	11553579	
REFERENCE	3 (bases 1 to 1071)	
AUTHORS	Hartsh,G. and Horwitz,M.A.	
TITLE	Direct Submission	
JOURNAL	Submitted (23-APR-1998) Medicine, UCLA, 10833 Le Conte Avenue, Los Angeles, CA 90095, USA	
REFERENCE	4 (bases 1 to 1071)	
AUTHORS	Tullius,M.V., Hartsh,G. and Horwitz,M.A.	
TITLE	Direct Submission	
JOURNAL	Submitted (24-JAN-2001) Medicine, UCLA, 10833 Le Conte Ave., Los Angeles, CA 90095, USA	
REMARK	Nucleotide sequence updated by submitter	
COMMENT	On Sep 24, 2001 this sequence version replaced gi:4321777.	
FEATURES	Location/Qualifiers	
source	1..1071	
	/organism="Mycobacterium smegmatis"	
	/strain="1-2c"	
	/db_xref="taxon:1772"	
CDS	<1..141	
	/note="similar to partial orf adjacent to Mycobacterium fortuitum soda gene"	
	/codon_start=1	
	/transl_table=11	
	/product="unknown"	
	/protein_id="FAL06643.1"	
	/db_xref="GI:15724848"	
	/translation="GSSSALPDPFEMWHTSGHLQTRHGVAFRLACVIAAILGLVAFIVW"	
gene	282..905	
	/gene="soda"	
CDS	282..905	
	/gene="soda"	
	/EC_number="1.15.1.1"	
	/codon_start=1	
	/transl_table=11	
	/product="superoxide dismutase"	
	/protein_id="FAD15825.2"	
	/db_xref="GI:15724847"	
	/translation="MAEYLPDLDYDYGALPEHISQINELHSHKHAATYKGVNDALAKSEBRANDHAIPLFNENKLAFLHGHNIHNSIMWNLSPPNGDKPTGLAAALIDDOAGSPKFRQAGFTAAANGSGGAAVIGSYSLGRLILFQIYDOAANPLGIPILOVDMEHAFLQYTKNKADYVAFNVAIVMDVDQNPAAATSKTSGILIFG"	
stem_loop	964..996	
BASE COUNT	205 a 349 c 315 g 202 t	
ORIGIN		
Alignment Scores:	3.1e-08	length: 1071
Pred. No.:	99.00	Matches: 16

Percent Similarity: 89.29%
 Best Local Similarity: 57.14%
 Query Match: 68.28%
 DB: 1
 Gaps: 0

US-09-987-190-2 (1-30) x AF061031 (1-1071)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheserAlaThrGluProTyrIleSergly 20
 Db 268 GAATACACCTCCCGAGCTGATTAACGACTGAGCCCTCGAGCCCATCTCTCCGT 347

Qy 21 GlnIleAsnGluIle**TyrThr 28
 Db 348 CAGATCAACGAGCTGCACACAGC 371

RESULT 13

MFSDA
 LOCUS MFSDA 1478 bp DNA linear BCT 21-MAY-1996
 DEFINITION M.fortuitum sod gene.
 ACCESSION X70914
 VERSION X70914.1 GI:950078
 KEYWORDS sod gene; superoxide dismutase.
 SOURCE Mycobacterium fortuitum.
 ORGANISM Mycobacterium fortuitum
 Bacteria; Firmicutes; Actinobacteriae; Actinobacteridae;
 Actinomycetales; Corynebacterineae; Mycobacteriaceae;
 Mycobacterium.

REFERENCE 1 (bases 1 to 1478)
 AUTHORS Menendez,M.C., Domenech,P., Prieto,J. and Garcia,M.J.
 TITLE Cloning and expression of the Mycobacterium fortuitum superoxide
 dismutase gene
 JOURNAL FEMS Microbiol. Lett. 134 (2-3), 273-278 (1995)
 MEDLINE 96102872
 PUBMED 8586279

REFERENCE 2 (bases 1 to 1478)
 AUTHORS Menendez,C.
 TITLE Direct Submission
 JOURNAL Submitted (15-FEB-1993) C. Menendez, School of Medicine, Autonoma
 University of Madrid, Dept of M. Preventive School of Medicine,
 ST/Arzobispo Morcillo, 4, 28029 Madrid, SPAIN

REMARK 3 (bases 1 to 1478)
 REFERENCE
 AUTHORS Garcia,M.
 TITLE Direct Submission
 JOURNAL Submitted (17-AUG-1995) M.Garcia, School of Medicine, Autonoma
 University of Madrid, Dept of M. Preventive School of Medicine,
 ST/Arzobispo Morcillo, 4, 28029 Madrid, SPAIN

FEATURES

source Location/Qualifiers

1..1478
 /organism="Mycobacterium fortuitum"
 /strain="ATCC 6841"
 /db_xref="taxon:1766"
 /clone="pmFV1"
 /clone_11b="E. coli TGI1"
 243..250
 257..880
 /gene="Sod"
 /gene="Sod"
 257..880
 /gene="Sod"
 /codon_start=1
 /transl_table=11
 /product="superoxide dismutase"
 /protein_id="CAA50266.1"
 /db_xref="GI:950078"
 /db_xref="SWISS-PROT:O59519"
 /translation="MAEYTLPLDLDYDALEPHISGQINELHSHKHAAYVKGVNDAY
 AKLDEBARANGDHAIFLNENKLAIFLGHVNHSTWKNLSPNGGDKPTGLADIDET
 FGSPDKFOAFTAAANGLOSGGMAVILGDSGLRLLTFQLDQOANVPLGIIPLLQVD
 MMEHAFYLOYNVADYVKAFMNVVNMEDVQNRVAAATSKNGLIFG"

BASE COUNT 260 a 486 c 452 g 280 t

Alignment Scores:

Pred. No.: 4,61e-08
 Score: 99.00
 Percent Similarity: 89.29%
 Best Local Similarity: 57.14%
 Query Match: 68.28%
 DB: 1
 Gaps: 0

US-09-987-190-2 (1-30) x MFSDA (1-1478)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheserAlaThrGluProTyrIleSergly 20
 Db 263 GAATACACTTTCGCGAGCTGATTAACGACTGAGCCCTCGAGCCCATCTCTCCGG 322

Qy 21 GlnIleAsnGluIle**TyrThr 28
 Db 323 CAGATCAACGAGCTGCACACAGC 346

RESULT 14

MLEPSOD
 LOCUS MLEPSOD 649 bp DNA linear BCT 10-FEB-1999
 DEFINITION Mycobacterium leprae DNA for manganese superoxide dismutase (EC
 1.15.1.1).
 ACCESSION X16453
 VERSION X16453.1 GI:44405
 KEYWORDS manganese superoxide dismutase; metalloenzyme; superoxide
 dismutase.
 SOURCE Mycobacterium leprae.
 ORGANISM Mycobacterium leprae
 Bacteria; Firmicutes; Actinobacteriae; Actinobacteridae;
 Actinomycetales; Corynebacterineae; Mycobacteriaceae;
 Mycobacterium.

REFERENCE 1 (bases 1 to 649)
 AUTHORS Thangaraj,H.S.
 TITLE Direct Submission
 JOURNAL Submitted (01-SEP-1989) Thangaraj H.S., National Institute for
 Medical Research, Laboratory of Leprosy and Mycobacterial Research,
 Mill Hill, London NW7 1AA, UK

REFERENCE 2 (bases 1 to 649)
 AUTHORS Thangaraj,H.S., Lamb,F.I., Davis,E.O. and Colston,M.J.
 TITLE Nucleotide and deduced amino acid sequence of Mycobacterium leprae
 manganese superoxide dismutase
 JOURNAL Nucleic Acids Res. 17 (20), 8378 (1989)
 MEDLINE 90045970
 PUBMED 2682526

FEATURES

source Location/Qualifiers

1..649
 /organism="Mycobacterium leprae"
 /db_xref="taxon:1769"
 /clone="Y3164 and pH77"
 /clone_11b="lambda gcl1 and pHCT9 cosmid"
 1..4
 /note="pot. ribosome binding site"
 14..637
 /note="superoxide dismutase (AA 1-207)"
 /codon_start=1
 /transl_table=11
 /protein_id="CAA34472.1"
 /db_xref="GI:581343"
 /db_xref="SWISS-PROT:P13367"
 /translation="MAEYTLPLDLDYDALEPHISGQINELHSHKHAAYVKGVNDAL
 AKLDEBARANGDHAIFLNENKLAIFLGHVNHSTWKNLSPNGGDKPTGLADIDET
 FGSPDKFOAFTAAANGLOSGGMAVILGDSGLRLLTFQLDQOANVPLGIIPLLQVD
 MMEHAFYLOYNVADYVKAFMNVVNMEDVQNRVAAATSKNGLIFG"

BASE COUNT 164 a 180 c 167 g 138 t

Alignment Scores:

Pred. No.: 2.53e-08
 Score: 98.00
 Percent Similarity: 92.86%
 Best Local Similarity: 57.14%
 Query Match: 67.59%
 DB: 1
 Gaps: 0

US-09-987-190-2 (1-30) x MLEP50D (1-649)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 20 GAATACACCTGCGCCGATTGGAGACTAGCAGCGCTGGAACACATATCTCTGGT 79

Qy 21 GluIleAnguile**TyrThr 28
Db 80 GAGATCAACGAGATCCACCACACC 103

RESULT 15

MLEPRTN1/c 344050 bp DNA linear BCT 20-FEB-2001
LOCUS Mycobacterium leprae strain TN complete genome; segment 1/10.
DEFINITION AL583917 AL450380
ACCESSION AL583917.1 GI:13092412
KEYWORDS

ORGANISM
Mycobacterium leprae.
Mycobacterium leprae
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium.

REFERENCE
1 (bases 1 to 344050)
Cole, S.T., Bigliamer, K., Parkhill, J., James, K.D., Thomson, N.R.,
Wheeler, P.R., Honore, N., Ganter, T., Churcher, C., Harris, D.,
Mungall, K., Basham, D., Brown, D., Chillingworth, T., Connor, R.,
Davies, R.M., Devlin, K., Duthoy, S., Felwell, T., Fraser, A.,
Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Jancsik, C.,
Maclean, J., Moule, S., Murphy, J., Oliver, Q., Qail, M.A.,
Rajandream, M.-A., Rutherford, K.M., Rutter, S., Seeger, K., Simon, S.,
Simmonds, M., Skelton, J., Squares, R., Squares, S., Stevens, K.,
Taylor, K., Whitehead, S., Woodward, J.R. and Barrell, B.G.
Massive gene decay in the leprosy bacillus
Nature 409 (6823), 1007-1011 (2001)

TITLE
JOURNAL
MEDLINE
PUBMED
2 (bases 1 to 344050)
Parkhill, J.
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT
Submitted on behalf of the Mycobacterium
leprae sequencing teams, The Sanger Centre, Wellcome Trust Genome
Campus, Hinxton, Cambridge, CB10 1SA, UK Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724, Paris Cedex, France. E-mail: parkhill@sanger.ac.uk
Notes:
Details of M. leprae sequencing at the Sanger Centre are available
from http://www.sanger.ac.uk/Projects/M_leprae/ A relational
database containing the M. leprae sequences is available from
<http://genolist.pasteur.fr/Leproma/>.

FEATURES
source
1. 344050
/organism="Mycobacterium leprae"
/strain="TN"
/db_xref="taxon:1769"
1. 1566
/gene="dnaa"
/note="ML0001"
1. 1566
/gene="dnaa"
/note="Similar to M. tuberculosis dnaa, chromosomal
replication initiator protein, SW:DNAA_MYCTU (P49993) (507
aa); Faeta score E(): 0, 87.2% identity in 507 aa overlap
and Mycobacterium smegmatis dnaa, SW:DNAA_MYCJM (P49992)
(495 aa); Faeta score E(): 0, 69.2% identity in 441 aa
overlap. Previously sequenced as SW:DNAA_MYCLE (P46388)
(521 aa); Faeta score E(): 0, 99.8% identity in 521 aa
overlap. Contains Pfam match to entry PF00308 bac_dnaa,
Bacterial dnaa protein. Contains PS00017 ATP/GMP-binding
site motif A (P-loop). Contains PS01008 Dnaa protein
signature."
/codon_start=1
/transl_table=11

/product="putative chromosomal replication initiator
protein"
/protein_id="CAC29509.1"
/db_xref="GI:13092413"
/translation="MPPPAKRPRIYNNQSDTSLADLSIGFTTWNAVYSELNGSEN
TDEATINDSTLVLPVQKRAMLVLPITLITSEFALLSPSSFVQVIRHMLPTIT
DALSRRLGQOIQLGVRILAPPSTDHIDNSSADVLALDDCGTDENYGGAPLGEYOG
LPTVFERPHHTSTVGTSLNRRYRFFVPGASRPFMAALAAIAAPAVANPL
FVNGESGLGTHLLHAAGYAORLPCMRKYVSTEEFTNDFINSLLDDKRVAFKRY
RDVDVILVDDIOPIEGKEGIOERFFHFNTHNANKIOIVISDRPPKQLATLEBLAT
RFEWGLITDQPPLETRIALIKKQAMELAPGDVLELAISIEINIEBELALR
VTAASLNTKTAIDALAEIVLRDILADSTWQISAATIMTATAYEDPTTLELNGPK
TRLAOSRQIAWYKACRELTDSLSPKIGQAGRHHTVVAQRKLISEAARRRVEFDH
KELTTRRSRKR"
544..1482
/gene="dnaa"
/note="Pfam match to entry PF00308 bac_dnaa, Bacterial
dnaa protein, score 712.20, E-value 8.3e-240"
664..687
/gene="dnaa"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)"
1426..1482
/gene="dnaa"
/note="PS01008 Dnaa protein signature"
2081..3280
/gene="dnaa"
/note="ML0002"
2081..3280
/gene="dnaa"
/EC_number="2.7.7.7"
/note="Similar to M. tuberculosis dnaa, DNA polymerase
III, [beta] subunit, SW:DP3B_MYCTU (Q50790) (402 aa);
Faeta score E(): 0, 80.9% identity in 403 aa overlap and
Mycobacterium smegmatis dnaa, SW:DP3B_MYCJM (P52651) (397
aa); Faeta score E(): 0, 77.3% identity in 397 aa overlap.
Previously sequenced as SW:DP3B_MYCLE (P46387) (399 aa);
Faeta score E(): 0, 100.0% identity in 399 aa overlap.
Contains Pfam match to entry PF00712 DNA_pol3_beta, DNA
polymerase III beta subunit."
/codon_start=1
/transl_table=11
/product="putative DNA polymerase III, [beta] subunit"
/protein_id="CAC29510.1"
/db_xref="GI:13092414"
/translation="MDLAKTNGCGSDLKFLARSPASVSWAKYLPTRPTVPLSG
VLRTGSDSGTITGPFDEYSAEYQVAEIALSSGSVNLGSLSDITATQVAPRPHRY
DGNRVALTGGSARFSLPTMAVEDYPTLPDERTGLPSVFPAAIQVAILAAGRDY
LPMATGIRISDVTVAATDIFRLAVRELKNSVLSDEASVLPVAKTLVEAKAG
TDSGVCISLAGVGKDLFGISGGKSTRLLDAEPKFKQLPAEHTAVATID
VAELTEIKLVAVADRGAVRMFPGGILRLSAGADVGRAEEDLAVAFGSELTIA
FNNVYLTDGLASVHSRVSFGFTTPSKPALRLRPSNDVHPTDGPALPTDVIYL
MPVRLPG"
2117..3214
/gene="dnaa"
/note="Pfam match to entry PF00712 DNA_pol3_beta, DNA
polymerase III beta subunit, score 592.70, E-value
2.2e-174"
3281..4438
/gene="recF"
/note="ML0003"
3281..4438
/gene="recF"
/note="Similar to M. tuberculosis recF, DNA replication
and SOS induction protein, SW:RECF_MYCTU (Q59586) (385
aa); Faeta score E(): 0, 76.4% identity in 385 aa overlap
and Mycobacterium smegmatis recF, SW:RECF_MYCJM (P50916)
(384 aa); Faeta score E(): 0, 70.0% identity in 383 aa
overlap. Previously sequenced as SW:RECF_MYCLE (P46391)
(385 aa); Faeta score E(): 0, 99.5% identity in 385 aa
overlap. Contains 2 Pfam matches to entry PF00670 RecF,
RecF protein. Contains PS00617 RecF protein signature 1.
Contains PS00617 ATP/GMP-binding site motif A (P-loop).
Contains PS00618 RecF protein signature 2."

```
/codon_start=1
/transl_table=1
/product="putative DNA replication and SOS induction
protein"
/protein_id="CAC29511.1"
/db_xref="GI:13092415"
/translation="MYVHFGRLRDFSRMDHDLBNPGRVFPQPNNGKTNLLEALW
YSTLSHSGVTDIPLIRAGTIRAVSTIVNERECADIEIAGRANRRLRSIV
RGMREVGVAALVFAPEDLALVCGDPANRRYVDLATVQPIYAARADYKVLRO
RTALKLSAARVSRDOGVLDLVDWDRRLAEHGAELMAATIDLVNOLAPEVKAOL
LAPGSRSTISYRASLDIGTAGVSSRRALLQDLADLAGSTRNVELERICVGRH
RDELELRGDQPAKGFASHGWSLALRLAAAYELLADGNEVLLDLDVFAELDAA
RCRALATVAESAEQVLTYSAAQEDI PVGMADKMTVDLRDSGRVSVYP"
3287..3415
/gene="recF"
/notes="Pfam match to entry PF00470 RecF, RecF protein,
score 18.90, E-value 0.00024"
3368..3391
/gene="recF"
/notes="PS00017 ATP/GTP-binding site motif A (P-loop)"
3614..3691
/gene="recF"
/notes="PS00617 RecF protein signature 1"
4100..4423
/gene="recF"
/notes="Pfam match to entry PF00470 RecF, RecF protein,
score 5.20, E-value 1.5"
4244..4297
/gene="recF"
/notes="PS00618 RecF protein signature 2"
4435..5004
/gene="ML0004"
4435..5004
/gene="ML0004"
/notes="Similar to hypothetical proteins from mycobacteria
e.g. M. tuberculosis Rv0004, hypothetical protein,
TR:P15173 (EMBL:AL123456) (187 aa); Fasta score E(): 0,
77.2% identity in 167 aa overlap. Previously sequenced as
TR:050181 (EMBL:Z70722) (199 aa); Fasta score E(): 0,
99.5% identity in 187 aa overlap."
/codon_start=1
/transl_table=1
/product="conserved hypothetical protein"
/protein_id="CAC29512.1"
/db_xref="GI:13092416"
/translation="MIESNESYSGDITPEIGTLTSGPDIYVRALFEARRAAACQGD
AGRGHVPPVPRVTRDRRNMSGPPDVRDQPGAKVAHDIAKRGMSAQVAEGRVG
QWASMGQIADHAFVGLNGVLSVTSSTAMATQIKIWOQLAKIAAIVGNGVVT
SLKITGPAPMRKGPWHIAGRGPRDTG"
5211..5216
/notes="possible RBS"
5229..7265
/gene="gyrB"
/notes="gyrB"
/notes="ML0005"
5229..7265
/gene="gyrB"
/BC_number="5.99.1.3"
/notes="Similar to M. tuberculosis gyrB, DNA gyrase subunit
B, SW:GYRB_MYCTU (P41514) (686 aa); Fasta score E(): 0,
87.5% identity in 679 aa overlap and to Mycobacterium
smegmatis gyrB, SW:GYRB_MYCSM (P48355) (675 aa); Fasta
score E(): 0, 85.0% identity in 679 aa overlap. Previously
sequenced as SW:GYRB_MYCLE (O59533) (697 aa); Fasta score
E(): 0, 100.0% identity in 678 aa overlap. Contains Pfam
match to entry PF00986 DNA_gyraseB_C, DNA gyrase B
subunit, carboxyl terminus. Contains Pfam match to entry
PF00204 DNA_topoisomII, DNA topoisomerase II (N-terminal
```

Alignment Scores:
Pred. No.: 6.03e-05 Length: 344050
Score: 98.00 Matches: 16
Percent Similarity: 92.86% Conservative: 10
Best Local Similarity: 57.14% Mismatches: 2

```
Query Match: 67.59% Indels: 0
DB: 1 Gaps: 0
US-09-987-190-2 (1-30) x MLEPRTNI (1-344050)

Qy 1 LysTYSerLeuPProGluLeuAspTyrGluPheSerAlaThrGluProTyrTlleSerGly 20
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 93264 GAATACACCCCTCCGATTTGAGCTGAGCTACGACGCTGGAACCAATATCTTGCT 93205
Qy 21 GlnLeaAngIuile**TyrThr 28
Db 93204 GAGATCAACGAGATCCACCAACC 93181

RESULT 16
MTSOD MTSOD 790 bp DNA linear BCT 03-MAY-1995
LOCUS M.tuberculosis SOD gene.
DEFINITION X52861.1 GI:794079
ACCESSION X52861.1
VERSION sod gene; superoxide dismutase.
KEYWORDS Mycobacterium tuberculosis.
SOURCE Mycobacterium tuberculosis
ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium tuberculosis complex.
1 (bases 1 to 790)
Zhang, Y.
REFERENCE
AUTHORS Submitted
TITLE Direct Submission
JOURNAL Submitted (23-APR-1990) Zhang Y., MRC TB & Related Infections Unit,
Cyclotron Bldg, Hammersmith Hospital, London W12 0HS, U K
2 (bases 1 to 790)
Zhang, Y., Lathigra, R., Garbe, T., Catty, D. and Young, D.
AUTHORS Genetic analysis of superoxide dismutase, the 23 kilodalton antigen
of Mycobacterium tuberculosis
TITLE Mol. Microbiol. 5 (2), 381-391 (1991)
JOURNAL 91251768
MEDLINE 1904126
PUBMED
COMMENT On May 4, 1995 this sequence version replaced gi:44678.
Data kindly reviewed (02-JUL-1990) by Zhang Y.
Related sequence: S36714.

FEATURES
Source
1..790
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
/db_xref="taxon:1773"
/clone="YA3P-9"
/clone_lib="lambda gt11"
20..25
/notes="putative"
99..105
112..735
/gene="SOD"
112..735
/gene="SOD"
/BC_number="1.15.1.1"
/BC_number="1.15.1.1"
/codon_start=1
/transl_except="(pos:112..114,aa:Met)
/transl_table=1
/product="superoxide dismutase"
/protein_id="CAA57042.1"
/db_xref="GI:581379"
/db_xref="SWISS-PROT:P17670"
/translation="MAEYTPDLDDWDYGLAEPLHISGOINELHSHKHATYVKANDAV
AKLEERAKSDHAAATTVQSSGNAALGMDTLGNKLLIFQYDHTQTNPLGLVPLLLD
FGSRDKRAQFHAATTVQSSGNAALGMDTLGNKLLIFQYDHTQTNPLGLVPLLLD
MWEIAFLQIKKRVKVDPAKFMVNVNADVQSRVAATSTQKGLIFG"
```

Alignment Scores:
Pred. No.: 1.72e-07 Length: 790
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10

Best Local Similarity: 53.57% Mismatches: 3
Query Match: 64.83% Gaps: 0
DB: 1

US-09-987-190-2 (1-30) x MTSOD (1-790)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 118 GAATACACCTTGCAGACCTGGACTGCGACTACGAGACCTGAACCCGACATCTCGGGT 177
Qy 21 GlnIleAengIuile***TyrThr 28
Db 178 CAGATCAACGAGCTTCACACAGC 201

RESULT 17
LOCUS AF077406 943 bp DNA linear BCT 26-JUL-1998
DEFINITION Mycobacterium bovis BCG superoxide dismutase (SOD) gene, complete cds.
ACCESSION AF077406
VERSION AF077406.1 GI:3342171
KEYWORDS Mycobacterium bovis BCG.
SOURCE Mycobacterium bovis BCG.
ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 943)
AUTHORS Kimble, E., Sanderson, R.J. and Gill, R.E.
TITLE Superoxide dismutase of M. bovis BCG.
JOURNAL Unpublished
PUBMED 2 (bases 1 to 943)
REFERENCE Kimble, E., Sanderson, R.J. and Gill, R.E.
AUTHORS Direct Submission
TITLE Submitted (10-JUL-1998) Microbiology, University of Colorado Health Sciences Center, 4200 E. 9th Ave., Denver, CO 80220-3706, USA
JOURNAL Location/Qualifiers
FEATURES
source 1..943
/organism="Mycobacterium bovis BCG"
/strain="Pasteur"
/db_xref="taxon:33892"
gene 307..943
/gene="SOD"
RBS 307..314
/gene="SOD"
/note="putative"
CDS 320..943
/gene="SOD"
/note="similar to Mycobacterium tuberculosis superoxide dismutase encoded by the sequence presented in GenBank Accession Number X52861"
/codon_start=1
/transl_table=1
/product="superoxide dismutase"
/protein_id="AAC27527.1"
/db_xref="GI:3342172"
/translation="MAEYTLPLDMDVYGALEPHISGOINELHSHKHAATVYKGANDAV AKLEBARAKEDSHAILINENKLAFNLAGHNHTIWKNSPNGDKRPTGELAIAIDA FGSFDRAPRAQFAAATTVOSSGNAALGMDTLGNKLLIFQYTDHQTNPGLGIVPLLLD MMEHAFYLYQYKNKVDPAKAFMVNVNADVQSRVAATSTQKGLIFG"

BASE COUNT 211 a 302 c 266 g 164 t

ORIGIN

Alignment Scores:
Pred. No.: 2,14e-07 Length: 943
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10
Best Local Similarity: 53.57% Mismatches: 3
Query Match: 64.83% Indels: 0
DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x AF077406 (1-943)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 326 GAATACACCTTGCAGACCTGGACTGCGACTACGAGACCTGAACCCGACATCTCGGGT 385
Qy 21 GlnIleAengIuile***TyrThr 28
Db 386 CAGATCAACGAGCTTCACACAGC 409

RESULT 18
LOCUS AF061030 1321 bp DNA linear BCT 03-MAR-1999
DEFINITION Mycobacterium tuberculosis superoxide dismutase (sodA) gene, complete cds.
ACCESSION AF061030
VERSION AF061030.1 GI:4321775
KEYWORDS Mycobacterium tuberculosis.
SOURCE Mycobacterium tuberculosis.
ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 1321)
AUTHORS Harth, G. and Horwitz, M.A.
TITLE Export of recombinant Mycobacterium tuberculosis superoxide dismutase is dependent upon both information in the protein and mycobacterial export machinery. A model for studying export of leaderless proteins by pathogenic mycobacteria
JOURNAL J. Biol. Chem. 274 (7), 4281-4292 (1999)
PUBMED 99134360
REFERENCE 2 (bases 1 to 1321)
AUTHORS Harth, G. and Horwitz, M.A.
TITLE Direct Submission
JOURNAL Submitted (23-APR-1998) Medicine, UCLA, 10833 Le Conte Avenue, Los Angeles, CA 90095, USA
FEATURES
source 1..1321
/organism="Mycobacterium tuberculosis"
/strain="Erdrman"
/db_xref="taxon:1773"
gene 542..1165
/gene="soda"
CDS 542..1165
/gene="soda"
/EC_number="1.15.1.1"
/codon_start=1
/transl_table=1
/product="superoxide dismutase"
/protein_id="AAD15824.1"
/db_xref="GI:4321776"
/translation="MAEYTLPLDMDVYGALEPHISGOINELHSHKHAATVYKGANDAV AKLEBARAKEDSHAILINENKLAFNLAGHNHTIWKNSPNGDKRPTGELAIAIDA FGSFDRAPRAQFAAATTVOSSGNAALGMDTLGNKLLIFQYTDHQTNPGLGIVPLLLD MMEHAFYLYQYKNKVDPAKAFMVNVNADVQSRVAATSTQKGLIFG"

BASE COUNT 266 a 429 c 382 g 244 t

ORIGIN

Alignment Scores:
Pred. No.: 3.25e-07 Length: 1321
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10
Best Local Similarity: 53.57% Mismatches: 3
Query Match: 64.83% Indels: 0
DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x AF061030 (1-1321)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 548 GAATACACCTTGCAGACCTGGACTGCGACTACGAGACCTGAACCCGACATCTCGGGT 607
Qy 21 GlnIleAengIuile***TyrThr 28
Db 1
Gaps: 0


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/product="IS1608", transposase"
/protein_id="AAK48323.1"
/db_xref="GI:13883844"
/translation="MTAENPGRSRTLVGIDAIATGHLAIRDDVGARSIRFEVPT
LAGRLTLDKLSGVDIDATVEPTSMVPLTIVAGDPMAGARHCRRLGALV
GKSDVYIDAEVLTRASEVFDLPTLPTPAQLALRSVIRRAQAVIDANRMRRLS
LAR"
complement(5255..5797)
/gene="MT3957"
complement(5255..5797)
/gene="MT3957"
/feature="identified by Glimmer2; putative"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAK48324.1"
/db_xref="GI:13883845"
/translation="MGLSKTIPRCRFLPLVGRGRSSILRCGDTYTPGSPPTMGK
EPGHEITASSDRVCNRIPCRQWCSACRFVRLHGVAVVAVGVDVGVQDFR
AAGGDRVAVGVAQLVGAAGDRHPRGAFQLAGDGLGVAMPGLGHQPVVERQVAG
RCAGQQADVGPFPQHRCRGR"
5778..5993
/gene="MT3958"
5778..5993
/gene="MT3958"
/feature="identified by Glimmer2; putative"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAK48325.1"
/db_xref="GI:13883846"
/translation="MVPDKPTVSCLSVSHFQRLFRVAQHNMMPVEIRRDYTHQHLDH
RDSGRRLTSSFPAPADATFORHSS"
complement(6207..6386)
/gene="MT3959"
complement(6207..6386)
/gene="MT3959"
/feature="identified by Glimmer2; putative"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAK48326.1"
/db_xref="GI:13883847"
/translation="MMRRSMGWGKKKSTAGLAQTANETLKEVLERAVHRESPVIRP
DVVVGIPAVDRRPRKQ"
6657..7280
/gene="MT3960"
6657..7280
/gene="MT3960"
/feature="similar to SP:P47201 PID:555746 PID:620090
PID:667039 SP:P53647; identified by sequence similarity;
putative"
/codon_start=1
/transl_table=11
/product="superoxide dismutase"
/protein_id="AAK48327.1"
/db_xref="GI:13883848"
/translation="MAEYTLPDLDMDVGALEPHISQINELHSHKHATYVKANDAV

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Alignment Scores:

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Pred. No.: 6.22e-06 Length: 14282
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10
Best Local Similarity: 53.57% Mismatches: 3
Query Match: 64.83% Gaps: 0
DB: 1

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US-09-987-190-2 (1-30) x AE007188 (1-14282)

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Cy 1 LysTyrSerLeuProGluLeuAspTyrGluPheserAlaThrGluProTyrIleSerGly 20
Db 6663 GAATACACCTTGCCAGACTGAGACTACGAGCACTGGAACCGACACATCTCGGGT 6722

```

```

Cy 21 GlnIleAsnGluIle***TyrThr 28
Db 6723 CAGATCAACGAGCTTACACACG 6746
RESULT 20
MTCY1A6
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NOTES:
DETAILS:
URL:
GENE DESIGNATIONS:
GENE PREDICTION:
IMPLEMENTED IN:
CAUTION:
INITIATION CODON:
BINDING SITE SEQUENCE:
INITIATION CODON:
FEATURES
SOURCE

```

```

scores, opt: 255, E(): 1.9e-11, (33.7% identity in 202aa
overlap). Contains possiblehelix-turn-helix motif from aa
34-55 (+4.97 SD)
/codon_start=1
/transl_table=11
/product="hypothetical protein Rv3830c"
/protein_id="CAB06211.1"
/db_xref="GI:1781127"
/db_xref="SPTREMBL:P96248"
/translation="MVRPPQTARSRTTEALROALVRFQAQVEATSEQIAEDADY
SLRTFYRFRSKHDLFPADYDAGLHWFRPAUDARPADSEITDSVOALFSPYVDAY
TKIASLRGELSPRIVSRHREVEADPADALQADLRNRNCIAGAPARLHIAYTARC
VAAVFGAMEAMMGSDRSGLRLARVCHALESLRVGISDWTTLTVSS"
749..1231
/gene="Rv3831"
749..1231
/gene="Rv3831"
/note="Rv3831" (MTCY01A6.38c), len: 160. Unknown"
/codon_start=1
/transl_table=11
/product="hypothetical protein Rv3831"
/protein_id="CAB06210.1"
/db_xref="GI:1781126"
/db_xref="SPTREMBL:P96247"
/translation="MVSLLVHAALGVVIVGIVSNPKVFTPRPAGSGWFSLPECVYV
VGIASIALGMYENIRFVOQVYAGALPLMGSGMAEYRLMTNPASAGODYTIAN
VILPLFSTTDGYRGLRPLWLYFSSLFTSFAPAFAYFATIERQRHHSRAIVGA
"
complement(1228..1803)
/gene="Rv3832c"
complement(1228..1803)
/gene="Rv3832c"
/note="Rv3832c" (MTCY01A6.37), len: 191. Unknown."
/codon_start=1
/transl_table=11
/product="hypothetical protein Rv3832c"
/protein_id="CAB06209.1"
/db_xref="GI:1781125"
/db_xref="SPTREMBL:P96246"
/translation="MAMNLLHRHSSAGMKAVANOLLPMALOHVELGPRTLTGRC
YGATLQALGLTASITLAVEVDNSMVERNNRYGQARLITRGDGTGTGPDHFTSVVC
FTMLHHVASAQLODQLFAEAYRVLPQGVGSGVPSLPRLIHIADTYPIAPADL
PGRRAVGFTHIVDVAGARLRWRATKEVAA"
1859..2650
/gene="Rv3833"
1859..2650
/gene="Rv3833"
/note="Rv3833" (MTCY01A6.36c), len: 263. Possible
transcriptional regulator, similar to e.g. YFIF_BACSU
P54722 hypothetical transcriptional regulator (314 aa),
fasta scores, opt: 171, E(): 8.5e-05, (30.2% identity in
126 aa overlap). Contains probable helix-turn-helix motif
from aa 165-186."
/codon_start=1
/transl_table=11
/product="hypothetical protein Rv3833"
/protein_id="CAB06208.1"
/db_xref="GI:1781124"
/db_xref="SPTREMBL:P96245"
/translation="MSENSHRRLATSTLTPPGARIERRHPSHOIYVPSAGAVSTT
HAGTWTPVNRRAIWI PACMWHQKHGHTGPGVALDQRRGSGPATPTVAVPLMK
ELVIAQSQADRTDDEHRLMALVODOLPTTSIREPLVPSPTRRRLHACALADNL
TOPLLTIOIGRIGVSORTLRLPLDELGMFPQWRQTLRIQHALVLAERHDVTSVA
SECGMATPSAIDTYRQAFGHTPGQAAKPMATRLTRLRARDKR"
complement(2647..3906)
/gene="sers"
complement(2647..3906)
/gene="sers"
/note="Rv3834c" (MTCY01A6.35), len: 419. Seryl-trna
synthetase, similar eg to SIS_BACSU P37464 (425 aa), fasta
scores, opt: 1015, E(): 0, (39.3% identity in 425 aa
overlap); contains P800179 Aminoacyl-transfer RNA
synthetases class-II signature 1"

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/codon_start=1
/transl_table=11
/product="sers"
/protein_id="CAB06207.1"
/db_xref="GI:1781123"
/db_xref="SWISS-PROT:P96244"
/translation="MIDKLRENPPAVRRSOLSRGEPALVDALLTADARRAVIST
ADSLRAEQKAASKVGASPEERAPLLRAKELAEQVKAADVEVEAAFTAAHLAI
SNVIYDGPVPAGEDDYAVLDVGPESYLENKDLEGEISLGIIMQRGAKVSGNRY
FLRGALLIOLGILQALKLAVNGEVPPTLPVLVPEWVGPGIQAAREYRVG
DGLYLVTSEVPLIAGHSGETLDSKGPLIYACHSSCFRRBASHGKDTGITRHQF
DKVEGFYCTPADEAHEHERLGMQOMLARIIEVPYKVIDVAAGDGSSAARFDECA
WITPGAYRELSTSNCTTFQARLIRYRDASGKQIATTAITLATTIRMLVAITLEN
HQRPDGSRVPADLVFPVGVEVEPVA"
complement(3067..3141)
/gene="sers"
/note="P800179 Aminoacyl-transfer RNA synthetases
class-II signature 1"
4039..5388
/gene="Rv3835"
4039..5388
/gene="Rv3835" (MTCY01A6.34c), len: 449. Unknown."
/codon_start=1
/transl_table=11
/product="hypothetical protein Rv3835"
/protein_id="CAB06206.1"
/db_xref="GI:1781122"
/db_xref="SPTREMBL:P96243"
/translation="MLDAPEQDPVDPDGPASPPHGEADQPLPGPRMPRALRSATRRA
LLTLALGGLIAGLIVTAIPAVGRAPERLAGYIASNVPSPGAKINASFNVASGDCIM
WPDGTPESAIVSCADEHREVAESIIMRTFPGMEYQONAPSPARIQOISEEQCA
AVRRYIGTKFDPNSKFTISMLWPGDAMRQAGSRMLCGLSGPPNQALPFGKVD
IDSKYVGPACTGIGDATTNQPIDVVDCAAPAMVSGVYNLAERPDALPSEPRD
GFTKDACTRMTDYLAPLKLRTTTLITLITLIPWSASGRVVASIGTLNGGGA
TLVNASGALLINGQVPEPPDIPEERLNPILPLDLPTRAPAPQOLPSTGRTQ
LPAQPVPTPTRPESHAPAAPASTQPPPDAGAPPAQSEATPPGAEAPAG"
5393..5806
/gene="Rv3836"
5393..5806
/gene="Rv3836" (MTCY01A6.33c), len: 137. Unknown;
containsP800142 Neutral zinc metalloproteinases,
zinc-binding region signature"
/codon_start=1
/transl_table=11
/product="hypothetical protein Rv3836"
/protein_id="CAB06205.1"
/db_xref="GI:1781121"
/db_xref="SPTREMBL:P96242"
/translation="MTVRMDPQRFDELVSADLILIPPELADAMDNVVLVANRHPQHE
NLGGYRGVALTERGSDYAGSLPDATTIYEAALLDQSDSEVDVQVAIVIEVANH
FGIDDERLDOLGWRDEPAPRGKNPDLASAPNANGP"
5672..5701
/gene="Rv3837"
/note="P800142 Neutral zinc metalloproteinases,
zinc-binding region signature"
complement(6001..6699)
/gene="Rv3837c"
complement(6001..6699)

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Alignment Scores:			
Pred. No.:	2,08e-05	Length:	37751
Scores:	94.00	Matches:	15
Percent Similarity:	89.29%	Conservative:	10
Best Local Similarity:	53.57%	Mismatches:	3
Query Match:	64.83%	Indels:	0
DB:	1	Gaps:	0

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US-09-987-190-2 (1-30) x MTCY1A6 (1-37751)
Oy 1 LysTYSerLeuPProGluLeuAspTy-GluuphSeSerIarhrgIupProTyriISerCy 20
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```

Qy	21	GlnIleAenGluIle***TyrThr 28
Db	15762	CAGATCAACGAGCTTCACCACAGC 15785
RESULT 21		
LOCUS	PFSD	567 bp DNA linear BCT 14-MAR-1996
DEFINITION	P. freudenreichii sod gene (partial).	
ACCESSION	X91650	
VERSION	X91650.1 GI:1061201	
KEYWORDS	sod gene; superoxide dismutase.	
SOURCE	Propionibacterium freudenreichii.	
ORGANISM	Propionibacterium freudenreichii Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Propionibacteriaceae; Propionibacteriinae; Propionibacteriaceae;	
REFERENCE	1 (bases 1 to 567)	
AUTHORS	Gabbianelli, R., Battistoni, A., Polizio, F., Carri, M.T., De Martino, A., Meier, B., Desideri, A. and Rottilo, G.	
TITLE	Metal uptake of recombinant cambialistic superoxide dismutase from <i>Propionibacterium shermanii</i> is affected by growth conditions of host <i>Escherichia coli</i> cells	
JOURNAL	Biochem. Biophys. Res. Commun. 216 (3), 841-847 (1995)	
MEDLINE	96074560	
PUBMED	7488202	
REFERENCE	2 (bases 1 to 567)	
AUTHORS	Gabbianelli, R.	
TITLE	Direct Submission	
JOURNAL	Submitted (19-SEP-1995) R. Gabbianelli, Dept. Biology, University of Vergata, Via Della Ricerca Scientifica, Rome, ITALY	
REMARK	revised by submitor 03-OCT-95	
FEATURES	Location/Qualifiers	
source	1..567	
gene	/organism="Propionibacterium freudenreichii"	
	/strain="P23"	
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	/db_xref="taxon:1744"	
	1..567	
	/gene="sod"	
	1..567	
	/EC_number="1.15.1.1"	
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	/product="superoxide dismutase"	
	/protein_id="CA62838.1"	
	/db_xref="GI:1061202"	
	/db_xref="SPTREMBL:O59673"	
	/translation="MAVYTLPELPIYDSALEPTYSIGETIMELHDKHKAAYVDGANTALDKLAERDKADFGAIINLEKDLAIAGVHDSVPMVNMAPKSAPEPDEIQAALIDKFAEPPNNMKQFPAALATGIGOGSSMASIYVNDPLGKRLINTLQFYDHNNLPAAGSLPILQLDMMHFAFYLDQYKNVKGDIYKSMNVNM"	
BASE COUNT	118 a 189 c 164 g 96 t	
ORIGIN		
Alignment Scores:		
Pred. NO.:	4e-07	Length: 567
Score:	91.00	Matches: 16
Percent Similarity:	84.62%	Conservative: 6
Best Local Similarity:	61.54%	Mismatches: 4
Query Match:	62.76%	Indels: 0
DB:	1	Gaps: 0
US-09-987-190-2 (1-30) x PFSD (1-567)		
Qy	2	TyrSerLeuProGluLeuAspYrGluPheSerAlaTrnGluProTyrIleSerGlyGln 21
Db	10	TACACGCTGCGGAGACTTCCTACACACTACTCGCCCTCGAGCCCTATCATCTCGGGTAG 69
Qy	22	IleAenGluIle***Tyr 27

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RESULT 22
Db 70 ATCATTGAGCTCCACCAT 87

PFSSOD
LOCUS P.freudenreichii sod gene, partial. 567 bp DNA linear BCT 15-MAY-1998
DEFINITION Y09012
ACCESSION Y09012
VERSION Y09012.1 GI:3135855
KEYWORDS cytoplasmatic protein, sod gene; superoxide dismutase.
SOURCE Propionibacterium freudenreichii.
ORGANISM Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Propionibacteriaceae; Propionibacteriaceae;
Propionibacterium.
1 (bases 1 to 567)
REFERENCE 1 (bases 1 to 567)
AUTHORS Gabbianelli, R.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-1996) R. Gabbianelli, Dept. of Biology,
UNIVERSITY TOR VERGATA, Via Della Ricerca Scientifica, Rome, ITALY
2 (bases 1 to 567)
Gabbianelli, R., Battistoni, A., Polizio, F., Carri, M.T., De
Martino, A., Meier, B., Desideri, A. and Rocilio, G.
Metabolic uptake of recombinant cambialistic superoxide dismutase from
Propionibacterium shermanii is affected by growth conditions of
host Escherichia coli cells
JOURNAL Biochem. Res. Commun. 216 (3), 841-847 (1995)
MEDLINE 96074560
PUBMED 7488202
FEATURES
source
location/Qualifiers
1..567
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/strain="PZ3"
/sub_species="Shermanii"
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1..567
/gene="sod"
1..>567
/EC_number="1.15.1.1"
/BC_number="1.15.1.1"
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/transl_table=1
/product="superoxide dismutase"
/protein_id="CAA70215.1"
/db_xref="GI:3135855"
/db_xref="SPTREMBL:O59673"
/translation="MAVYTLPELPYDSALPEYISGEIMELHDKHKAAYVDGANTALL
DKLAARDKADPGAINLEKDIKEDIAENLAGIYNHVSFEMKQMAPKSARPRDEIGALID
EFPSGPNMAAQPTLAATGTIGSGMSAIYWDPLKRIINTLIQFYDHNNLPAGSIPLIQ
LDMWEHAFYIQTYNKVDYKSVKNNVNM"
BASE COUNT 118 a 189 c 164 g 96 t
ORIGIN
Alignment Scores:
Pred. No.: 4e-07 Length: 567
Score: 91.00 Matches: 16
Percent Similarity: 84.62% Conservative: 6
Best Local Similarity: 61.54% Mismatches: 4
Query Match: 62.76% Indels: 0
Gaps: 0
1
US-09-987-190-2 (1-30) x PFSSOD (1-567)
OY 2 TyrsrLeuPProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 10 TACACGCTGCGCGAACTTCCTACGACACTCTGGCCCTGAGCCGTACATCTCGSGTAG 69
OY 22 TleangIuile***Tyr 27
Db 70 ATCATGAGCTCCACCAT 87
RESULT 23
LOCUS AB079877
AB079877 655 bp mRNA linear INV 19-FEB-2002

```

DEFINITION Marsupenaeus japonicus sod-1 mRNA for superoxide dismutase like protein, complete cds.

ACCESSION AB079877

VERSION AB079877.1 GI:18700488

KEYWORDS

SOURCE Marsupenaeus japonicus cDNA to mRNA.

ORGANISM Marsupenaeus japonicus

REFERENCE 1 Soma,G., Inagawa,H., Nishizawa,T., Honda,T., Nomura,Y., Uenobe,M., Takahashi,Y., Iteami,T. and Yokomizo,Y. Kurema shrimp cDNA similar to superoxide dismutase protein Published Only in Database (2002)

JOURNAL 2 (bases 1 to 655)

REFERENCE Soma,G., Inagawa,H., Nishizawa,T., Honda,T., Nomura,Y., Uenobe,M., Takahashi,Y., Iteami,T. and Yokomizo,Y. Direct Submission Submitted (15-FEB-2002) Hirocyki Inagawa, Tokushima Bunri University, Institute for Health Sciences; Yamashiro-cho Nishihama-bouji, Tokushima, Tokushima 770-8514, Japan (E-mail:pinac@okushima.bunri-u.ac.jp, Tel:81-86-622-9611(ex.1104), Fax:81-86-622-3217)

COMMENT This study was supported by Grant-in-Aid of Recombinant Cytokine's Project provided by the Ministry of Agriculture, Forestry and Fisheries, Japan (RCP2001-2230).

FEATURES

source Location/Qualifiers

1..655

/organism="Marsupenaeus japonicus"

/db_xref="taxon:27405"

1..655

/gene="sod-1"

32..637

/gene="sod-1"

/codon_start=1

/product="superoxide dismutase like protein"

/protein_id="BAB85211.1"

/db_xref="GI:18700489"

/translation="MAEKAAYISILEKLAELGIEVDQIKKQFANAADEAVIGE MATYVEGIVQAGVQAQAGTYSPOIAQFPHINLEGERAHALPLPKIDFNALIEP ISGMIEIHTKHIOGTYNINLIATKIKVEAANDVSEANMALLPAIKENGHNLHT IFMTNMAPDAGEPQGAIAQAIIDSLHSVPOGQFSAASYE"

BASE COUNT 173 a 156 c 169 g 157 t

ORIGIN

Alignment Scores:

Score: 4.76e-05 Length: 655

Percent Similarity: 80.00 Matches: 15

Best Local Similarity: 77.78% Conservative: 6

Query Match: 55.56% Mismatches: 6

DB: 55.17% Indels: 0

Gaps: 0

US-09-987-190-2 (1-30) x AB079877 (1-655)

Qy 2 TyrsrleupProgluleuaspTyrgluPheseralathrgluProtyrIleesergly 21

Db 290 CATGCTTGCCTCTCTCAAGTACGCTTAATGCGCTCGAACACACATTTGGGCATG 349

Qy 22 llaengluile**TyrThr 28

Db 350 ATCATGAGATTCATCACAC 370

RESULT 24

AB001693

LOCUS AB001693 954 bp mRNA linear MAM 14-DEC-1999

DEFINITION Equus caballus Mn-SOD mRNA for manganese superoxide dismutase, complete cds.

ACCESSION AB001693

VERSION AB001693.1 GI:4589877

KEYWORDS Mn-SOD; manganese superoxide dismutase.

SOURCE Equus caballus (strain:Thoroughbred) adult male testis cDNA to

ORGANISM Equus caballus

REFERENCE 1 Ishida,N., Katayama,Y., Sato,F., Hasegawa,T. and Mukoyama,H. The cDNA sequences of equine antioxidant enzyme genes Cu/Zn-SOD and Mn-SOD, and these expressions in equine tissues

JOURNAL J. Vet. Med. Sci. 61 (3), 291-294 (1999)

REFERENCE 2 (bases 1 to 954)

REFERENCE Ishida,N. Direct Submission Submitted (07-MAR-1997) Nobuhige Ishida, JRA Equine Research Institute, Laboratory of Molecular and Cellular Biology, 321-4, Tokami-cho, Utsunomiya, Tochigi 320-0856, Japan (E-mail:noi@idcenter.equinist.go.jp, Tel:81-28-647-0662, Fax:81-28-647-0686)

FEATURES

source Location/Qualifiers

1..954

/organism="Equus caballus"

/strain="Thoroughbred"

/db_xref="taxon:9796"

/sex="male"

/tissue_type="testis"

/dev_stage="adult"

/note="domestic horse"

1..954

/gene="Mn-SOD"

70..738

/gene="Mn-SOD"

/codon_start=1

/product="manganese superoxide dismutase"

/protein_id="BAA76922.1"

/db_xref="GI:4589878"

/translation="MLCRAACSTSRKLVLPALGSLGRQKSLPDLQYDGLALPYINA QIQQLHHSKHAAYVNNLVNLTBEKYGQALAKGVTAQIALQPLKRNKGGHINHTTFW TNLSPNGGEGPKGLDPAIKRDGSEDFKFKELTASAGVSGMGWLGFPNKQGRIG IVACPNDPLQGTGTLIPLLGIDVWEHAYVLQKNVRPDPYLKAIMVINVENSERYM ACKK"

BASE COUNT 235 a 223 c 256 g 240 t

ORIGIN

Alignment Scores:

Score: 7.59e-05 Length: 954

Percent Similarity: 80.00 Matches: 13

Best Local Similarity: 78.57% Conservative: 9

Query Match: 46.43% Mismatches: 6

DB: 55.17% Indels: 0

Gaps: 0

US-09-987-190-2 (1-30) x AB001693 (1-954)

Qy 1 lvsTyrsrleupProgluleuaspTyrgluPheseralathrgluProtyrIleesergly 20

Db 142 AAGCAGCCCTCCCGCAGCTTCAGTATGATGAGCCCTCGAGCCCTACATCACGCC 201

Qy 21 glulleangluile**TyrThr 28

Db 202 CAGATCATGACGTGCACACAGC 225

RESULT 25

GSP312188

LOCUS GSP312188 4439 bp DNA linear BCT 21-MAY-2002

DEFINITION Gordonia sp. K02 sodA gene, ORF1, ORF2 and ORF3 (partial).

ACCESSION AJ312188

VERSION AJ312188.1 GI:21104320

KEYWORDS ATP-binding protein; Mn-superoxide dismutase; ORF1; ORF2; ORF3; sodA gene; transmembrane protein.

SOURCE Gordonia sp. K02.

ORGANISM Gordonia sp. K02

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Gordoniaceae; Gordonia.

REFERENCE 1
AUTHORS Berekaa, M.M.
JOURNAL Thesis (2001) Department of Institut fuer Mikrobiologie,
Westfaelische Wilhelms-Universitaet Muenster, Muenster, Germany

REFERENCE 2
AUTHORS Berekaa, M.M., Priefert, H. and Steinbuechel, A.
TITLE Identification and characterization of an extracellular
Mn-superoxide dismutase encoding gene (sod) of Gordonia sp. strain
K02: A radical scavenger enzyme produced during rubber degradation
Unpublished
3 (bases 1 to 4439)
REFERENCE Berekaa, M.M.
AUTHORS Direct Submission
TITLE Submitted (21-MAY-2001) Berekaa M.M., Institut fuer Mikrobiologie,
Westfaelische Wilhelms-Universitaet, Corrensstrasse 3,
48149-Muenster, D-48149, GERMANY
JOURNAL location/Qualifiers
1. .4439
/organism="Gordonia sp. K02"
/strain="K02"
/db_xref="taxon:160824"
/country="Germany: Muenster"
/note="rubber degrading bacterium"
1. .640
/gene="soda"
1. .3
/gene="soda"
11. .640
/gene="soda"
/function="radical scavenger enzyme"
/codon_start=1
/evidence=experimental
/transl_table=1
/product="Mn-superoxide dismutase"
/protein_id="CAC85367.1"
/db_xref="GI:21104321"
/translation="MAEYTLADLDYDALEPHISGIMELHSHKHATYVKANDTL
EKLAAREDSIAGKVGGLSATLSFHLGHTNHSI FWNLSPNGSGEPGLAAITE
QFGGFDKRFHATTAATLQSGWAILGYDPIGKLVILQITDQSGNI PAALIPVWML
DMMEHAPLYDQNKPDYVAKMMVVMMAADAGEFRGAKTQSGSLIIPA"
complement (725. .1519)
/function="hypothetical ABC transport system"
/note="ORF1"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="CAC85368.1"
/db_xref="GI:21104322"
/translation="MHSRAVRLGRCPMTWTVPLRQVPGDSFVHRLMAGTKLVYL
ILGIMTVLPSWPAIGVAAIVITLALAGIPLGAI RPPMFWGLIGI GAVNASFA
ILGALIVLPAITLALVAVASSIIVITTPADVAPALRLMRELRLLPVENWAVA
IALCMRGLPLIEELAVLRAAHLRPRAKGRSDHSPAMGIMDITAMSSALRSASB
MAELTRAGGTGRITAMPARGRSDALALFVIYVACTVATVTITL"
complement (1516. .3765)
/function="hypothetical ABC transport system"
/note="ORF2"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="CAC85369.1"
/db_xref="GI:21104323"
/translation="MCWYPSAGSIRTAEPSCDARLHAI RPTGTRGRSPAGPAUT
RHGPPEVLASAGMEFASVAFGLTVAANVIVSVIHRAGRAARGRSPDPGPA
ABALITATVATTAFAFAMAGTAMATVIGSALIGIVGDIKRGRGALGATVAV
PVLGVSIVLIVLVEPLRTITTEAMTNSLHGVAKMLGKPEPTDVGALMSRSTIS
HMMIWMVSGTGVTAISLVAAWMTLGA SSPACPARHAI DGRGRDVAAPLARS
NTSLILOPARGHVLHDIIDIDPGRVAVVANGSGKSTLKL IAGRPSTGVHPEL
AGLVHGTALVLOPPEIOMIGSRVADVVGGLPGADVVEALIAVGLSGDRET
TDLSGQOORLAIAALARPRLIADETSMVDEGRGOLILALPVRGIAVYL
ITHRGSEAAADARVILHAGRVVPHPRAMPDPTDIHRPAPADSSATSLAAGPHV
DOLAARPHLGGELVLDHYGVANLPSSPWEVALTIDICLVTRGEBLIVGKGSRK
TTLAMIAGLISPTSGTCHLSSGKTPAAGPDGEPVTDHVGAVGLGQHALQIQ
KTVVDEIMAAAGEKVGTAEVAVLIELVGLPRQMAATKVDLLSGQMRVVLAIAR

HPYMLVINEPLAGLNPARRRSVSLIPALRADGMTIIVISHDFSLDSVCTRRVLY
DGAVAAQDP"
complement (1524. .1526)
/note="ORF1"
complement (3772. .3773)
/note="ORF2"
3819. .3822
/note="ORF3"
3832. .>4439
/function="unknown"
/note="ORF3"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="CAC85370.1"
/db_xref="GI:21104324"
/translation="MOSIPLELTPQHEGLNGLISGRPESTLEKTHSVGSRVIG
CRPGLPTITLIVGEORPARSADETVGMVAISNTTDSFVAGRLNPPALMLH
PRSRFTLCCGVFGRLRVLAAGPTELGELHRAWGAEATHRELAHVIGIDPVPTKV
LACSSSLGPAPKPCPTGSTRSAROLGPDSDQTSRCRSRLILV"

BASE COUNT 771 a 1508 c 1524 g 636 t
ORIGIN

Alignment Scores:
Pred. No.: 0.000511 Length: 4439
Score: 80.00 Matches: 13
Percent Similarity: 85.71% Conservative: 11
Best local Similarity: 46.43% Mismatches: 4
Query Match: 55.17% Indels: 0
DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x GSP312188 (1-4439)

Qy 1 LysTYrSerLeuProGluLeuAspTYrGluPheSerAlaThrGluProtyrIleSercly 20
Db 17 GAATPACGCGCTTCCGAGATCGATTACGACTACGGGACTCGAGCCGACATCTCCGCG 76

Qy 21 GlnIleAsnGluIle***TYrThr 28
Db 77 AGATCATGAGCTCCACACAGC 100

RESULT 26
E15569
LOCUS 812 bp, DNA linear PAT 28-JUL-1999
DEFINITION cDNA encoding Malassezia antigen protein MF-4.
ACCESSION E15569
VERSION E15569.1 GI:5710252
KEYWORDS JP 1998077296-A/4.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 812)
AUTHORS Takesako, K., Daimon, H., Kuroda, M., Katou, I., Yasueda, H., Akiyama, K.
and Yamaguchi, H.
TITLE RECOMBINANT MALASSEZIA ANTIGENIC PROTEIN AND ITS GENE
JOURNAL Patent: JP 1998077296-A 4 24-MAR-1998;
TAKARA SHUZO CO LTD
OS Malassezia furfur
PN JP 1998077296-A/4
PF 05-SEP-1998 JP 1996257613
PI TAKESAKO KAZUTADA, DAIMON HISASHI, KURODA MASANOBU, PI KATOU
IKUNOSHIN,
PI YASUEDA HIROSHI, AKIYAMA KAZUO, YAMAGUCHI HIDEYO PC
C07K14/195, A61J39/35, C07H21/04, C07K7/08, C12N15/09, C12Q1/68, PC
G01N33/53,
CC GOIN33/569;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key location/Qualifiers

FT source 1. .812
FT /strain='TIMM2782', /organism='Malassezia furfur' FT
FT mat_peptide 2. .673
FT /product='Malassezia antigen protein MF-4',
FEATURES
source
1. .812
/organism='unidentified'
/db_xref='taxon:32644'
BASE COUNT 235 a _245 c 218 g 114 t
ORIGIN

Alignment Scores:
Pred. No.: 9.45e-05 Length: 812
Score: 79.00 Matches: 15
Percent Similarity: 70.37% Conservative: 4
Best Local Similarity: 55.56% Mismatches: 8
Query Match: 54.48% Indels: 0
DB: 6 Gaps: 0

US-09-987-190-2 (1-30) x E15569 (1-812)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 74 AAGTACACGCTCCGCCGCTGACGACGAGCGCGCTGAGCGCGGCGATCTCGGCG 133

Qy 21 GlnIleAsnGluIle***Tyr 27
Db 134 GAGATCATGAGACGACATC 154

RESULT 27
AX123311 600 bp DNA linear PAT 11-MAY-2001
LOCUS
DEFINITION Sequence 3227 from Patent EP1108790.
ACCESSION AX123311
VERSION AX123311.1 GI:14040799
KEYWORDS
SOURCE
ORGANISM
Corynebacterium glutamicum.
Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Corynebacteriaceae;
Corynebacterium.
1 (bases 1 to 600)
AUTHORS Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
Yokoi,H., Tareishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
TITLE Novel polynucleotides
JOURNAL Patent: EP 1108790-A 3227 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
FEATURES
source
1. .600
/organism='Corynebacterium glutamicum'
/db_xref='taxon:1718'
BASE COUNT 143 a _197 c 146 g 114 t
ORIGIN

Alignment Scores:
Pred. No.: 0.00015 Length: 600
Score: 77.00 Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
DB: 6 Gaps: 0

US-09-987-190-2 (1-30) x AX123311 (1-600)

Qy 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 21
Db 10 TACGAATCCCGAATCGATACGATACGACGCTCTGACACACATCCCGCTGAA 69

Qy 22 IleAsnGluIle***TyrThr 28
Db 70 ATCATGAGACTTCACCATC 90

RESULT 28
RABMSD 606 bp mRNA linear MAM 11-FEB-1994
LOCUS
DEFINITION Oryctolagus cuniculus manganese superoxide dismutase mRNA, partial
cds.
ACCESSION L28808
VERSION L28808.1 GI:454174
KEYWORDS manganese superoxide dismutase.
SOURCE Oryctolagus cuniculus (strain NZ white) cDNA to mRNA.
ORGANISM Oryctolagus cuniculus
Bukaryaota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE
AUTHORS Jackson,R.M.
JOURNAL 1 (bases 1 to 606)
Unpublished (1994)
FEATURES
source
Location/Qualifiers
1. .606
/organism="Oryctolagus cuniculus"
/strain="NZ white"
/db_xref="taxon:9986"
CDS
<1..>606
/codon_start=1
/product="manganese superoxide dismutase"
/protein_id="AA031401.1"
/db_xref="GI:454175"
/translation="HGRGMKHSLPDLPYDGALEPHINAQIMELHSHKHHAAVYNNLN
ATREKREALARGDVTAAVAALOPALKEKGGHINHTIPWNTLS PNGSGEPKGLLEAI
KRDPGSPDKRELTAVSVGVSGMGWGLFENKEOGLDIAACANDPLOGTGLIPL
LGIDVMEHATYLDQKNRPDYLRKINMVTIMENVTERIMACK"
BASE COUNT 155 a _162 c 178 g 111 t
ORIGIN

Alignment Scores:
Pred. No.: 0.000152 Length: 606
Score: 77.00 Matches: 13
Percent Similarity: 78.57% Conservative: 9
Best Local Similarity: 46.43% Mismatches: 6
Query Match: 53.10% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x RABMSD (1-606)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 16 AAGCACAGCCTCCCGACCTGCTGACGACGAGCGCGCTGAGCCGACATCAAGCG 75

Qy 21 GlnIleAsnGluIle***TyrThr 28
Db 76 CAGATCATGAGACTGACACACG 99

RESULT 29
AB055218 960 bp DNA linear BCT 02-AUG-2001
LOCUS
DEFINITION Corynebacterium glutamicum gene for superoxide dismutase, complete
cds.
ACCESSION AB055218
VERSION AB055218.1 GI:15076595
KEYWORDS
SOURCE
ORGANISM
Corynebacterium glutamicum (strain:ATCC 13032) DNA.
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
1
AUTHORS Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Hattori,M.,
Shiba,T., Sakaki,Y., Yokoi,H. and Ozaki,A.
TITLE SOD of Corynebacterium glutamicum ATCC 13032
JOURNAL Published Only in Database (2001)
REFERENCE
AUTHORS Nakagawa,S.
JOURNAL Direct Submission
Submitted (01-FEB-2001) Satochi Nakagawa, Kyowa Hakko Kogyo Co.
Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida,

Tokyo 194-8533, Japan (E-mail: snakagawa@kyowa.co.jp,
Tel:81-42-725-2555(ex.2165), Fax:81-42-726-8330)

FEATURES

source

CDS

```

1..960
/organism="Corynebacterium glutamicum"
/strain="ATCC 13032"
/db_xref="taxon:1718"
154..756
/EC_number="1.15.1.1"
/codon_start=1
/transl_table=1
/product="superoxide dismutase"
/protein_id="BAB62412.1"
/db_xref="GI:15076596"
/translation="MAVVELPELDYADALEPHIAIMELHSHKHATYVAGANAL
EALAKAREGTPQIRALSKNLAFNIGTHNVPMKNSPNGGEPTELAIR
DFGFAFQDHPNSAALGDSGNAVGYDHSGLVIBOLTDQGNISVDITFVLM
DMEHAFYLYQKVKADYKAVNVPFWDAAAFPAASK"

```

ALIGNMENT SCORES:

```

Pred. No.: 0.000268 Length: 960
Score: 77.00 Matches: 13
Percent Similarity: 74.07% Conserved: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
DB: 1 Gaps: 0

```

US-09-987-190-2 (1-30) x AB055218 (1-960)

Qy 2 TyserleuprogulueapTyrgluPheserAathrgluProTyrlIserglyln 21

Db 163 TACGAAGTCCAGAACTGACATACGACGCTCTCGAGCCACACATCGCGCTGAA 222

Qy 22 Ileaengulie***TyrrThr 28

Db 223 ATCATGAGCTTCACCACTCC 243

RESULT 30

AX136077 1143 bp DNA linear PAT 30-MAY-2001

LOCUS AX136077

DEFINITION Sequence 1 from Patent EP1077261.

ACCESSION AX136077

VERSION AX136077.1 GI:14272487

KEYWORDS

ORGANISM

source

FEATURES

source

CDS

1..1143

/organism="Corynebacterium melassecola"

/db_xref="taxon:41643"

/note="ATCC 17965"

338..940

/note="unnamed protein product"

/codon_start=1

/transl_table=1

/protein_id="CAC39682.1"

/db_xref="GI:14272488"

/translation="MAVVELPELDYADALEPHIAIMELHSHKHATYVAGANAL

EALAKAREGTPQIRALSKNLAFNIGTHNVPMKNSPNGGEPTELAIR

DFGFAFQDHPNSAALGDSGNAVGYDHSGLVIBOLTDQGNISVDITFVLM

DMEHAFYLYQKVKADYKAVNVPFWDAAAFPAASK"

BASE COUNT 273 a 323 c 288 g 259 t

ALIGNMENT SCORES:

```

Pred. No.: 0.000333 Length: 1143
Score: 77.00 Matches: 13
Percent Similarity: 74.07% Conserved: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
DB: 6 Gaps: 0

```

US-09-987-190-2 (1-30) x AX136077 (1-1143)

Qy 2 TyserleuprogulueapTyrgluPheserAathrgluProTyrlIserglyln 21

Db 347 TACGAAGTCCAGAACTGACATACGACGCTCTCGAGCCACACATCGCGCTGAA 406

Qy 22 Ileaengulie***TyrrThr 28

Db 407 ATCATGAGCTTCACCACTCC 427

RESULT 31

BD011434 1143 bp DNA linear PAT 31-JAN-2002

LOCUS BD011434

DEFINITION DNA, amino acid sequence, coryneform microorganism, shuttle vector, method of potentiating superoxide dismutase activity and method of producing metabolite.

ACCESSION BD011434

VERSION BD011434.1 GI:18639807

KEYWORDS JP 2001078788-A/1.

SOURCE JP 2001078788-A/1.

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

OS Corynebacterium melassecola ATCC 17965

PN JP 2001078788-A/1

PF 27-MAR-2001

PR 14-AUG-2000 JP 2000246077

PI 13-AUG-1999 US 09/373731

PC C12N15/09,C12N1/21,C12N9/02,C12P13/08,C12P19/32, PC

C12Q1/68//

PC C12N9/10,C12N9/88,(C12N15/09,C12R1:15),(C12N9/02,C12R1:15), PC

(C12P13/08,C12R1:15),C12N15/00,(C12N15/00,C12R1:15) CC

FH Key

FT CDS

Location/Qualifiers

1..1143

/organism="unidentified"

/db_xref="taxon:32644"

273 a 323 c 288 g 259 t

ALIGNMENT SCORES:

Pred. No.: 0.000333 Length: 1143

Score: 77.00 Matches: 13

Percent Similarity: 74.07% Conserved: 7

Best Local Similarity: 48.15% Mismatches: 7

Query Match: 53.10% Indels: 0

DB: 6 Gaps: 0

US-09-987-190-2 (1-30) x BD011434 (1-1143)

Qy 2 TyserleuprogulueapTyrgluPheserAathrgluProTyrlIserglyln 21

Db 347 TACGAAGTCCAGAACTGACATACGACGCTCTCGAGCCACACATCGCGCTGAA 406

AUTHORS Nakagawa, S.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-2002) Satoshi Nakagawa, Kyowa Hako Kogyo Co.
Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida,
Tokyo 194-8533, Japan (E-mail: snakagawa@xagen.com,
Tel:81-44-823-3031, Fax:81-44-813-1651)
COMMENT This sequence is conducted by collaboration of Kyowa Hako Kogyo
Co. Ltd. And Kitasato University.
location/Qualifiers
FEATURES
source
1. .325651
/organism="Corynebacterium glutamicum ATCC 13032"
/strain="ATCC 13032"
/db_xref="taxon:196627"
/note="ATCC 13032"
complement(135. .773)
/gene="Cg12799"
complement(135. .773)
/gene="Cg12799"
/note="P01025:GrpE"
/codon_start=1
/transl_table=11
/product="molecular chaperone GrpE (heat shock protein)"
/protein_id="BAC00193.1"
/db_xref="GI:21325572"
/translation="MPDNFGDPENTDEPATSADRAEQAEAAARQAEESEFQASSE
EISPELAEIINDLSVDPLDGDGEVSASVETQAERTEDLQRTAAYANRRTERE
RQGIIDTARAGVYQLPLDDDLAEQHDNLGKPLSLDKLINILGKLVESFGS
IGSAFDEIHEHVAVDLSQGVKVLGTVLRKQYLRGDRVIRAVLIDPEES"
complement(792. .2648)
/gene="Cg12800"
complement(792. .2648)
/gene="Cg12800"
/note="P00012:Hsp70 protein"
/codon_start=1
/transl_table=11
/product="molecular chaperone and 70 kDa heat shock
chaperonin protein dnak"
/protein_id="BAC00194.1"
/db_xref="GI:21325573"
/translation="MGRVAGIDLTGTSVSVLEGGPVTYANAGSRTPSPVAFK
NGEVLGQSAKNQAVNVDRITRSVKHIGIDMSVAIDDKYTSQESASRTIMLKRD
AEALGSDVDVAVTVPAFEDSQKATKEGQJAGLVNLVNEPTAALAVLEKGS
EQEQTILVFDGGSTFVSLLEIGDVEVATSGDNELGGDDORIIVMLVEKFS
SNGIDLTAKKALQRLREAAEKAKIELSSQSANINLPYITADKNPLFDELTFS
BFGQITODLARTKTPNOVYKDGAVSEIDHYVLVGSGTRMPAVTELVLELGRSE
PKGVNPDEVAVGALQAGVLRGEVVDVILDVPLSLIGETGVMTKLIBENTTI
PYRSERTTAEDNQPSVOIQVPGREIRATANKLISFELGAIAPAPRGVPIETVF
DIRNAGIVHTAKDKGTGKENTYITIQSGISODEIDRMIKDAHADDEDKREEOE
VRNNAESLVYQTRKFEVENSEKSEDEKAKVEEAKGVEEALKGEDEIAIKAAVEKLN
TESQEMKAIYEADAAAGATQADAGAGAADNVDAVEVEDDAADNGEDKK"
3084. .4418
/gene="Cg12801"
3084. .4418
/gene="Cg12801"
/note="P01594:Domain of unknown function DUF20"
/codon_start=1
/transl_table=11
/product="Predicted permease"
/protein_id="BAC00195.1"
/db_xref="GI:21325574"
/translation="MPDTVLDALGNEFPPLNTOKSAVPPNAEATVEADSEGTDRSV
ILSGDGRMLSGMALRFIVLAVIALRMGLFWGILPVLLALVCTVAMPVKMR
EHKIPALAVITILGFPAIIGVFAIAPSVSOTROWDQATVGIEDMDVQGP
FNIDISQFEGALNDITSMLOSLOSISGVSGSISTASIVTTLAVMLVITFFLKG
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KKYFHAHLSBLLGEEFAGLSLPHPPPAKAAADIDATREFIKOMEGRDVEYAIRM
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GRADUGDDEARVRLRFHSDVAPAGLTDLEVPLSNCEIQEPOVILMVNLDSFLM
PLWPGVITAGAGYRAVDIVRGYPFSNGRLLYGDDLDLDFKILDGVRSHVPITESVL
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DKOIDNNEAELRCENQIVGILRSYLETWANKADAOAEPFGEAINRGLRSRL
AERTAKFLGLAMENSTRNLQISRLRDAREIEBEREPIINASLASEPREGRIHID
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Pred. No.:	Score:	Length:	Matches:
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Query Match:	53.10%	Indels:	0
DB:	1	Gaps:	0

US-09-987-190-2 (1-30) x AP005283 (1-325651)

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Oy 22 Ileaengluile**TyrThr 28
Db 142712 ATCATGAGCTTCACACATCC 142732
RESULT 35
AF521909 663 bp mRNA linear INV 07-JUN-2002
LOCUS Trichinella pseudospiralis Mn superoxide dismutase mRNA, complete
DEFINITION cde.
ACCESSION AF521909
VERSION AF521909.1 GI:21702728
KEYWORDS Trichinella pseudospiralis.
SOURCE Trichinella pseudospiralis.
ORGANISM Eukaryota; Metazoa; Nematoda; Enoplia; Trichocephalida;
REFERENCE 1 (bases 1 to 663)
AUTHORS Wu,H.W.K., Ko,R. and Mak,C.H.
TITLE Characterization and molecular cloning of Mn- superoxide dismutase

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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 663)
AUTHORS Wu,H.W.K., Ko,R. and Mak,C.H.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2002) Zoology, The University of Hong Kong, Pokfulam, Hong Kong, China
FEATURES
source
1..663
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BASE COUNT 178 a 147 c 162 g 176 t
ORIGIN
Alignment Scores:
Pred. No.: 0.00258 Length: 663
Score: 76.00 Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 52.41% Indels: 0
DB: 3 Gaps: 0
US-09-987-190-2 (1-30) x AF521909 (1-663)
Oy 1 LysTyrsertleuprogulenuaspytYtGluPheserAathrGluProtyrTlleserGly 20
Db 58 AAGACACGTTACCCGATTCGCTGATGACTTCGATCGTCTCGAACCCTGATATCTGCT 117
Oy 21 Glnleaugluile**Tyr 27
Db 118 GAATTTATGCGATTGATCAT 138
RESULT 36
DLA278864 761 bp mRNA linear PLN 24-AUG-2000
LOCUS Digitalis lanata partial mRNA for manganese superoxide dismutase
DEFINITION Digitalis lanata partial mRNA for manganese superoxide dismutase (Mn-SOD gene).
ACCESSION A0278864
VERSION A0278864.1 GI:9929160
KEYWORDS manganese superoxide dismutase; Mn-SOD gene.
SOURCE Digitalis lanata.
ORGANISM Digitalis lanata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Veronicaceae; Digitalis.
REFERENCE 1 (bases 1 to 761)
AUTHORS Gruner,B., Reva,V.A. and Mueller-Urli,F.
TITLE Stress-induction of Mn-dependent SOD and CAT in Digitalis lanata (Ehrh.) during somatic embryogenesis
JOURNAL Unpublished
JOURNAL 2 (bases 1 to 761)
REFERENCE Gruner,B.
AUTHORS Gruner,B.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Gruner B., Institute of Pharmaceutical Biology, University of Halle, Hoher Weg 8; Halle /Saale, D-06120, GERMANY
FEATURES
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/gene="MN-SOD"

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CDS

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 DVLATKGAISLVPLIGIDVWEHAYLQYKARPPYLKINIKMNMWKTASRYQKECP"

BASE COUNT 219 a 172 c 181 g 189 t

Alignment Scores:

Pred. No.: 0.000306 Length: 761
 Score: 76.00 Matches: 14
 Percent Similarity: 77.78% Conservative: 6
 Best Local Similarity: 51.85% Mismatches: 0
 Query Match: 52.41% Indels: 0
 Gaps: 0

US-09-987-190-2 (1-30) x DLA278864 (1-761)

QY 1 LyeTySerLeuProGluLeuAspTyrgluPheSerAlaThrGluProTyrlleSergly 20
 Db 44 AAGATTTCGCTGCCCGCTGAGCTGACATTAACGCCGCTTGAGCCAGTATACAGCGGC 103
 QY 21 GlnlleasnGluile***Tyr 27
 Db 104 GAGATCATGCAATTCACAC 124

RESULT 37
 LOCUS AX469763 325 bp DNA linear PAT 16-JUL-2002
 DEFINITION Sequence 11 from Patent WO0240498.
 ACCESSION AX469763
 VERSION AX469763.1 GI:21901883
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Oberley, L.W., Weydert, C.J. and Smith, B.B.
 TITLE Reduction of antioxidant enzyme levels in tumor cells using
 antisenese oligonucleotides
 JOURNAL Patent: WO 0240498-A 11 23-MAY-2002;
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
 FEATURES
 source 1. .325
 Location/Qualifiers

BASE COUNT 76 a 99 c 98 g 52 t
 ORIGIN
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 /db_xref="taxon:9606"

Alignment Scores:

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 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 Gaps: 0

US-09-987-190-2 (1-30) x AX469763 (1-325)

QY 1 LyeTySerLeuProGluLeuAspTyrgluPheSerAlaThrGluProTyrlleSergly 20
 Db 113 AAGACAGCGCTCCCGCTGAGCTGACATTAACGCCGCTTGAGCCAGTATACAGCGC 172
 QY 21 GlnlleasnGluile***TyrThr 28
 Db 173 CAGATCATGCGCTGACACACAGC 196

RESULT 38
 LOCUS S78832S1 535 bp DNA linear ROD 24-OCT-1995
 DEFINITION Sod-2=manganese superoxide dismutase [mice, C3H/HeJ, Genomic, 535
 nt, segment 1 of 4].

ACCESSION S78832
 VERSION S78832.1 GI:1037116
 KEYWORDS
 SEGMENT 1 of 4
 SOURCE Mus sp. C3H/HeJ.
 ORGANISM

REFERENCE 1
 AUTHORS Disilverstre, D., Kleeberger, S.R., Johns, J. and Levitt, R.C.
 TITLE Structure and DNA sequence of the mouse MnSOD gene
 JOURNAL Mamm. Genome 6 (4), 281-284 (1995)
 MEDLINE 95337589
 PUBMED 7613035
 REMARK Genbank staff at the National Library of Medicine created this
 entry [NCBI gblseq 169396] from the original journal article.
 This sequence comes from Fig. 1.
 Map location: 17.

FEATURES
 source Location/Qualifiers
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BASE COUNT 96 a 166 c 171 g 99 t 3 others
 ORIGIN

Alignment Scores:
 Pred. No.: 0.000456 Length: 535
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 Gaps: 0

US-09-987-190-2 (1-30) x S78832S1 (1-535)

QY 1 LyeTySerLeuProGluLeuAspTyrgluPheSerAlaThrGluProTyrlleSergly 20
 Db 210 AAGCAGCGCTCCCGCTGAGCTGACATTAACGCCGCTTGAGCCAGTATACAGCGC 269

QY 21 GlnlleasnGluile***TyrThr 28
 Db 270 CAGATCATGCGCTGACACACAGC 293

RESULT 39
 LOCUS AR130379 594 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 1 from patent US 6190658.
 ACCESSION AR130379
 VERSION AR130379.1 GI:14118704
 KEYWORDS
 SOURCE Unknown.
 ORGANISM

REFERENCE 1 (bases 1 to 594)
 AUTHORS McCord, J.M., Gao, B. and Flores, S.C.
 TITLE Genetically modified manganese superoxide dismutase for treating
 oxidative damage
 JOURNAL Patent: US 6190658-A 1 20-FEB-2001;
 Location/Qualifiers

FEATURES
 source 1. .594
 Location/Qualifiers
 1. .594
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 BASE COUNT 166 a 144 c 154 g 130 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.000519 Length: 594
 Score: 74.00 Matches: 12

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Computron Ltd.

OM protein - protein search, using sw model

Run on: April 9, 2003, 13:56:15 ; Search time 5.09174 Seconds

(without alignments)
173.357 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 145

Sequence: 1 KYSLPEIDYFSATEPYISQINEIXYTX 30

Scoring table: BLAST62

Searched: 262574 seqs, 29422922 residues

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued_Patents_AA.*

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- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	100	69.0	233	US-08-928-692-31	Sequence 31, Appli
3	100	69.0	233	US-09-339-972-31	Sequence 31, Appli
4	79	54.5	30	US-09-091-097-52	Sequence 52, Appli
5	79	54.5	224	US-09-091-097-8	Sequence 8, Appli
6	74	51.0	198	US-09-075-019-2	Sequence 2, Appli
7	74	51.0	198	US-08-47-10	Patent No. 5240847
8	74	51.0	198	US-08-47-11	Patent No. 5240847
9	74	51.0	222	US-08-365-486A-28	Sequence 48, Appli
10	74	51.0	222	US-08-023-980B-44	Sequence 44, Appli
11	74	51.0	222	US-08-486-953A-52	Sequence 52, Appli
12	74	51.0	222	US-08-927-230A-2	Sequence 2, Appli
13	74	51.0	222	US-08-927-230A-3	Sequence 3, Appli
14	74	51.0	222	US-09-151-052-2	Sequence 2, Appli
15	74	51.0	222	US-09-151-052-3	Sequence 3, Appli
16	74	51.0	222	US-09-126-109-2	Sequence 2, Appli
17	74	51.0	222	US-08-880-342-28	Sequence 28, Appli
18	74	51.0	226	US-09-075-019-7	Sequence 7, Appli
19	71	49.0	188	US-09-262-856A-6	Sequence 6, Appli
20	70	48.3	46	US-08-47-24	Patent No. 5240847
21	69	47.6	230	US-08-928-692-30	Sequence 30, Appli
22	69	47.6	230	US-09-339-972-30	Sequence 30, Appli
23	62	42.8	206	US-09-091-097-6	Sequence 6, Appli
24	58	40.0	214	US-09-411-578-1	Sequence 1, Appli
25	57	39.3	201	US-09-134-001C-3584	Sequence 3584, App
26	56	38.6	190	US-08-679-493A-184	Sequence 184, Appl
27	53	36.6	204	US-08-445-909A-17	Sequence 17, Appl

28	53	36.6	204	1	US-08-445-909A-29	Sequence 29, Appli
29	50	34.5	371	4	US-09-605-785-708	Sequence 708, App
30	50	34.5	553	4	US-09-020-956-113	Sequence 113, App
31	50	34.5	553	4	US-09-030-607-113	Sequence 113, App
32	50	34.5	553	4	US-09-605-785-113	Sequence 113, App
33	50	34.5	553	4	US-09-429-113-113	Sequence 113, App
34	50	34.5	553	4	US-09-352-616A-113	Sequence 113, App
35	50	34.5	553	4	US-09-602-877A-101	Sequence 101, App
36	50	34.5	553	4	US-09-232-149A-113	Sequence 113, App
37	48	33.1	885	1	US-08-042-747A-8	Sequence 8, Appli
38	48	33.1	885	3	US-08-804-439A-23	Sequence 23, Appli
39	48	33.1	885	3	US-08-720-229-23	Sequence 23, Appli
40	48	33.1	885	3	US-08-446-345-36	Sequence 36, Appli
41	46	31.7	1009	4	US-09-693-146-4	Sequence 4, Appli
42	45.5	31.4	203	3	US-08-331-625A-11	Sequence 11, Appli
43	45.5	31.4	203	4	US-09-484-151-11	Sequence 11, Appli
44	45.5	31.4	208	4	US-08-896-933-30	Sequence 30, Appli
45	45.5	31.4	208	4	US-08-896-933-30	Sequence 30, Appli

ALIGNMENTS

RESULT 1
US-09-262-856A-2
Sequence 2, Application US/09262856A
Patent No. 6333164
GENERAL INFORMATION:
APPLICANT: TAKESAKO, Kautech
APPLICANT: WIZUTANI, Shigetoshi
APPLICANT: ENDO, Masahito
APPLICANT: KATO, Ikumoshin
TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
FILE REFERENCE: 1422-372P
CURRENT APPLICATION NUMBER: US/09/262,856A
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 30
TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
OTHER INFORMATION: residues 26, 39, 30 = unknown
US-09-262-856A-2

Query Match 97.2%; Score 141; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.9e-17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 KYSLPEIDYFSATEPYISQINEIXYTX 28
US-09-262-856A-2
Sequence 2
Sequence 31; Application US/08928692
Patent No. 5958727
GENERAL INFORMATION:
APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamma, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 59587272 No. 59587272disk of No. 5958727th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA

```

ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928.692
FILING DATE: 12-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambda16, Eliae J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5958727e
US-08-928-692-31

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Oy      1 KSLPELDYEFSSATEPIYISQINEIXYT 28
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Db      27 KATLPDLKWDGALPEYISQINEIHYT 54

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RESULT 3
 US-09-339-972-31
 Sequence 31, Application US/09339972
 Patent No. 6323002
 GENERAL INFORMATION:
 APPLICANT: Brody, Howard
 APPLICANT: Yaver, Deborah S.
 APPLICANT: Lamsa, Michael
 APPLICANT: Hansen, Kim
 TITLE OF INVENTION: Methods for Modifying the Production of
 TITLE OF INVENTION: a Polypeptide
 NUMBER OF SEQUENCES: 80
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6323002o No. 6323002disk of No. 6323002th America, Inc
 STREET: 405 Lexington Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10174
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/339, 972
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/928, 692
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias J
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4944.200-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655

```

; INFORMATION FOR SEQ ID NO: 31:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 233 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: No. 6323002e
;
US-09-339-972-31

Query Match          69.0%; Score 100; DB 4; Length 233;
Beet Local Similarity 64.3%; Pred. No. 8.5e-09;
Matches 18; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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QY      1 KSLPELDYEFSSATEPYISGQINEIXYT 28
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Db      27 KVTLPDLKWDFCALFPYISGQINELHYT 54

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RESULT 5
US-09-091-097-8
; Sequence 8, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI
; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; TITLE OF INVENTION: MALASSEZIA
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,097
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; 09-091-097-8

Query Match 54.5%; Score 79; DB 4; Length 224;
Best Local Similarity 55.6%; Pred. No. 2.4e-05;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 KXSLPDLPEFSATEPYISQINEIXYT 27
Db 25 KYTLPLPYDYGALPAISGIMETHY 51

RESULT 6
US-09-075-019-2
; Sequence 2, Application US/09075019
; Patent No. 6190658
; GENERAL INFORMATION:
; APPLICANT: UTC IR459
; TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
; TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO

COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2848-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-075-019-2

Query Match 51.0%; Score 74; DB 4; Length 198;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXSLPDLPEFSATEPYISQINEIXYT 28
Db 1 KXSLPDLPYDYGALPHINQIMQLHHS 28

RESULT 7
5240847-10
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEYAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSSTEK, EDELTRAUD; MAURER-FOG, INGRID;
; WITCHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO: 10:
; LENGTH: 198
; 5240847-10

Query Match 51.0%; Score 74; DB 6; Length 198;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXSLPDLPEFSATEPYISQINEIXYT 28
Db 1 KXSLPDLPYDYGALPHINQIMQLHHS 28

RESULT 8
5240847-11
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEYAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSSTEK, EDELTRAUD; MAURER-FOG, INGRID;
; WITCHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO: 11:

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-126-109-2

Query Match 51.0%; Score 74; DB 4; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00016;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXSLPELDYERSATEPYISQINIEIXYT 28
DB 25 KXSLPELDYIDYGALEPHINQIMQLHHS 52

RESULT 17
US-08-880-342-28
Sequence 28, Application US/08880342
Patent No. 6218179

GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-880-342-28

Query Match 51.0%; Score 74; DB 4; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00016;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXSLPELDYERSATEPYISQINIEIXYT 28
DB 25 KXSLPELDYIDYGALEPHINQIMQLHHS 52

RESULT 18
US-09-075-019-7
Sequence 7, Application US/09075019
Patent No. 6190658

GENERAL INFORMATION:
APPLICANT: UTC IR459
TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,019
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2848-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 226 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-075-019-7

Query Match 51.0%; Score 74; DB 4; Length 226;
Best Local Similarity 42.9%; Pred. No. 0.00016;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXSLPELDYERSATEPYISQINIEIXYT 28
DB 3 KXSLPELDYIDYGALEPHINQIMQLHHS 30

RESULT 19
US-09-262-856A-6
Sequence 6, Application US/09262856A
Patent No. 633164
GENERAL INFORMATION:
APPLICANT: TAKESAKO, Kazuo
APPLICANT: MIZUTANI, Shigetoshi
APPLICANT: ENDO, Masahiro
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
FILE REFERENCE: 1422-372P
CURRENT APPLICATION NUMBER: US/09/262,856A
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 188
TYPE: PRT
ORGANISM: Candida albicans
US-09-262-856A-6

Query Match 49.0%; Score 71; DB 4; Length 188;
Best Local Similarity 81.2%; Pred. No. 0.00041;

Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 13 ATEPISGOINEIXYT 28
Db 1 ATEPITTCOMNEIHYT 16

RESULT 20
5240847-24
Patent No. 5240847
APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
ZOPHEL, ANDREAS; KRISTEK, EDELTRAUD; MADLER-FOGY, INGRID;
WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
(HNM-SOD)
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/167,261
FILING DATE: 11-MAR-1988
SEQ ID NO: 24
LENGTH: 46
40847-24

Query Match 48.3%; Score 70; DB 6; Length 46;
Best Local Similarity 54.5%; Pred. No. 9.6e-05;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KYSLPELDYFESATEPISGOI 22
Db 25 KHSLPDLPYDGALEPHINAQI 46

RESULT 21

US-08-928-692-30
Sequence 30, Application US/08928692
Patent No. 5958727
GENERAL INFORMATION:
APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamaa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958727o No. 5958727disk of No. 5958727th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944,200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

; MOLECULE TYPE: No. 5958727e
US-08-928-692-30

Query Match 47.6%; Score 69; DB 2; Length 230;
Best Local Similarity 48.1%; Pred. No. 0.0011;
Matches 13; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KYSLPELDYFESATEPISGOINEIXY 27
Db 36 KATLPDLAYDGALEPSISGKIMELH 62

RESULT 22
US-09-339-972-30
Sequence 30, Application US/09339972
Patent No. 6323002
GENERAL INFORMATION:
APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamaa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6323002o No. 6323002disk of No. 6323002th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,972
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,692
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944,200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6323002e
US-09-339-972-30

Query Match 47.6%; Score 69; DB 4; Length 230;
Best Local Similarity 48.1%; Pred. No. 0.0011;
Matches 13; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KYSLPELDYFESATEPISGOINEIXY 27
Db 36 KATLPDLAYDGALEPSISGKIMELH 62

RESULT 23
US-09-091-097-6
Sequence 6, Application US/09091097
Patent No. 6432407
GENERAL INFORMATION:

```

; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI
; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; TITLE OF INVENTION: MALASSEZIA
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESS: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-091-097-6
;
Query Match          42.8%; Score 62; DB 4; Length 206;
Best Local Similarity 40.7%; Pred. No. 0.014;
Matches 11; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
1 YSLPELDYFSATEPYISQINEIXY 27
:|||||:|||||:
6 EYTLPLPYAVDALEPFSKEIMTVHH 32
;
RESULT 24
US-09-411-578-1
; Sequence 1, Application US/09411578
; Patent No. 6203801
; GENERAL INFORMATION:
; APPLICANT: Schaap, Theodorus C
; APPLICANT: Kuiper, Catharina M
; APPLICANT: Vermeulen, Arnoldus N
; TITLE OF INVENTION: Coccidioides Vaccines
; FILE REFERENCE: schaad
; CURRENT APPLICATION NUMBER: US/09/411,578
; CURRENT FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 98203384.7
; EARLIER FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: 98203457.1
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
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; ORGANISM: Eimeria tenella
;
US-09-411-578-1
;
Query Match          40.0%; Score 58; DB 4; Length 214;
Best Local Similarity 46.2%; Pred. No. 0.068;
Matches 12; Conservative 2; Mismatches 12; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATEPYISQINEIXY 27
:|||||:|||||:
DB 3 FELPPLPYADALEPFSKETLEHYH 28
;
RESULT 25
US-09-134-001C-3584
; Sequence 3584, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13/064,964
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3584
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
;
US-09-134-001C-3584
;
Query Match          39.3%; Score 57; DB 4; Length 201;
Best Local Similarity 42.3%; Pred. No. 0.092;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATEPYISQINEIXY 27
:|||||:|||||:
DB 5 FELPPLPYADALEPHIDKQMEITHH 30
;
RESULT 26
US-08-679-493A-184
; Sequence 184, Application US/08679493A
; Patent No. 6303295
; GENERAL INFORMATION:
; APPLICANT: Taylor, Ethan W.
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
; FILE REFERENCE: 55-95
; CURRENT APPLICATION NUMBER: US/08/679,493A
; CURRENT FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 60/001203
; PRIOR FILING DATE: 1995-07-14
; PRIOR APPLICATION NUMBER: 60/003,112
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 184
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Entamoeba dispar
;
US-08-679-493A-184
;
Query Match          38.6%; Score 56; DB 4; Length 190;
Best Local Similarity 38.5%; Pred. No. 0.12;
Matches 10; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATEPYISQINEIXY 27
:|||||:|||||:
DB 3 FOLPPLPYAVNALEPHISKETLEFHH 28
```

RESULT 27

US-08-445-909A-17
; Sequence 17, Application US/08445909A
; Patent No. 5772396
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, Antony
; TITLE OF INVENTION: Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Superoxide Dismutase from Bacillus
; TITLE OF INVENTION: Stearothermophilus and Bacillus Caldorena
; NUMBER OF SEQUENCES: 29
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,909A
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,697
; FILING DATE: 02-FEB-1993
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-445-909A-17

Query Match 36.6%; Score 53; DB 1; Length 204;
Best Local Similarity 37.0%; Pred. No. 0.43;
Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 2 YSLPELDYFSAATPEYISQGINEIXYT 28

Db 3 FELPALPYDALBPHIDKEMTNNIHT 29

RESULT 28
US-08-445-909A-29
; Sequence 29, Application US/08445909A
; Patent No. 5772396
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, Antony
; TITLE OF INVENTION: Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Superoxide Dismutase from Bacillus
; TITLE OF INVENTION: Stearothermophilus and Bacillus Caldorena
; NUMBER OF SEQUENCES: 29
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,909A
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,697
; FILING DATE: 02-FEB-1993
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-445-909A-29

Query Match 36.6%; Score 53; DB 1; Length 204;

Best Local Similarity 37.0%; Pred. No. 0.43;
Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 2 YSLPELDYFSAATPEYISQGINEIXYT 28

Db 3 FELPALPYDALBPHIDKEMTNNIHT 29

RESULT 29

US-09-605-785-708
; Sequence 708, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 708
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-605-785-708

Query Match 34.5%; Score 50; DB 4; Length 371;
Best Local Similarity 45.0%; Pred. No. 2.9;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 YSLPELDYFSAATPEYISQ 21

Db 150 YLPAIDWTSALAPYIGTQ 169

RESULT 30
US-09-020-956-113
; Sequence 113, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
-09-020-956-113

Query Match 34.5%; Score 50; DB 4; Length 553;
Best Local Similarity 45.0%; Pred. No. 4.9;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 YSLPELDYEFSEATPYISQ 21
Db 176 YLPAIDWDTSLAPYLGQT 195

RESULT 31
US-09-030-607-113
Sequence 113, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Xu, JIANGCHUN
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-607-113

Query Match 34.5%; Score 50; DB 4; Length 553;
Best Local Similarity 45.0%; Pred. No. 4.9;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 YSLPELDYEFSEATPYISQ 21
Db 176 YLPAIDWDTSLAPYLGQT 195

RESULT 32
US-09-605-785-113
Sequence 113, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, JIANGCHUN
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 113
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapien
US-09-605-785-113

Query Match 34.5%; Score 50; DB 4; Length 553;
Best Local Similarity 45.0%; Pred. No. 4.9;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 YSLPELDYEFSEATPYISQ 21
Db 176 YLPAIDWDTSLAPYLGQT 195

RESULT 33
US-09-439-313-113
Sequence 113, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, JIANGCHUN
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9

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; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-439-313-113

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Query Match          34.5%; Score 50; DB 4; Length 553;
Best Local Similarity 45.0%; Pred. No. 4.9;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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```

Qy      2 YSLPELDYEFSEATEPYISQ 21
      176 YLLPAIDWDTSLAPYLGTO 195

```

```

RESULT 34
-09-352-616A-113
Sequence 113, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-352-616A-113

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Query Match          34.5%; Score 50; DB 4; Length 553;
Best Local Similarity 45.0%; Pred. No. 4.9;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

```

```

Qy      2 YSLPELDYEFSEATEPYISQ 21
      176 YLLPAIDWDTSLAPYLGTO 195

```

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RESULT 35
US-09-602-877A-101
Sequence 101, Application US/09602877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602,877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-602-877A-101

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```

Query Match          34.5%; Score 50; DB 4; Length 553;

```

```

Best Local Similarity 45.0%; Pred. No. 4.9;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

```

```

Qy      2 YSLPELDYEFSEATEPYISQ 21
      176 YLLPAIDWDTSLAPYLGTO 195

```

```

RESULT 36
US-09-232-149A-113
Sequence 113, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-232-149A-113

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Query Match          34.5%; Score 50; DB 4; Length 553;
Best Local Similarity 45.0%; Pred. No. 4.9;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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Qy      2 YSLPELDYEFSEATEPYISQ 21
      176 YLLPAIDWDTSLAPYLGTO 195

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RESULT 37
US-09-028-934-31
Sequence 31, Application US/09028934
; Patent No. 6117670
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Lam, Steven T.
; APPLICANT: Hammer, Philip B.
; APPLICANT: van Pee, Karl-Heinz
; APPLICANT: Kirner, Sabine
; APPLICANT: Young, Thomas R.
; TITLE OF INVENTION: Pyrolytic Biosynthesis Genes and Uses
; FILE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 611767artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/028,934
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/729,214
; FILING DATE: 09-Oct-1996
; PRIOR APPLICATION DATA:

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; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,229
; FILING DATE: 26-SEP-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schief, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 29938-20002.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 885 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-720-229-23

Query Match      33.1%; Score 48; DB 3; Length 885;
Best Local Similarity 34.8%; Pred. No. 19;
Matches 8; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSEKTEPYISQINE 24
Db 582 YSRPLVSFRYEDGPLVEGQLGE 604

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Search completed: April 9, 2003, 14:01:34
 Job time : 7.09174 secs